

28488

Access DB# _____

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: S. Devi Examiner #: S. Devi Date: 08 May 00
Art Unit: 1641 Phone Number 308-9347 Serial Number: 09/240,675
Mail Box and Bldg/Room Location: CM1-7E15 Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Monoclonal antibodies against the Interferon Receptor
Inventors (please provide full names): Patrick Benoit et al.

Earliest Priority Filing Date: 03.31.92

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please ask Ms. Beverly Shears to perform this search.

Please perform a Sequence & an Interference search on the SEQ ID NO: 1 and 2 and portions or analogues thereof.
Claims are enclosed.

Thanks.

Point of Contact:
Beverly Shears
Technical Info. Specialist
CM1 12C14 Tel: 308-4994

SLIS
signature

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Type of Search

Vendors and cost where applicable

Searcher: Beverly 24995 STN: _____
Searcher Phone #: _____ AA Sequence (#) _____ Dialog _____
Searcher Location: _____ Structure (#) _____ Questel/Orbit _____
Date Searcher Picked Up: _____ Bibliographic _____ Dr. Link _____
Date Completed: 06-05-00 Litigation _____ Lexis/Nexis _____
Searcher Prep & Review Time: 12 Fulltext _____ Sequence Systems _____
Clerical Prep Time: _____ Patent Family _____ WWW/Internet _____
Online Time: 20 Other _____ Other (specify) CGN

201 AACTGGATGATTAATGGATAAATTGCTGGGTGCAGATAATACTA 250
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67 sthrglymetaspasnrtrpleylsleuserglycysglinsnlethrs 84
251 GTACCAATGCACTTTTCTCAGTCAGAGCTGATGTTATGAGAAAT 300
|||||
84 erthrlyscysasnpheserleuylsleuasnvaltrygluile 100
301 AATTCGCTATAGAGCAGAAAAAAGAAACCTCTTCATGATGAGCT 350
|||||
101 lysleuarrgilleargalaglulysglinsnrthrsersertrpyrgluva 117
351 TGACTCATTTACACATTTTCGCAAGCTCAGATTGCTCTCCAGAGTA 399
|||||
117 laspserphethrprophearglysalaglinleclgyproprogluval 133
seq_name: A_Geneseq_36:R14487

seq_documentation_block:
ID R14487 standard; Protein: 436 AA.
AC R14487;
DT 16-JAN-1992 (first entry)
DE Soluble interferon-alpha/beta receptor.
KW IFN: autoimmune disease; graft rejection; histocompatibility.
OS Homo sapiens.
PN FR2657881-A.
PD 09-AUG-1991.
PF 05-FEB-1990; FR-001298.
PR (EUBI-) LAB EURO BIOTECHNO.
PI EID P. Gresser I, Lutfalla G, Meyer F, Mogensen KE;
PI Tovey M, Uze G;
DR WPI: 91-31978/44.
DR N-PSDB: Q14239.
PT New water-soluble polypeptide(s) with affinity for IFN-alpha and
PT beta - used to treat e.g. lupus erythematosus, Behcet's disease,
PT aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.
PS Claim 2: Page 45; 52pp. French.
CC The transmembrane and cytoplasmic domains of the native IFN receptor
CC have been deleted to obtain a soluble, circulating form of the
CC receptor. Potentially immunogenic epitopes have thus been eliminated.
CC Derivatives obtained by substitution or deletion of this sequence
CC are also claimed as are hybrid molecules comprising the soluble
CC receptor (or deriv.) and an immunoglobulin such as IgG1.
CC See also Q14240.
SQ Sequence 436 AA;

alignment_scores:
Quality: 692.00 Length: 133
Ratio: 5.203 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-240-675-1_COPY_27_427 x R14487

Align seg 1/1 to: R14487 from: 1 to: 436

1 ATGATGCTGCTCCTCGTGGCGGAGACCCCTAGTGTCTGCGCCGTGG 50
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1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
51 CCCATGGGTGTGTCGCGACCGCAGGTGGAATAATCTTCTCTC 100
|||||
17 yprotirpValleuserAlaAlaGlyGlyAsnLeuLysSerProG 34
101 AAAAGTAGAGTCGACATGATGACAACTTATCTGAGGTGAAC 150
|||||
34 IntlysValGluValAspIlelleaspaspasnphelleuarrtrpash 50
151 AGGAGCATGAGTGTCTGCGGAATGTGACTTTTTCATTGATTCAAAA 200
|||||
51 ArggersaspgluserValGlyAsnValThrPheserPheserpyrglnly 67

201 AACTGGATGATTAATGGATAAATTGCTGGGTGCAGATAATACTA 250
|||||
67 sthrglymetaspasnrtrpleylsleuserglycysglinsnlethrs 84
251 GTACCAATGCACTTTTCTCAGTCAGAGCTGATGTTATGAGAAAT 300
|||||
84 erthrlyscysasnpheserleuylsleuasnvaltrygluile 100
301 AATTCGCTATAGAGCAGAAAAAAGAAACCTCTTCATGATGAGCT 350
|||||
101 lysleuarrgilleargalaglulysglinsnrthrsersertrpyrgluva 117
351 TGACTCATTTACACATTTTCGCAAGCTCAGATTGCTCTCCAGAGTA 399
|||||
117 laspserphethrprophearglysalaglinleclgyproprogluval 133
seq_name: A_Geneseq_36:R28495

seq_documentation_block:
ID R28495 standard; Protein: 436 AA.
AC R28495;
DT 31-MAR-1993 (first entry)
DE Sequence of a soluble form of the Interferon (IFN) receptor
DE with a high affinity for IFN-alpha and -beta.
KW Interferon receptor; alpha-interferon; beta-interferon.
OS Synthetic.
PN WO9218626-A.
PD 29-OCT-1992.
PF 17-APR-1991; F00318.
PR (EUBI-) LAB EURO BIOTECHNOLOGIE.
PI EID P. Gresser I, Lutfalla G, Meyer F, Mogensen KE;
PI Tovey M, Uze G;
DR WPI: 92-382110/46.
DR N-PSDB: Q30532.
PT Water soluble polypeptide(s) strongly bind interferon(s) alpha
PT and beta - useful as immunosuppressants, for treating auto-immune
PT diseases and transplant rejection
PS Claim 2: Fig 1: 58pp. English.
CC DNA encoding the water-soluble polypeptide with a high affinity for
CC IFN-alpha and -beta is isolated by PCR, using appropriate
CC oligonucleotides as primers and cloned cDNA as template. For example,
CC bacteriophage lambda ZAP, containing the entire coding sequence of
CC the IFN-alpha and -beta receptor (Q30533), was incubated with oligos
CC Q30534 and Q30535. R28496 represents the complete receptor. R28495
CC lacks the transmembrane and cytoplasmic domains. Both forms bind
CC IFN in the same way as antibodies and so are immunosuppressants e.g. for
CC treating autoimmune diseases and graft rejection. They lack the
CC toxic side-effects of known immunosuppressants such as steroids.
SQ Sequence 436 AA;

alignment_scores:
Quality: 692.00 Length: 133
Ratio: 5.203 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-240-675-1_COPY_27_427 x R28495

Align seg 1/1 to: R28495 from: 1 to: 436

1 ATGATGCTGCTCCTCGTGGCGGAGACCCCTAGTGTCTGCGCCGTGG 50
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
51 CCCATGGGTGTGTCGCGACCGCAGGTGGAATAATCTTCTCTC 100
|||||
17 yprotirpValleuserAlaAlaGlyGlyAsnLeuLysSerProG 34
101 AAAAGTAGAGTCGACATGATGACAACTTATCTGAGGTGAAC 150
|||||

seq_name: A_Geneseq_36:R11958

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1 ATGATGGTCGTCCTCTGGGCGCAGCACTACTGCTGCGCCGTGGG 50
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
51 CCCATGGGTGTTCGCCGACCGCAGGTGAAAAATCTAAATCTCTCTC 100
17 yProTrrValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
101 AAAAGTAGAGTCGACATCATAGATGACAACTTATCTTGAAGTGAC 150
34 InLysValGluValAspIleIleAspAspAsnPhelLeuAlaGtrPasn 50
151 AGAGCGATGAGTCGTGGGAAATGTGCTTTCATTCGATATCAAAA 200
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnL 67
201 AACTGGATGATTAATGGATAAATGTGCTGCTCAGATATTAATA 250
67 sThrGlyMetAspAsnTrrPileLysLeuSerGlyCysGlnAsnIleHrs 84
251 GTACCAATGCAACTTTCTTCACTCACTGAGTGAATGTTATGAAGA 300
84 eTrrHrLysCysAsnPheserSerLeuLysLeuAsnValTyrGluIle 100
301 AATTCGATTAAGACAGCAAAAAAACAACCTTCTTCATGGTATGAG 350
101 LysLeuArgIleArgAlaGluLysGluAsnThrSerTrrPyrGluVal 117
351 TGACATATTACACATTTGCGAAAGCTGAGTTGGTCTCCAGAGTA 399
117 LAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluVal 133

```

seq_documentation_block:

ID R11958 standard; Protein: 557 AA.

AC R11958;

DT 18-JUL-1991 (first entry)

DE Human alpha-interferon receptor protein.

KW Human alpha IFN; IFN agonists; antiviral; anti tumour agent;

OS Homo sapiens.

FT Key Location/Qualifiers

FT peptide 1..27

FT /label= signal peptide

PN W09105862-A.

PD 02-MAY-1991.

PR 13-OCT-1990; F00758.

PR 20-OCT-1989; FR-013770.

PA (CNRS) CNRS CENT NAT RECH SCI.

PI Mogensen KE, Uze G, Lutfalla G, Gresser I;

DR N-PSDB: Q11701.

DR N-PSDB: Q11701.

PT New human alpha-interferon receptor protein - useful for testing.

PT Interferon agonists and in treatment or diagnosis

PS Disclosure: fig 4; 30pp; French.

CC This recombinant human alpha interferon (IFN) receptor protein is

CC useful for the testing of IFN agonists and for treatment and diag-

CC nosis of viral diseases and tumours. Antibodies raised against

CC this protein can be used for blocking the receptor when required,

CC eg where overexpression of alpha-IFN is harmful. The Abs are

CC also useful for eg drug targeting. Variants of the protein,

CC having residue 164 (Thr) replaced by Arg and an Asp inserted

CC between residues 479 and 480, are also useful.

CC Sequence 557 AA:

alignment_scores: 692.00 Length: 133

Ratio: 5.203 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignement_block:

us-09-240-675-1_copy_27_427 x R11958

Align seg 1/1 to: R11958 from: 1 to: 557

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1 ATGATGGTCGTCCTCTGGGCGCAGCACTACTGCTGCGCCGTGGG 50
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
51 CCCATGGGTGTTCGCCGACCGCAGGTGAAAAATCTAAATCTCTCTC 100
17 yProTrrValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
101 AAAAGTAGAGTCGACATCATAGATGACAACTTATCTTGAAGTGAC 150
34 InLysValGluValAspIleIleAspAspAsnPhelLeuAlaGtrPasn 50
151 AGAGCGATGAGTCGTGGGAAATGTGCTTTCATTCGATATCAAAA 200
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnL 67
201 AACTGGATGATTAATGGATAAATGTGCTGCTCAGATATTAATA 250
67 sThrGlyMetAspAsnTrrPileLysLeuSerGlyCysGlnAsnIleHrs 84
251 GTACCAATGCAACTTTCTTCACTCACTGAGTGAATGTTATGAAGA 300
84 eTrrHrLysCysAsnPheserSerLeuLysLeuAsnValTyrGluIle 100
301 AATTCGATTAAGACAGCAAAAAAACAACCTTCTTCATGGTATGAG 350
101 LysLeuArgIleArgAlaGluLysGluAsnThrSerTrrPyrGluVal 117
351 TGACATATTACACATTTGCGAAAGCTGAGTTGGTCTCCAGAGTA 399
117 LAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluVal 133

```

seq_name: A_Geneseq_36:R14488

seq_documentation_block:

ID R14488 standard; Protein: 557 AA.

AC R14488;

DT 16-JAN-1992 (first entry)

DE Complete interferon-alpha/beta receptor.

KW IFN; autoimmune disease; graft rejection; histocompatibility.

OS Homo sapiens.

FT Key Location/Qualifiers

FT domain 437..457

FT /label= transmembrane

FT domain 458..557

FT /label= cytoplasmic

PN FR2657881-A.

PD 09-AUG-1991.

PR 05-FEB-1990; Q01298.

PR 05-FEB-1990; FR-001298.

PA (EUBI-) LAB EURO BIOTECHNO.

PI Tovey MG, Uze G;

DR N-PSDB: Q14240.

DR N-PSDB: Q14240.

PT New water-soluble polypeptide(s) with affinity for IFN-alpha and

PT beta - used to treat e.g. lupus erythematosus, Behcet's disease,

PT aplastic anemia, diabetes mellitus, rheumatoid arthritis, etc.

PS Disclosure: Page 47; 52pp; French.

CC The invention covers derivatives of the interferon-alpha and/or beta

CC receptor obtained by deleting the transmembrane and cytoplasmic domains

CC of the native receptor or by substitution. Potentially immunogenic

CC epitopes are eliminated and the deriv. can be secreted from

CC transformed cells. Soluble deriv.s block the activity of IFN alpha/beta

CC and can be used to treat autoimmune diseases or to inhibit graft

CC rejection. See also Q14239.

CC Sequence 557 AA:

alignment_scores:

Quality: 692.00 Length: 133
Ratio: 5.203 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_427 x R14488 ..

Align seg 1/1 to: R14488 from: 1 to: 557

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1 ATGATGTCGTCCTCTGGGGCGAGACCTAGTCGTCGCCGTGGG 50
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
51 CCCATGGGTGTGTCCGACGCCGAGGTGGAATAAATCTAAATCTCCTC 100
|||||
17 YProTPrValLeuSerAlaAlaLeuGlyGlyLysAsnLeuLysSerProG 34
101 AAAAAGTAGAGGTGCACATCATAGATGACAACCTTATCTCGAGTGGAC 150
|||||
34 InLysValGluValAlaSpIleIleAspAspAsnPhelIleLeuArgTrpAsn 50
151 AGGAGCGATGAGTCGTGGGGAATGTGACTTTTCATTCGATTATCAAAA 200
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTrpGlnLys 67
201 AACTGGGATGATTAATTGATAAATTTGCTGGGTGCAGATATTACTTA 250
|||||
67 sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS 84
251 GTACCAATGCACACTTTTCTTCACTCAAGCTGAATGTTATGAGAAATT 300
|||||
84 eThrIlyscysAsnPheserSerLeuLysLeuAsnValTrpGluGluIle 100
301 AAATTGCGTATAGAGCAGAAAAAGAAACACTTCTTCATGATGATGAGCT 350
|||||
101 LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTrpGluVal 117
351 TGACTCATTTACACCATTTCCGCAAGCTCAGATTGGTCTCCAGAACTA 399
|||||
117 LAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluVal 133

```

seq_name: A_Geneseq_36:R28496

seq_documentation_block:

ID R28496 standard; Protein: 557 AA.
AC R28496:
DT 31-MAR-1993 (first entry)
DE Sequence of a soluble form of the interferon (IFN) receptor with a high affinity for IFN-alpha and -beta.
KW Interferon receptor; alpha-interferon; beta-interferon.
OS Synthetic.
PN MO9218626-A.
PD 29-OCT-1992.
PF 17-APR-1991; F00318.
PR 17-APR-1991; WO-F00318.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
PI Eld P, Gresser I, Luftalla G, Meyer F, Mogensen KE, Tovey M, Uze G.
PI MPI: 92-382110/46.
DR N-PDB: Q30533.
DR Water soluble polypeptide(s) strongly bind interferon(s) alpha and beta - useful as immunosuppressants, for treating auto-immune diseases and transplant rejection
PS Claim 3: Fig 2: 58pp. English.
CC DNA encoding the water-soluble polypeptide with a high affinity for IFN-alpha and -beta is isolated by PCR, using appropriate oligonucleotides as primers and cloned cDNA as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and -beta receptor (Q30533), was incubated with oligos Q30534 and Q30535. R28496 represents the complete receptor. R28495 lacks the transmembrane and cytoplasmic domains. Both forms bind

CC IFN in the same way as antibodies so are immunosuppressants e.g. for
CC treating autoimmune diseases and graft rejection. They lack the
CC toxic side-effects of known immunosuppressants such as steroids.
SQ Sequence 557 AA:

alignment_scores:

Quality: 692.00 Length: 133
Ratio: 5.203 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_427 x R28496 ..

Align seg 1/1 to: R28496 from: 1 to: 557

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1 ATGATGTCGTCCTCTGGGGCGAGACCTAGTCGTCGCCGTGGG 50
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1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
51 CCCATGGGTGTGTCCGACGCCGAGGTGGAATAAATCTAAATCTCCTC 100
|||||
17 YProTPrValLeuSerAlaAlaLeuGlyGlyLysAsnLeuLysSerProG 34
101 AAAAAGTAGAGGTGCACATCATAGATGACAACCTTATCTCGAGTGGAC 150
|||||
34 InLysValGluValAlaSpIleIleAspAspAsnPhelIleLeuArgTrpAsn 50
151 AGGAGCGATGAGTCGTGGGGAATGTGACTTTTCATTCGATTATCAAAA 200
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTrpGlnLys 67
201 AACTGGGATGATTAATTGATAAATTTGCTGGGTGCAGATATTACTTA 250
|||||
67 sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS 84
251 GTACCAATGCACACTTTTCTTCACTCAAGCTGAATGTTATGAGAAATT 300
|||||
84 eThrIlyscysAsnPheserSerLeuLysLeuAsnValTrpGluGluIle 100
301 AAATTGCGTATAGAGCAGAAAAAGAAACACTTCTTCATGATGATGAGCT 350
|||||
101 LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTrpGluVal 117
351 TGACTCATTTACACCATTTCCGCAAGCTCAGATTGGTCTCCAGAACTA 399
|||||
117 LAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluVal 133

```

seq_name: A_Geneseq_36:R42635

seq_documentation_block:

ID R42635 standard; Protein: 557 AA.
AC R42635:
DT 20-APR-1994 (first entry)
DE Human interferon receptor.
KW IFN-R; extracellular domain; monoclonal antibody; viral infection; cell proliferation; allograft rejection; systemic lupus erythematosus; psoriasis; multiple sclerosis; Behcet's Disease; aplastic anaemia; immunodeficiency; measles virus; interferon-alpha-beta.
KW Homo sapiens.
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 1..436
FT /label= extracellular domain
FT /note= "soluble, immunogenic form of IFN-R"
PN EP-563487-A.
PD 06-OCT-1993.
PF 31-MAR-1992; 400902.
PR 31-MAR-1992; EP-400902.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
PI Benoit P, Maguire D, Meyer F, Plavec I, Tovey MG.
PI MPI: 93-312951/40.
DR P-PDB: R42635.
DR Monoclonal antibody to human interferon type-I receptor - having

PT neutralising activity against human type I interferon, used for
PT therapy and diagnosis
PS Disclosure; Fig 3; 21pp; English.
CC Monoclonal antibodies produced against soluble forms of the human
CC interference alpha-beta receptor based on the full-length human IFN-R
CC sequence are claimed. The antibodies are useful for treatment and
CC prophylaxis of disorders involving cell proliferation and/or viral
CC infection.
SQ Sequence 557 AA;

alignment_scores:
Quality: 692.00 Length: 133
Ratio: 5.203 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_427 x R42635 ..

Align seg 1/1 to: R42635 from: 1 to: 557

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1 ATGATGTCGTCCTCTCGGCGGAGACCCCTAGTGTCTGCGCGGTGGG 50
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
51 CCCATGGGTGTGTCGCCGAGCCGAGTGGAAAAAATCTAAATCTCTC 100
|||||
17 yPrrtPrpAlLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
101 AAAAAGTAGAGTCGATCATAGATGACAACTTATCTCTGAGGTGGAAC 150
|||||
34 InLysValGluValAspIleIleAspAspAsnPhelIleuArgTrpAsn 50
151 AGGAGCGATGAGTCTGCGGAAATGTGACTTTTCATTCGATTATCAAA 200
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGluLy 67
201 AACGCGGATGATTAATGGATAAATTTGCTGGGTGTGAGATATTACTA 250
|||||
67 sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleHis 84
251 GTACCAATGCAACTTTCTTCACTCAAGCTGAATGTTATGAAGAAAT 300
|||||
84 eThrLysCysAsnPheserSerLeuLysLeuAsnValTyrGluGluIle 100
301 AAATTCGCTATAAGACGAGAAAAAAGAAACCTTCTTCATGTGATGAGT 350
|||||
101 LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrGluVa 117
351 TGACATATTACACCTTTCGCAAGCTCAGATGTGCTCCAGAAAGTA 399
|||||
117 lAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluVal 133
```

seq_name: A_Geneseq_36:R75356

seq_documentation_block:

ID R75356 standard; Protein: 557 AA.
AC R75356;
DT 16-OCT-1995 (first entry)
DE Human IFN receptor.
KW IFN receptor; interferon receptor; interferon-alpha;
KW interferon-beta; monoclonal antibody; immunomodulator; AIDS.
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 1..436
FT /label= Extracellular_domain
PD W0507716-A.
PD 23-MAR-1995.
PF 16-SEP-1994; E03114.
PF 17-SEP-1993; EP-402279.
PR (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
PI Benizri EJ, Tovey MG;
DR WPI, 95-131187/17.

DR N-PSDB: 086458.
PT Compsn. of monoclonal antibodies against interferon receptor
PT useful as immuno-modulator, eg. for treating AIDS
PS Disclosure; Fig 3A-2B; 105pp; English.
CC The amino acid sequence of human interferon class I receptor is
CC given in R75356. A recombinant soluble form of the extracellular
CC domain of this receptor (R71723) has been used to raise
CC immunomodulatory monoclonal antibodies.
SQ Sequence 557 AA;

alignment_scores:
Quality: 692.00 Length: 133
Ratio: 5.203 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_427 x R75356 ..

Align seg 1/1 to: R75356 from: 1 to: 557

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1 ATGATGTCGTCCTCTCGGCGGAGACCCCTAGTGTCTGCGCGGTGGG 50
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
51 CCCATGGGTGTGTCGCCGAGCCGAGTGGAAAAAATCTAAATCTCTC 100
|||||
17 yPrrtPrpAlLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
101 AAAAAGTAGAGTCGATCATAGATGACAACTTATCTCTGAGGTGGAAC 150
|||||
34 InLysValGluValAspIleIleAspAspAsnPhelIleuArgTrpAsn 50
151 AGGAGCGATGAGTCTGCGGAAATGTGACTTTTCATTCGATTATCAAA 200
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGluLy 67
201 AACGCGGATGATTAATGGATAAATTTGCTGGGTGTGAGATATTACTA 250
|||||
67 sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleHis 84
251 GTACCAATGCAACTTTCTTCACTCAAGCTGAATGTTATGAAGAAAT 300
|||||
84 eThrLysCysAsnPheserSerLeuLysLeuAsnValTyrGluGluIle 100
301 AAATTCGCTATAAGACGAGAAAAAAGAAACCTTCTTCATGTGATGAGT 350
|||||
101 LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrGluVa 117
351 TGACATATTACACCTTTCGCAAGCTCAGATGTGCTCCAGAAAGTA 399
|||||
117 lAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluVal 133
```

seq_name: A_Geneseq_36:W21804

seq_documentation_block:

ID W21804 standard; Protein: 557 AA.
AC W21804;
DT 23-SEP-1997 (first entry)
DE Transmembranal interferon alpha-receptor.
KW Interferon alpha-receptor; IFNAR.
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 1..436
FT /label= Extracellular_domain
FT domain 437..457
FT /label= Transmembrane_domain
FT domain 458..557
FT /label= Intracellular_domain
PD A09475977-A.
PD 11-MAR-1995.
PF 20-OCT-1994; 075977.
PF 24-OCT-1993; IL-107378.

PA (YEDA) YEDA RES & DEV CO LTD.
 PA (ABRA/) ABRAVOVICH C.
 PI Abramovich C, Ratovitski E, Revel M;
 DR WPI: 95-200634/27.
 PT New mammalian soluble interferon alpha-receptor forms - used for
 PT inhibiting, modulating or modifying the activities of interferon(s)
 PS Disclosure: Fig 7: 46pp; English.
 CC Human transmembrane Interferon alpha receptor (IFNAR) (W21804)
 CC includes a 21-amino acid transmembrane region. Novel, splice-
 CC deleted IFNAR forms 1 (W21805) and 2 (W21806) have been detected
 CC that lack this transmembrane domain. These, soluble non-membrane
 CC bound polypeptides can be expressed in host cells and used to
 CC inhibit, modulate or modify the activities of interferons alpha
 CC and beta in cells, tissues and organisms, or for diagnostic
 CC purposes.
 SQ Sequence 557 AA;

alignment_scores:
 Quality: 692.00 Length: 133
 Ratio: 5.203 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_427 x W21804 ..

Align seg 1/1 to: W21804 from: 1 to: 557

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1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
51 CCCATGGGTGTGTCGCGAGCCGCGAGGTGGAATAATCTAAATCTCCTC 100
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17 ProTyrValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
101 AAAAAGTAGAGGTGAGCATCATGATGACAACTTATCTGAGGTGAGAC 150
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101 LysLeuArgIleArgAlaGlnLysGlnAsnThrSerTyrTyrGlnVal 117
351 TGACTCATTTACACCATTTCCAAAGCTCAGATTGCTCTCCAGAGA 399
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seq_name: A_Geneseq_36:W79159

seq_documentation_block:

ID W79159 standard; Protein: 553 AA.

AC W79159;

DE 20-NOV-1998 (first entry)

KW zcytor7 cytokine receptor polypeptide.

KW type 2 cytokine receptor; ligand-binding polypeptide; kidney; pancreas;

KW agonist; cell proliferation family; CRF2; prostate tissue; nervous tissue;

KM neural disease; pancreatic disease.

OS Homo sapiens.

PH key Location/Qualifiers

FT Domain 30..250
 FT /note= "extracellular (ligand-binding) domain;
 FT sequence claimed in claim 1."
 FT Domain 275..553
 FT /note= "intracellular domain"

PN WO9837193-A1.
 PD 27-AUG-1998.
 PF 18-FEB-1998; 003029.
 PR 02-OCT-1997; US-943087.
 PR 20-FEB-1997; US-803305.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RU, Farran TM, Jelmberg AC, Kho CJ, Lok S,
 PI Whitmore TE;
 DR WPI: 98-480798/41.
 DR N-PSDB: V57515.
 PT Novel human zcytor7 DNA encodes a type 2 cytokine receptor - useful
 PT for treating renal, neural, pancreatic and prostatic diseases
 PS Claim 1, Pages 55-59; 72pp; English.
 CC This represents the zcytor7 cytokine receptor. Zcytor7 is a ligand-
 CC binding receptor polypeptide and is a novel member of the type 2 cytokine
 CC receptor family (CRF2). An expression vector containing the zcytor
 CC polynucleotide, operably linked to transcription promoter, a sequence
 CC encoding a transmembrane and intracellular domain, or both, and a
 CC transcriptional terminator can be used to transform host cells for the
 CC recombinant production of the polypeptide. The sequences can be used to
 CC study the zcytor7 gene and to isolate ligands binding to it. Zcytor7 is
 CC preferentially expressed in the kidney, pancreas, prostate or nervous
 CC tissue. Agonists of zcytor7 can be used to stimulate proliferation and
 CC differentiation of cell in these organs. The antagonists and agonists can
 CC also be used in the treatment of renal, neural, pancreatic and prostate
 CC diseases.
 SQ Sequence 553 AA;

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 Quality: 146.00 Length: 127
 Ratio: 1.848 Gaps: 4
 Percent Similarity: 62.205 Percent Identity: 29.921

alignment_block:

US-09-240-675-1_COPY_27_427 x W79159 ..

Align seg 1/1 to: W79159 from: 1 to: 553

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49 snMetLysAsnValLeuGlnThrProProGlnGlyLeuGlnGlyVal 65
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319 GAAAAAAGAACTTCTCATGATGATGATGATGATGATGATGATGAT 368
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116 TrpLysThrLysCysSerLysTyrPalaGlnSerGlyArgPheThrPro 132
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251 GTACCAAAATGCAACTTTTCTCAGCTCAGCTGATGTATGAGAAAT 300
84 eThrlyscysAsnPheserSerleuLysLeuAsnValIlyrGlnGluIle 100
301 AAATGCGTATAAGACAGCAAAAAAAGAAACACTTCTTCATGTAGAGT 350
101 LysLeuArGileArGlaGluLysGlnAsnThrSerSerTrpTyrGlnVal 117
351 TGACGTATTACACCATTTCCGAAAGCTGAGATGGTCTCCGAGAGTA 399
117 LaspSerPheThrProPheArGlySalGlnIleGlyProProGluVal 133
seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-307-588-2
seq_documentation_block:
Sequence 2, Application US/08307588
Patent No. 5919453
GENERAL INFORMATION:
APPLICANT: BENOIT, Patrick
APPLICANT: MEYER, Francois
APPLICANT: MAGUIRE, Deborah
APPLICANT: PLAVEC, Ivan
APPLICANT: TOVEY, Michael G.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00770
FILING DATE: 30-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92400902.0
FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 17283/117/GUPL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-307-588-2

alignment_scores:
Quality: 692.00 Length: 133
Ratio: 5.203 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
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17 yProTrpAlleuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerPro 34
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101 LysLeuArGileArGlaGluLysGlnAsnThrSerSerTrpTyrGlnVal 117
351 TGACGTATTACACCATTTCCGAAAGCTGAGATGGTCTCCGAGAGTA 399
117 LaspSerPheThrProPheArGlySalGlnIleGlyProProGluVal 133
seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-328-256-12
seq_documentation_block:
Sequence 12, Application US/08328256
Patent No. 5643749
GENERAL INFORMATION:
APPLICANT: REVEL, Michel
APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVIJSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
ZIP: 20004
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.
 REGISTRATION NUMBER: REVEL-13
 REFERENCE/DOCKET NUMBER: 25,618
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 496 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-328-256-12

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 Quality: 692.00 Length: 133
 Ratio: 5.203 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

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seq_name: /cgn2_6/ptodata/1/laa/5A_COMB.pep:US-08-328-256-10

seq_documentation_block:

; Sequence 10, Application US/08328256
 ; Patent No. 5643749

; GENERAL INFORMATION:

; APPLICANT: REVEL, Michel

; APPLICANT: ARAHOVITCH, Carolina

; APPLICANT: RATOVTSKI, Edward

; TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NETMARK

STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/328,256
 FILING DATE: 24-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: IL 107378
 FILING DATE: 24-OCT-1993

ATTORNEY/AGENT INFORMATION:
 NAME: BROWDY, Roger L.
 REGISTRATION NUMBER: REVEL-13
 REFERENCE/DOCKET NUMBER: 25,618
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 TELEX: 248633

INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 557 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-328-256-10

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 Quality: 692.00 Length: 133
 Ratio: 5.203 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

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; STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-466-974-2

alignment_scores:
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Ratio: 5.203 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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seq_documentation_block:
Sequence 2, Application US/08471453
Patent No. 5886153

GENERAL INFORMATION:
APPLICANT: NOGENSEN, Knud E.
APPLICANT: UZE, Gilles
APPLICANT: LUTFALLA, Georges
APPLICANT: GRESSER, Ion
TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
NUMBER OF SEQUENCES: 2
PREPARATION OF THE CORRESPONDING PROTEIN
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHUYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,453
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-453-2

alignment_scores:
Quality: 692.00 Length: 133
Ratio: 5.203 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
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Align seg 1/1 to: US-08-471-453-2 from: 1 to: 557

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101 LysLeuArgIleArgAlaGluLysGlnAsnThrSerSerTrpTyrGluVal 117
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seq_documentation_block:
Sequence 4, Application US/08307588

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Patent No. 5919453
GENERAL INFORMATION:
APPLICANT: BENOIT, Patrick
APPLICANT: MEYER, Francois
APPLICANT: MACUIRE, Deborah
APPLICANT: PLAVEC, Ivan
APPLICANT: TOVEY, Michael G.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INT
TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY
TITLE OF INVENTION: INTERFERON
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00770
FILING DATE: 30-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92400902.0
FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: SAYE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 17283/117/GUPL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-307-588-4

Alignment_scores:
Quality: 692.00 Length: 133
Ratio: 5.203 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

Alignment_block:
US-09-240-675-1_COPY_27_427 x US-08-307-588-4 ..
Align seg 1/1 to: US-08-307-588-4 from: 1 to: 557

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seq_documentation_block:
GENERAL INFORMATION:
  APPLICATION: PC/TUS9414277
  APPLICANT: Agnet, Michel
  APPLICANT: Bonini, Ruth
  APPLICANT: Hemmi, Silvio
  TITLE OF INVENTION: Receptor Subunit Polypeptides
  NUMBER OF SEQUENCES: 8
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Genentech, Inc.
    STREET: 460 Point San Bruno Blvd
    CITY: South San Francisco
    STATE: California
    COUNTRY: USA
    ZIP: 94080
  COMPUTER READABLE FORM:
    MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: patin (Genentech)
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: PCT-US94/14277
    FILING DATE: 07-DEC-1994
  CLASSIFICATION:
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: 08/164596
      FILING DATE: 09-DEC-1993
    ATTORNEY/AGENT INFORMATION:
      NAME: Love, Richard B.
      REGISTRATION NUMBER: 34,659
      REFERENCE/DOCKET NUMBER: 866PCT
      TELECOMMUNICATION INFORMATION:
        TELEPHONE: 415/225-5530
        TELEFAX: 415/952-9881
      TELEX: 910/371-7168
  INFORMATION FOR SEQ ID NO: 3:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 202 amino acids
      TYPE: amino acid
      TOPOLOGY: linear

PCT-US94-14277-3

alignment_scores:
  Quality: 273.50      Length: 107
  Ratio: 3.552         Gaps: 1
  Percent Similarity: 71.963      Percent Identity: 48.598

alignment_block:
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1 GluAsnLeuysProProGluAsnIleAsp***TyrIleIleAspSps 17
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17 nTyrIleLeuysIlePserSerHisGlyUserMetGlySerValThr 34
182 TTTCATTCGATTATCAAAAACTGGGATGATTAATGGATAAATGTCT 231
34 heserIleGlyTyrArgThrLysAspGluArgLysIlePLeuys**Pro 50
232 GGGTCGACAGATATTAAGTACCAATGCACTTTCTTCATCAACGT 281
51 GlucySGlnHisThrThrThrLysCysGlnPheSerLeuAspThr 67
282 GAATGTTATGAAGAATTAATGCGCTATAGACAGAAAAAGAAAC. 330
67 rAsn**TyrIleLysThrGlnPheArgValArgIleGluGlyAsn 84
331 .ACTTCTCATGGTATGAGGTGACTCATTTACACCATTTCCAAAGCT 378
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101 HisMetSerProProGluVal 107
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seq_documentation_block:
; Sequence 2, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Fairah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
; US-08-943-087-2
alignment_scores:
    Quality: 146.00    Length: 127
    Ratio: 1.848      Gaps: 4
    Percent Similarity: 62.205    Percent Identity: 29.921
alignment_block:
US-09-240-675-1_COPY_27_427 x US-08-943-087-2 ..
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75 AGGTGAAAAAATCTAAATCTCTCAAAAGTAGAGTGCATCATAG 124
34 rGlyGly.....LeuProLysProAlaAsnIleThrPheLysSerIleA 49
125 ATGACACACTTATCTGAGGTGGAACAGACGATGACTGTCCGG... 171
49 smetLysAsnValLeuGlnTrpThrProProGluGlyLeuGlnGlyVal 65
172 AATGTCATTTTCATTCATTCATCAAAAAAGTGGATGATTAATGAT 221
66 LysValThrTyrThrValGlnTyrPheIleTyrGlyGlnLysIleStrple 82
222 AAATGTCGTGGGTGACAGATATTAAGTACCAAAATGCACTTTCTT 271
82 uAsnLysSerGlyCysArgAsnIleAsnArgThrTyrCysAspLysSerA 99
272 CACTCAAGCTGAATGTTTATGAAGAAATTAATGGCTTAAGAGA... 318
99 IadIuThrSerAspTyrGluHisGlnTyrTyrAlaLysValLysAlaIle 115
319 GAAAAAGAAACACTCTTCATGATGATGATGATGATGATGATGAT 368
116 TrpGlyThrLysCysSerLysTrpAlaGluSerGlyArgPheTyrProPh 132
369 TCCGAAAGCTCAGATTGTCCTCCAGAGTA 399
132 eleuGluThrGlnIleGlyProProGluVal 142
seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-943-087-14
seq_documentation_block:
; Sequence 14, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Fairah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0

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CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/943,087
  FILING DATE:
  CLASSIFICATION: 536
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/803,305
  FILING DATE: 20-FEB-1997
  ATTORNEY/AGENT INFORMATION:
  NAME: Lunn, Paul G
  REGISTRATION NUMBER: 32,743
  REFERENCE/DOCKET NUMBER: 96-24C1
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: 206-442-6627
  TELEFAX: 206-442-6678
  TELEX:
  INFORMATION FOR SEQ ID NO: 14:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 553 amino acids
  TYPE: amino acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  MOLECULE TYPE: protein
  FRAGMENT TYPE: internal
US-08-943-087-14

alignment_scores:
  Quality: 146.00      Length: 127
  Ratio: 1.848        Gaps: 4
  Percent Similarity: 62.205      Percent Identity: 29.921

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75 AGGTGGAAGAAATCTAAATCTCTCAAAAAGTAGAGTGCACATCATAG 124
34 TGLYGLY.....LeuProLysProAlaAsnIleThrPheLeuSerIleA 49
125 ATGACACATTATCTCAGTGTGAGGAGACAGAGCATGAGTGTGCGG... 171
49 smetLysAsnValLeuGlnTTPThrProProGluGlyLeuGlnGlyVal 65
172 AATGTGACATTTCATTCGATTATCAAAAACTGGGATGATTAATGGAT 221
66 LysValThrThrValGlnTTPThrPheIleTyrGlyGlnLysLysTyrPle 82
222 AAAATGTCGTCGTCGAGATATATACAGTACCAATGCAACTTTCTT 271
82 uAsnLysSerGluCysArgAsnIleAsnArgThrTyrCysAspLeuSerA 99
272 CACTCAAGCTGAATGTTATGAGAAATTAATGCGTATAAGACA... 318
99 IeGluThrSerAspTyrGlnIleGlnTTPThrAlaLysValLysAlaLe 115
319 GAAAAAGAAACACTTCTTCATGTGTAGAGTGTACATTCATTACACATT 368
116 TTPGlyThrLysCysSerLysTyrPalaGlnSerGlyArgPheTyrProPh 132
369 TCGCAAGCTCAGATTGTCTCTCCAGAACTA 399
132 eLeuGlnThrGlnIleGlyProProGluVal 142

seq_name: /cgn2_6/prodata/1/laa/5B_COMB.pep:US-08-943-087-16
seq_documentation_block:
; Sequence 16, Application US/08943087
; Patent No. 5945311
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GENERAL INFORMATION:
  APPLICANT: Lok, Si
  APPLICANT: Kho, Choon J.
  APPLICANT: Jelnberg, Anna C.
  APPLICANT: Adams, Rodyn L.
  APPLICANT: Whitmore, Theodore E.
  APPLICANT: Farrah, Theresa M.
  TITLE OF INVENTION: CYTOKINE RECEPTOR
  NUMBER OF SEQUENCES: 60
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: ZymoGenetics, Inc.
  STREET: 1201 Eastlake Avenue East
  CITY: Seattle
  STATE: WA
  COUNTRY: USA
  ZIP: 98102
  COMPUTER READABLE FORM:
  MEDIUM TYPE: Diskette
  COMPUTER: IBM Compatible
  OPERATING SYSTEM: DOS
  SOFTWARE: FastSeq for Windows Version 2.0
  CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/943,087
  FILING DATE:
  CLASSIFICATION: 536
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/803,305
  FILING DATE: 20-FEB-1997
  ATTORNEY/AGENT INFORMATION:
  NAME: Lunn, Paul G
  REGISTRATION NUMBER: 32,743
  REFERENCE/DOCKET NUMBER: 96-24C1
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: 206-442-6627
  TELEFAX: 206-442-6678
  TELEX:
  INFORMATION FOR SEQ ID NO: 16:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 553 amino acids
  TYPE: amino acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  MOLECULE TYPE: protein
  FRAGMENT TYPE: internal
US-08-943-087-16

alignment_scores:
  Quality: 146.00      Length: 127
  Ratio: 1.848        Gaps: 4
  Percent Similarity: 62.205      Percent Identity: 29.921

alignment_block:
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Align seq 1/1 to: US-08-943-087-16 from: 1 to: 553

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75 AGGTGGAAGAAATCTAAATCTCTCAAAAAGTAGAGTGCACATCATAG 124
34 TGLYGLY.....LeuProLysProAlaAsnIleThrPheLeuSerIleA 49
125 ATGACACATTATCTCAGTGTGAGGAGACAGAGCATGAGTGTGCGG... 171
49 smetLysAsnValLeuGlnTTPThrProProGluGlyLeuGlnGlyVal 65
172 AATGTGACATTTCATTCGATTATCAAAAACTGGGATGATTAATGGAT 221
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319 GAAAAAGAAAACACTTCTCATGTATGAGGTTGACTCATTTACACATT 368
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116 trpglythrlyscysserlystrpialagluserglyargphetyrproph 132
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132 eleugluthrignilleglyproprogluval 142
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seq_name: /cgn2_6/prodata/1/laa/5B_COMB.pep:US-08-943-087-18

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seq_documentation_block:
; Sequence 18, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, S1
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELE:
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-943-087-18
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alignment_scores:
Quality: 146.00      Length: 127
Ratio: 1.848         Gaps: 4
% Similarity: 62.205 Percent Identity: 29.921
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alignment_block:
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Align seg 1/1 to: US-08-943-087-18 from: 1 to: 553

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172 AATGTGACTTTTTCATTGATTATCAAAAACCTGGGATGATTAATGAT 221
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82 uasnlysserlucysargasnilleasnargthryrcysaspleusera 99
272 CACTCAAGCTGAATGTTATTAAGAAATTAATGCGTATAGACA... 318
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99 lagluthseraspyrgluthisgintyrrtyralalysvalysalle 115
319 GAAAAAGAAAACACTTCTCATGTATGAGGTTGACTCATTTACACATT 368
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116 trpglythrlyscysserlystrpialagluserglyargphetyrproph 132
369 TCGCAAGCTGAGATTGCTCTCCAGAAAGTA 399
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132 eleugluthrignilleglyproprogluval 142
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seq_name: /cgn2_6/prodata/1/laa/5B_COMB.pep:US-08-943-087-20

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seq_documentation_block:
; Sequence 20, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, S1
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
```

REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-943-087-20

alignment_scores:
Quality: 146.00 Length: 127
Ratio: 1.848 Gaps: 4
Percent Similarity: 62.205 Percent Identity: 29.921

alignment_block:
US-09-240-675-1_COPY_27_427 x US-08-943-087-20 ..

Align seg 1/1 to: US-08-943-087-20 from: 1 to: 553

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172 AATGTGACTTTTCATTCGATTATCAAAAAAAGTGGATGATTAATGAT 221
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82 uAsnLysSerGluCysArgAsnIleAsnArgThrTyrcysAspLeuSerA 99
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272 CACTCAAGCTGAATGTTATGAAGAATTAATGCGTATAGACA... 318
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99 lAcIuThrSerAspTyrGluHisGlnIleTyrTyraLysValLysAlaIle 115
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319 GAAAAAGAAACACTTCTTCATGATGATGAGGTGACATTCATTCACCAT 368
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116 TrpGlyThrLysCysSerLysTyrAlaGluSerLysArgPheTyrProPh 132
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seq_documentation_block:
Sequence 22, Application US/08943087
Patent No. 5945511
GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Kho, Choon J.
APPLICANT: Jeimberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Farrah, Theodore M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:

ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-943-087-22

alignment_scores:
Quality: 146.00 Length: 127
Ratio: 1.848 Gaps: 4
Percent Similarity: 62.205 Percent Identity: 29.921

alignment_block:
US-09-240-675-1_COPY_27_427 x US-08-943-087-22 ..

Align seg 1/1 to: US-08-943-087-22 from: 1 to: 553

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|||||:|||||:|||||:|||||:|||||:|||||:
82 uAsnLysSerGluCysArgAsnIleAsnArgThrTyrcysAspLeuSerA 99
|||||:|||||:|||||:|||||:|||||:|||||:
272 CACTCAAGCTGAATGTTATGAAGAATTAATGCGTATAGACA... 318
|||||:|||||:|||||:|||||:|||||:|||||:
99 lAcIuThrSerAspTyrGluHisGlnIleTyrTyraLysValLysAlaIle 115
|||||:|||||:|||||:|||||:|||||:|||||:
319 GAAAAAGAAACACTTCTTCATGATGATGAGGTGACATTCATTCACCAT 368
|||||:|||||:|||||:|||||:|||||:|||||:
```

116 TTPGlyThrIysCysSerIysSTrPAIaGluSerGlyArgPheTyrProPh 132
369 TCACAAGCTCAGATTGTCCTCCAGAACTA 399
| ::::::::::::::::::::::::::::|
132 eLeuGluThrGlnIleGlyProProGluVal 142

OM of: US-09-240-675-1_COPY_27_427 to: PIR-63:*

out-format : pfs

Date: Jun 1, 2000 12:36 AM

About: Results were produced by the Gencore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

```
-MODEL-frame+_n2p_model -DEV-xlp
-O/cgn2_1/USPTO_spool/US09240675/runat_30052000.164312_24623/app_query.fasta.1
-DB-PIR-63 -OPT-fastan -SUFFIX-modif.rpr -GAPOP-12.000
-GAPEXT-4.000 -MINMATCH-0.100 -LOOPEXT-0.000
-OGAPOP-4.500 -OGAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500
-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-DELOP-6.000 -DELEXT-7.000 -START-1 -MATRIX-biosum62
-TRANS-human40.ccd -LIST-45 -DOCALIGN-200 -THR_SCORE-pct
-ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext -MINLEN-0
-MAXLEN=1000000 -USER-US09240675 -NCPU-6 -ICPU-3 -NO_XLPHY -WAIT
-THREADS=1
```

Search information block:

```
Query: US-09-240-675-1_COPY_27_427
Query length: 401
Database: PIR-63:*
Database sequences: 168808
Database length: 58629743
Search time (sec): 85.570000
```

score_list:

Sequence	Strd Orig	ZScore	EScore	Len	Documentation
PIR2:A32694	+	692.00	5.3e-69	557	Interferon alpha/beta receptor
PIR2:A27387	+	454.00	1.8e-42	560	Interferon alpha receptor type
PIR2:A45283	+	366.50	7.1e-32	590	Interferon alpha/beta receptor
PIR2:C01418	+	136.50	260.76	273	Cytokine receptor family II, me
PIR2:A47003	+	136.50	259.27	323	Cytokine receptor family I, cy
PIR2:A49947	+	127.00	5.2e-06	349	Interferon receptor class II cy
PIR2:A38500	+	104.50	226.06	332	Interferon gamma receptor beta
PIR2:A31555	+	85.50	194.90	337	Interferon gamma receptor acces
PIR2:A27934	+	84.00	128.17	489	Interferon gamma receptor precu
PIR2:A57242	+	84.00	128.16	6831	Interferon gamma receptor ZK617.1a
PIR2:A27935	+	84.00	127.77	6839	Interferon gamma receptor ZK617.1b
PIR2:A25698	+	83.50	153.68	306	Interferon gamma receptor ZK617.1c
PIR2:A04591	+	83.00	148.15	520	Interferon gamma receptor ZK617.1d
PIR2:A04239	+	82.50	149.87	378	Interferon gamma receptor ZK617.1e
PIR2:A20106	+	81.50	138.36	1152	Interferon gamma receptor ZK617.1f
PIR2:A38344	+	80.00	108.46	26926	Interferon gamma receptor ZK617.1g
PIR2:A04240	+	79.50	136.82	380	Interferon gamma receptor ZK617.1h
PIR2:A44257	+	79.50	136.29	918	Interferon gamma receptor ZK617.1i
PIR2:A61165	+	79.00	141.53	442	Interferon gamma receptor ZK617.1j
PIR2:A56215	+	78.00	137.24	578	Interferon gamma receptor ZK617.1k
PIR2:A23031	+	78.00	131.88	1083	Interferon gamma receptor ZK617.1l
PIR2:A67208	+	77.50	130.59	1120	Interferon gamma receptor ZK617.1m
PIR2:A26351	+	76.50	143.56	194	Interferon gamma receptor ZK617.1n
PIR2:A14222	+	76.50	139.42	315	Interferon gamma receptor ZK617.1o
PIR2:A49667	+	76.50	134.28	575	Interferon gamma receptor ZK617.1p
PIR2:A36337	+	76.50	130.29	918	Interferon gamma receptor ZK617.1q
PIR2:A28336	+	75.50	133.34	508	Interferon gamma receptor ZK617.1r
PIR2:A28336	+	75.50	133.34	508	Interferon gamma receptor ZK617.1s
PIR2:A37892	+	75.50	131.08	662	Interferon gamma receptor ZK617.1t
PIR2:A20901	+	74.50	111.19	6805	Interferon gamma receptor ZK617.1u
PIR2:A50037	+	74.50	137.79	212	Interferon gamma receptor ZK617.1v
PIR2:A36638	+	73.50	131.61	389	Interferon gamma receptor ZK617.1w
PIR2:A20265	+	73.50	129.83	426	Interferon gamma receptor ZK617.1x
PIR2:A07648	+	71.50	127.05	408	Interferon gamma receptor ZK617.1y
PIR2:A09337	+	71.50	128.71	746	Interferon gamma receptor ZK617.1z
PIR2:A20204	+	71.00	120.17	304	Interferon gamma receptor ZK617.1aa
PIR2:A50807	+	71.00	123.16	828	Interferon gamma receptor ZK617.1ab
PIR2:A61405	+	70.50	127.28	316	Interferon gamma receptor ZK617.1ac
PIR2:A11734	+	70.50	125.34	406	Interferon gamma receptor ZK617.1ad
PIR2:A34355	+	70.50	122.31	572	Interferon gamma receptor ZK617.1ae

```
PIR1:164231 + 70.00 125.08 11.76 368 | high affinity transport s
PIR2:A48584 + 70.00 106.79 14.41 313 | transmission blocking ta
PIR2:A45731 + 69.50 132.26 12.21 141 | comc-alpha protein - phag
PIR2:JC2339 + 69.50 129.41 12.61 197 | neutrophil gelatinase-ass
```

seq_name: PIR2:A32694

seq_documentation_block:

```
Interferon alpha/beta receptor precursor - human
C.Species: Homo sapiens (man)
C.Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 22-Oct-1999
C.Accession: A32694; S17112
R.Uze, G.; Lutfalla, G.; Gresser, I.
Cell 60, 225-234, 1990
A.Title: Genetic transfer of a functional human interferon alpha receptor into mou
A.Reference number: A32694; MUID:90124632
A.Accession: A32694
A.Molecule type: mRNA
A.Residues: 1-557 <UZE>
A.Cross-references: GB:J01171; NID:q184645; PIDN:AAA52730.1; PID:q306914
R.Lutfalla, G.
Submitted to the EMBL Data Library, July 1991
A.Description: The structure of the human interferon alpha/beta receptor gene.
A.Reference number: S17112
A.Accession: S17112
A.Molecule type: DNA
A.Residues: 1-16, 'A', '18-329, 'V', '343-557 <UZE>
A.Cross-references: EMBL:X60459; NID:q32671
C.Genetics:
A.Gene: GDB:IFNAR1; IFNAR; IFRC
A.Cross-references: GDB:120078; OMIM:107450
A.Map position: 21q22.1-21q22.1
A.Intons: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3
C.Keywords: cytokine receptor; glycoprotein; transmembrane protein
F.1-2/Domain: transmembrane #status predicted <RNI>
F.437-455/Domain: transmembrane #status predicted <RNI>
F.558-581/88,110,172,254,313,314,376,416,433,507,518,537/Binding site: carboxydra
```

alignment_scores:

```
Quality: 692.00 Length: 133
Ratio: 5.203 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
US-09-240-675-1_COPY_27_427 x A32694
```

Align seg 1/1 to: A32694 from: 1 to: 557

```
1 ATGATGTCCTCTCTGCGGCGGAGACCGCTAGTCTGTCGCGCGTGGG 50
|||||
1 MethetvalValLeuLeuGlyAlaThrThrLeuValValValAlaValG 17
51 CCATGGGCTTGTTCGCGACCGCGAGTGAAGAAAAATCTTAATCTCTC 100
|||||
17 yProtrPvalLeuSerAlaAlaAlaGlyGlyValValValValSerProG 34
101 AAAAGTAGAGTGCACATCATGATGACACACTTATCTCGAGTGAAC 150
|||||
34 InlyValGluValAlaPilellelaspaspaspshelleleuAlaGTPasp 50
151 AGAGCGATGATGCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAA 200
|||||
51 ArgSeraspIuSerValGlyAsnValThrPheSerPheaspIyrcInly 67
201 AACTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 250
|||||
67 strInGlyMeCaspaspaspaspaspaspaspaspaspaspaspaspasp 84
251 GTCACCAATGCACTTTCTTCACAGCTGATGATGATGATGATGATGATGAT 300
|||||
84 ertThrlyCysasnpheserSerleuLysleuasnValIyrgInguInuile 100
```

```

301 AATTGCGTATAGAGCAGAAAAACACTTCTTCATGATGAGT 350
|||||
101 LysleuArGleArGAlaGluGluAsnThrSerTyrGluVal 117
|||||
351 TGACTCATTTACACCATTTGCGAAAGCTCAGATTGGTCTCCAGAGTA 399
|||||
117 LAspSerPheThrProPheArGlySalAGlnIleGlyProProGluVal 133
|||||
seq_name: p1r2:527387

```

seq_documentation_block:

```

Interferon alpha receptor type 1 precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S27387; S33770
R:Mouchel-Vielh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G.
FEBS Lett. 313, 255-259, 1992
A:Title: Specific antiviral activities of the human alpha interferons are determined at
A:Reference number: S27387; MUID:93076908
A:Accession: S27387
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-560 <MOU>
A:Cross-references: EMBL:X68443; NID:9431; PIDN:CAA48484.1; PID:9432
A:Experimental source: MDBK cells
R:Lim, J.K.; Langer, J.A.
Biochim. Biophys. Acta 1173, 314-319, 1993
A:Title: Cloning and characterization of a bovine alpha interferon receptor.
A:Reference number: S33770; MUID:93305725
A:Accession: S33770
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-421, 'V', 423-560 <LIW>
A:Cross-references: EMBL:L06320; NID:9163187; PIDN:AA02571.1; PID:9163188
A:Experimental source: Lung
C:Keywords: antiviral; cytokine receptor; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-560/Product: interferon alpha receptor type 1 #status predicted <MAT>

```

alignment_scores:

```

Quality: 454.00 Length: 134
Ratio: 3.914 Gaps: 4
Percent Similarity: 86.567 Percent Identity: 69.403

```

alignment_block:

```

US-09-240-675-1_COPY_27_427 x S27387 ..

```

```

Align seg 1/1 to: S27387 from: 1 to: 560

```

```

4 ATGGTGCTCTCTGCGCGGCGAGCCATAGTCTGCGCGGCGGCC 53
|||||
1 MetLeuAlaLeuLeuGluAlaThrTrpLeuMetLeuValAla...GLYAr 16
|||||
54 ATGGGTGTTGTCGCGAGCGCGAGGTGGAATAATCTAAATCTCTCAAA 103
|||||
16 gtrValIleuProAlaIleSerGlyIuAlaAsnLeuLys...ProGluA 32
|||||
104 AACTAGAGTCGACATCATAGATGACAACCTTATCTCTGAGTGAACAG 153
|||||
32 snValGluIleLysIleIleAspAspAsnPhePheLeuLysTrpAsnSer 48
|||||
154 AGGAGATGAGTCTGCGGAATGAGCTTTTCATTCGATTCATCAAAAC 203
|||||
49 SerSerGluSerValLysAsnValIlnPheSerAlaAspTyrIlnIlele 65
|||||
204 TGGATGATGAATGATGAATAATGCTGGGTCAAGATATATACAGTA 253
|||||
65 uGlyThrAspAsnTrpLysLysLeuSerGlyCysGlnHisIleThrSer 82
|||||
254 CCAATGCACTTTCTCTCACTCAAGCTG...AATGTTATGAAGAAT 300
|||||
82 hTrpLysCysAsnPheSerSerValGluLeuGluAsnValPheGluLysIle 98
|||||

```

```

301 AATTGCGTATAGAGCAGAAAA...GAAACACTTCTTCATGATGA 347
|||||
99 GluLeuArGleArGAlaGluGluAsnThrSerThrTyrGrl 115
|||||
348 GGTGACTCATTTACACCATTTGCGAAAGCTCAGATTGGTCTCCAGAG 397
|||||
115 uValGluProPheValProPheLeuGluAlaGlnIleGlyProProAspV 132
|||||
398 TA 399
132 at 132

```

```

seq_name: p1r2:A45283

```

seq_documentation_block:

```

Interferon alpha/beta receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A45283; I48423; I48424; I48425; I48426; I48427; I48428; I48429
R:Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992
A:Title: Behavior of a cloned murine interferon alpha/beta receptor expressed in hon
A:Reference number: A45283; MUID:92262522
A:Accession: A45283
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-590 <UZE>
A:Cross-references: GB:M89641; NID:9194111; PIDN:AAA37890.1; PID:9194112
A:Note: Sequence extracted from NCBI backbone (NCBIN:102354, NCBIPI:102357)
R:Lutfalla, G.; Uze, G.
Gene 148, 343-346, 1994
A:Title: Structure of the murine interferon alpha/beta receptor-encoding gene: high
A:Reference number: I48423; MUID:95047447
A:Accession: I48423
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 127-224 <RE2>
A:Cross-references: EMBL:U06238; NID:9497104; PIDN:AA01749.1; PID:9755811
A:Accession: I48425
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 243-264 <RE3>
A:Cross-references: EMBL:U06239; NID:9497106; PIDN:AAA65004.1; PID:9510261
A:Accession: I48426
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 265-375 <RE4>
A:Cross-references: EMBL:U06240; NID:9497108; PIDN:AAA65005.1; PID:9510262
A:Accession: I48427
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 397-424 <RE5>
A:Cross-references: EMBL:U06241; NID:9497110; PIDN:AAA65006.1; PID:9755812
A:Accession: I48428
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 426-445 <RE6>
A:Cross-references: EMBL:U06242; NID:9497112; PIDN:AAA65007.1; PID:9755813
A:Accession: I48429
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 473-590 <RE7>
A:Cross-references: EMBL:U06244; NID:9497114; PIDN:AAA65008.1; PID:9510265
C:Genetics:
A:Gene: IFNAR
A:Introns: 177/3; 331/1
C:Keywords: cytokine receptor; transmembrane protein

```

alignment_scores:

Quality: 366.50 Length: 133
Ratio: 3.524 Gaps: 1
Percent Similarity: 78.195 Percent Identity: 52.632

alignment_block:

US-09-240-675-1_COPY_27_427 x A45283 ..

Align seg 1/1 to: A45283 from: 1 to: 590

```

4 ATGTCGTCCTCCGCGCGGAGACCCCTAGTCGTCGCGCGGCGCC 53
|||||
1 MetLeuAlaValValGlyAlaAlaLeuValAlaValAlaGlyAlaPr 17
54 ATGGGTGTGTCGCGCGGAGACCCGAGAAATCTAAATCTCTCAA 103
|||||
17 OTPrValLeuProSerAlaAlaGlyGlyGluAsnLeuLysProProGluA 34
104 AAGTAGAGTCGACATCATAGATGACAATTATCTGAGGTGAGACAG 153
|||||
34 snlLeuAspValTyrIleIleAspAspAsnTyrThrLeuLysTyrSer 50
154 AGGCATGAGTCGTCGCGGAGATGACATTTTCATTCGATTTCAGAAAAC 203
|||||
51 HisGlyLysSerMetGlySerValThrPheSerAlaGlyTyrArgThrLy 67
204 TGGGATGATATGATATAAATGTGCGGTGTCAGAAATATCTAGTA 253
|||||
67 sAspGluAlaLysTyrPheLysValProGlyGlyGlnHisThrThrThrT 84
254 CCAATGCCAATTTCTTCTCACTCAAGCTGAATGTTTGAAGAAATTA 303
|||||
84 hrlYsCysGluPheSerLeuLeuAspThrAsnValTyrIleLysThrGln 100
304 TTGGCTATAGACGAGAAAAAGAAAC...ACTTCTTCATGCTATGAGCT 350
|||||
101 PheAlrValAlaArgAlaGluGlnGlyAsnSerThrSerSerTyrPasnGluVa 117
351 TGACTCATTTTACACCATTTTCGCAAGCCACATGGTCTCCAGAGTA 399
|||||
117 lAspProPheIleProPheTyrThrAlaHisMetSerProGluVal 133

```

seq_name: p1r2:G01418

seq_documentation_block:

cytokine receptor family II, member 4 - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
C:Accession: G01418
R:LutTalla, G.
submitted to the EMBL Data Library, April 1994
A:Reference number: G06935
A:Accession: G01418
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-273 <LUT>
A:Cross-references: EMBL:U08988; NID:g571295; PID:g571296
C:Genetics:
A:Gene: GDB:CRFB4; CRF2-4
A:Cross-references: GDB:138166; OMIM:123889
A:Map position: 21q22.1-21q22.2
A:Introns: 17/1; 58/2; 111/1; 166/3; 216/1

alignment_scores:

Quality: 136.50 Length: 121
Ratio: 1.896 Gaps: 5
Percent Similarity: 59.504 Percent Identity: 33.058

alignment_block:

US-09-240-675-1_COPY_27_427 x G01418 ..

Align seg 1/1 to: G01418 from: 1 to: 273

```

55 TGGGTGTGTCGCGCGGAGACCCGAGAAATCTAAATCT..... 96
|||||
3 TrpSerLeuGlySerThrLeuGlyGlyCysLeuLeuValSerAlaLeuG 19
97 .....CTCAAAAGTAGAGTCGACATCATAGATGAGACACT 133
|||||
19 yMetValProProProGluAsnValAlaArgMetAsnSerValAsnPhelYsA 36
134 TTATCTGAGGTGGAACGAGGACGATGATCTGCGGAATGACATTTT 183
|||||
36 snlLeuGlnTyrGlySerProAlaPheAlaLysGlyAsnLeuThrPhe 52
184 TCATTCGATATCAAAAAAGTCGATGATATGCTAAATGCTCG 233
|||||
53 ThrAlaGlnTyr.....LeuSerTyrArgTllePheGlnAspLy 65
234 GTGTCAGAAATATTTAGTACCAATGCAACTTTTCTCACTCAAGCTGA 283
|||||
65 sCysMetAsnThrThrLeuThrGlyCysAspPheSer.....LeuS 80
284 ATGTTTATGAGAAATTAATTCGCTATTAAGACAGAA...AAGAAAC 330
|||||
80 eLysTyrGlyAspPheThrLeuAlaGlyAlaArgAlaGluPheAlaAspGlu 96
331 ACTTCTTCAGGTATGAGCTGACATTCATTCACACCATTCGCAAGCTCA 380
|||||
97 HisSerAspTyrValAsnIle...ThrPheCysProValAspAspThrI 112
381 GATTGTCCTCA 393
|||||
112 eLleGlyProPro 116

```

seq_name: p1r2:A47003

seq_documentation_block:

cytokine receptor family class II protein CRF2-4 precursor - human
C:Species: Homo sapiens (man)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 10-Sep-1997
C:Accession: A47003
R:LutTalla, G.; Gardiner, K.; Uze, G.
Genomics 16, 366-373, 1993
A:Title: A new member of the cytokine receptor gene family maps on chromosome 21 at
A:Reference number: A47003; MUID:93300510
A:Accession: A47003
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-325 <LUT>
A:Cross-references: GB:217227; NID:g393378; PID:g393379
C:Genetics:
A:Map position: 21q
C:Keywords: transmembrane protein

alignment_scores:

Quality: 136.50 Length: 121
Ratio: 1.896 Gaps: 5
Percent Similarity: 59.504 Percent Identity: 33.058

alignment_block:

US-09-240-675-1_COPY_27_427 x A47003 ..

Align seg 1/1 to: A47003 from: 1 to: 325

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55 TGGGTGTGTCGCGCGGAGTCGAGAAAAATCTAAATCT..... 96
|||||
3 TrpSerLeuGlySerThrLeuGlyGlyCysLeuLeuValSerAlaLeuG 19
97 .....CTCAAAAGTAGAGTCGACATCATAGATGAGACACT 133
|||||
19 yMetValProProProGluAsnValAlaArgMetAsnSerValAsnPhelYsA 36

```

134 TTATCTGAGGTGACAGAGCGATGAGTCTGCGGAATGACTTT 183
 |||||
 36 snlleuGlntrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe 52
 |||||
 184 TCATTGATATCAAAAACTGCGATGATTAATGATTAATGCTGCG 233
 |||||
 53 ThrAlaGlnTyr.....LeuSerTyrArgIlePheGlnAspIly 65
 |||||
 234 GTGTCAGAAATTTACTAGTACCAATGCAACTTTTCTTCACTCA 283
 |||||
 65 scyGlnSerAsnThrLeuThrGlnCysAspPheSer.....LeuS 80
 |||||
 284 ATGTTTAGCAAGAAATTAATTCGCTATAGACAGAA...AAGA 330
 |||||
 80 eLysTyrGlyAspHisThrLeuArgValArgAlaGlnPheAlaSpI 96
 |||||
 331 ACTTCCTCATGATGAGTGCATCATCTTACACCATTTCCCAAGCT 380
 |||||
 97 HisSerAspTrpValAsnIle...ThrPheCysProValAspAspThr 112
 |||||
 381 GATTGCTCTCCA 393
 |||||
 112 eileGlyProPro 116

seq_name: p1r2:JC6311

seq_documentation_block:

Interferon receptor class II cytokine receptor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
 C:Accession: J06311
 R:Gibbs, V.C.; Pennica, D.
 Gene 186, 97-101, 1997
 A:Title: CRF2-4: Isolation of cDNA clones encoding the human and mouse proteins.
 A:Reference number: J06311
 A:Accession: J06311
 A>Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-349 <GIB>
 A:Cross-references: GB:U53696

alignment_scores:
 Quality: 127.00 Length: 121
 Ratio: 1.693 Gaps: 6
 Percent Similarity: 61.983 Percent Identity: 30.579

alignment_block:
 US-09-240-675-1_COPY_27_427 x JC6311 ..

Align seg 1/1 to: JC6311 from: 1 to: 349

46 GTGGCCCATGGGTGTGTCGCCAGCCGAGTGGAAAAATCTAAATC 95
 |||||
 9 LeuGlyGlyPheLeuLeuValProAlaLeuGly.....MetIleProPr 23
 |||||
 96 TCCTCAAAAGTAGAGTGCATCATCTATAGTCAACTTTATCTAGGT 145
 |||||
 23 oProGluLysValArgMetAsnSerValAsnPheLysAsnIleLeuGln 40
 |||||
 146 GGAACAGAGCGATGAGTCTGTCGGAATGATGATTTTCACTGATAT 195
 |||||
 40 rProIleValProAlaPheProLysThrAsnLeuThrPheThrAlaGlnTyr 56
 |||||
 196 CAA.....AAACGTGGATGATTAATGATTAATTTGCTGGGTCA 239
 |||||
 57 GluSerTyrArgSerPheGlnAspHis.....CysIly 67
 |||||
 240 GATTATTACAGTACCAAAATGCAACTTTTCTTCACTCAAGCTGATGTT 289
 |||||
 67 sArgTrpAlaSerThrGlnCysAspPheSer.....HisLeuSerLysT 82

290 ATGAGAAATTAATTCGCTATAGACAGAA...AAGAAAACTCT 316
 |||||
 82 yrcGlyAspTyrThrValArgValArgAlaGlnLeuAlaLysSer 98
 |||||
 337 TCATGATGATGAGTGTGATCATCTTACACCATTTTCGCAAGCTGATG 386
 |||||
 99 GluTrpAlaAsnVal...ThrPheCysProValGluAspThrIleLeu 114
 |||||
 387 TCCTCCAGAGTA 399
 |||||
 114 yProProGlnMet 118

seq_name: p1r2:A49947

seq_documentation_block:

Interferon gamma receptor beta subunit - mouse
 N:Alternate names: IFN-gamma R beta chain; IFN-gamma R species-specific cofactor; ty
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
 C:Accession: A49947
 R:Hemmi, S.; Bohni, R.; Stark, G.; Di Marco, F.; Aguet, M.
 Cell 76, 803-810, 1994
 A:Title: A novel member of the interferon receptor family complements functionality
 A:Reference number: A49947; MIM:94170381
 A:Accession: A49947
 A>Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-332 <HEM>
 A:Cross-references: GB:S69336; NID:954584; PIDN:AAB30165.1; PID:9545842
 A:Experimental source: early B-cell line 116
 A:Note: sequence extracted from NCBI backbone (NCBIN:145654, NCBI:145656)
 C:Keywords: cytokine receptor

alignment_scores:
 Quality: 120.00 Length: 130
 Ratio: 1.500 Gaps: 8
 Percent Similarity: 61.538 Percent Identity: 30.769

alignment_block:
 US-09-240-675-1_COPY_27_427 x A49947 ..

Align seg 1/1 to: A49947 from: 1 to: 332

61 TTGTCGCGAGCCGAGGTGGA.....AAAACTTAAATCTCC 98
 |||||
 16 LeuGlyAlaAlaAlaSerProAspSerPheSerGlnLeuAlaIlePr 32
 |||||
 99 TCMAAAAGTAGAGTGCATCATCTATAGTCAACTTTTCTGAGGTGGA 148
 |||||
 32 OLeuAsnProArgLeuHisLeuTyrAsnAspGlnGlnIleLeuThrTrpG 49
 |||||
 149 ACAGAGCGATGAGTCT.....GTGCGAATGTGACT 180
 |||||
 49 LuProSerProSerSerAsnAspProArgProValIleTyrGlnValGlu 65
 |||||
 181 TTTTCATTCGATTAACAAAACTGGATGAT...AATGATTAATTT 227
 |||||
 66 TyrSerPhe.....IleAspGlySerTrpHisArgIle 76
 |||||
 228 G.....TCTGGGTCTCAGAATATTACTAGTACCAAAATGCAACTTTTCT 271
 |||||
 76 uLeuGluProAsnCysThrAspIleThrGlnThrLysCysAspLeuTrpG 93
 |||||
 272 CA.....CTCAAGCTGAATGTTTATGAA...GAATTAATTTGCGT 309
 |||||
 93 IyGlyGlyArgLeuLysLeuPheProHisProPheThrValPheLeuArg 109
 |||||
 310 ATTAGAGCAGAAAAAGAAAC...ACTTCTTCATGATGATGAGTTGACTC 356
 |||||
 110 ValArgAlaLysArgGlyAsnLeuThrSerLysTrpValGlyLeuGluPr 126
 |||||
 357 ATTACACCATTTCCCAAGCTCAAGATGCTCCTCCAGAA 396

126 oPhenclHisTyrGIuaSnValThValGIyProProlys 139
seq_name: p1r2:138500

seq_documentation_block:
Interferon gamma receptor accessory factor-1 precursor - human
C:Species: Homo sapiens (man)
C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 05-Nov-1999
C:Accession: 138500; 138501
R:Sch, J.; Donnelly, R.J.; Kokenko, S.; Mariano, T.M.; Cook, J.R.; Wang, N.; Emanuel, S.
Cell 76, 793-802, 1994
A:Title: Identification and sequence of an accessory factor required for activation of
A:Reference number: A49946; MUID:94170380
A:Accession: 138500
A:Molecule type: mRNA
A:Residues: 1-337 <RES>
A:Cross-references: EMBL:U05875; NID:g463549; PIDN:AAA16955.1; PID:g463550
A:Experimental source: clone pSK1
A:Accession: 138501
A:Molecule type: mRNA
A:Residues: 1-63, 'Q', 65-337 <RE2>
A:Cross-references: EMBL:U05877; NID:g463551; PIDN:AAA16956.1; PID:g463552
A:Experimental source: clone pJ53
C:Genetics:
A:Map position: 21
C:Keywords: cytokine receptor

alignment_scores:
Quality: 104.50 Length: 145
Ratio: 1.393 Gaps: 7
Percent Similarity: 51.724 Percent Identity: 25.517

alignment_block:
US-09-240-675-1_COPY_27_427 x 138500 ..

Align seg 1/1 to: 138500 from: 1 to: 337

```
34 GTGCTCGCCGCGGCGCCATGGGTGTTCGCGAGCCGAGTGA.. 81
9 LeuLeuLeuLeuLeuGlyValPheAlaAlaAlaAlaAlaProPheAs 25
82 .....AAAAATCTAAATCTCCTCAAAAAGTAGAGTGCACATCATAG 124
25 ProLeuSerGlnLeuProAlaProGlnHisProLysIleArgLeuTyrA 42
125 ATGCAACTTATCTCTGAGGTG.....ACACAGAGC 156
42 snAlaGlnGlnValLeuSerTrpGluProValAlaAlaLeuSerAsnSerThr 58
157 GATGAGTCTGTGGGAATGTGACTTTTTCATTCGATTATCAAAAACGCG 206
59 ArgProValValTyrArgValGlnPheLysTyrThrAspSerLys.... 73
207 GATGAGTAATGTGATAAATGTCT.....GGGTCTC 238
74 .....TriPheThrAlaAspIleMetSerIleGlyValAsnGlySer 87
239 AGAATATTACAGTACCAATGCAACTTTTCTTCA..... 273
87 hrgInIleThrAlaThrGlnLysAspPheThrAlaAlaSerProSerAla 103
274 .....CTCAGCTGAATGTTATGAGAAGAAATTAATGCGTATTAAG 314
104 GlyPheProMetAspPheAsnVal.....ThrLeuAspGlnLeuArg 116
315 AGCAGAAAAAGAAAAACACT...TCCTCATGCTATGAGGTGACTCATTTA 361
116 gAlaGlnIleGlnGlyAlaLeuHisSerAlaIleTrpValThrMetProTrpPheG 133
362 CACCATTTTCGAAAGCTCAGATTGTCTCTCAGAA 396
```

133 InHisTyrArgAsnValThValGIyProProGlu 144
seq_name: p1r2:A31555

seq_documentation_block:
Interferon gamma receptor precursor - human
C:Species: Homo sapiens (man)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 23-Jul-1999
C:Accession: A31555
R:Agnet, M.; Dembic, Z.; Merlín, G.
Cell 55, 273-280, 1988
A:Title: Molecular cloning and expression of the human interferon-gamma receptor.
A:Reference number: A31555; MUID:89003065
A:Accession: A31555
A:Molecule type: mRNA
A:Residues: 1-489 <AGU>
A:Cross-references: GB:J03143; NID:g184650; PIDN:AAA52731.1; PID:g306915
C:Genetics:
A:Gene: GDB:IFNGR1; IFNGR
A:Cross-references: GDB:120688; OMIM:107470
A:Map position: 6q23-q24
C:Superfamily: Interferon gamma receptor
C:Keywords: cytokine receptor; transmembrane protein

alignment_scores:
Quality: 85.50 Length: 136
Ratio: 1.018 Gaps: 5
Percent Similarity: 61.765 Percent Identity: 24.265

alignment_block:
US-09-240-675-1_COPY_27_427 x A31555 ..

Align seg 1/1 to: A31555 from: 1 to: 489

```
7 GTGCTCTCTGCGGCGGAGACACCTAGTCTGTCGCGCGCGCCATG 56
1 MetalLeuLeuPheLeuLeuProLeuValMetGlnGlyValSerArgAl 17
57 GGTCTTCTCCGCAACC...GCAGTGGAAAAAATCTTAAATCTCCTCAA 103
17 agLLeuGlyThrAlaAspLeuGlyProSerSerValProThrProThra 34
104 AAGTAGAGGCGACATCATGATGACAACCTTATCTCGAGGTGAACAG 153
34 snValThrIleGlnSerTyrAsnMetAsnProIleValTyrTrpGluTyr 50
154 AGCGATGAGTCTGTGCGGAATGTG...ACTTTTCATTCGATTATCAAA 200
51 .....GlnIleMetProGlnValProValPheThrValGlnValLysAs 65
201 AACTGGGATGATTAATGATAAATTCGTCTGGGTCTCAAAATTAATACT 250
65 nTyrGlyValLysAsnSerGlnTrpIleAspAlaCysIleAsnIleSerH 82
251 GTACCAAAATGCAACTTTCTTCTCACTCAAGCTGATGTTATGAAGAAT 300
82 IshIstYrCysAsnIleSerAspHisValGlnLysProSerAsnSerLeu 98
301 AAATTCGCTTAAGACA.....GAAAAAGAAAAACACTTCTTCATG 341
99 TrpValArgValLysAlaArgValGlnGlnLysGlu.....SerAlaTy 113
342 GTATGAGGTGACTCAATTTACACCATTTGCGCAAGCTCAGATGCGCTC 391
113 fAlaLysSerGlnGlnPheAlaValAlaCysArgAspGlyLysIleGlyPro 130
392 CAGAGTA 399
130 rOlyLysLeu 132
seq_name: p1r2:T27934
```


A:Cross-references: MIPS:YDL108w; SGD:S0002266
A:Map position: 4L
A:Introns: 10/1
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:5-259/Domain: protein kinase homology <Kin>
F:13-21/Region: protein kinase ATP-binding motif

Alignment_scores:
Quality: 83.50 Length: 102
Ratio: 1.606 Gaps: 4
Percent Similarity: 50.980 Percent Identity: 26.471

Alignment_block:
US-09-240-675-1_COPY_27_427 x A25698

Align seg 1/1 to: A25698 from: 1 to: 306

```
115 GACATCATGATGACACCTTATCCGTGAGTGGACAGGAGCGATGAGTC 164
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
159 GUILLEUTHSERRASVALVATHRATGTPITYRATGALAPROGLU.. 174
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
165 TGTGGGAATGTGACTTTTTCATTCGATTATCAAAAAGCTGGATGATA 214
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
175 .....LeuLeuPheGLyAlaLysHsYrThrSerAlaIleAspI 188
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
215 ATTGATTAATTTGCTGGGTGTCAGATATTCTGACCAATATCAAC 264
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
188 IETRP.....SerValGIyAlaIle 194
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
265 TTTTCTCACTCAAGCTG.....AATCTTA 290
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
195 PHEALGILUETHLEUARGILEPTOTYRLEUPROGLINASNPYA 211
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
291 TGAAGAAATTAATTCGATTAAGACAGAAAAAACAACCTCT...T 337
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
211 IASPGIMETGLUVALTHRPHEARGALALEUGLYTHPROTHRASPARGA 228
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
338 CATGGATATGAGTTGACTCTATTACACCATTTGCGAAAGCTGATGG 387
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
228 SPIRPROGLIUALSERSETPHEMETHTRYASNLYSLUENILLETYR 244
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
388 CCTCA 393
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
245 PROPRO 246
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
```

seq_name: p1r2:T04591

seq_documentation_block:
ferulate-5-hydroxylase (EC 1.-.-.-) - Arabidopsis thaliana
N:Alternate names: cytochrome P450-dependent monooxygenase; protein F23E13.110
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 29-Sep-1999
C:Accession: T04591
R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Jesse, T.
submitted to the Protein Sequence Database, March 1998
A:Reference number: 215378
A:Accession: T04591
A:Molecule type: DNA
A:Residues: 1-520 <BEV>
A:Cross-references: EMBL:AL022141
A:Experimental source: cultivar Columbia; BAC clone F23E13
C:Genetics:
A:Map position: 4
A:Introns: 11/1; 314/3
A>Note: F23E13.110
C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C:Keywords: heme; iron; oxidoreductase
F:458/Binding site: heme iron (Cys) (axial ligand) #status predicted

alignment_scores:

Quality: 83.00 Length: 156
Ratio: 1.137 Gaps: 6
Percent Similarity: 46.795 Percent Identity: 21.154

Alignment_block:
US-09-240-675-1_COPY_27_427 x T04591

Align seg 1/1 to: T04591 from: 1 to: 520

```
1 ATGATGCTGCTCCTCGGGCGGACGACCACTTATGCTCGTGGCGGG 50
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
313 ILEMETASPYALMETPHEGLYTHGLUTHRALALASERATALLE.. 328
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
51 CCCATGGGTGTTCGCCAGCCGAGGTGGAAAAATCTTAATCTCTC 100
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
329 GLUTRIPALAEUTHR.....GLULeuLeuArgSerProG 340
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
101 AAAAAAGTAGAGTCGACATCATAGATGACAACTTATCTGAGGTGAA 150
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
340 IUAAPLEULYS..... 343
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
151 AGAGCGCATGAGTCTGCGGAGATGACTTTTCATTCGATTATCAAA 200
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
344 ARGVALGLINGLULLEUALGLUVAL..... 352
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
201 AACTGGATGATATGATTAATTTGCTGGGTGTCAGAAATATCTA 250
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
353 VALGILEUNSPARGVALGLUGLUSERASPILGLULYSLEUTHR 369
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
251 GTACCAATGCAACTTTCTTCACTCAAGCTGAATGTTTANGAANAAT 300
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
369 YLEULYSCYSYTHREULYSGLU...THREUARGMETHISPROFOLLE 384
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
301 AATGCGCTATAAGACGAGAAAAAACAACCTCT..... 336
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
365 PROLEULEUHLISGLUTHRALAGLUSPHRISERILEASPGLYPHEPH 401
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
336 ..... 336
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
401 EILEROLYSYSERARGVALMETILEASNALPHEALILEGLYARGA 418
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
337 .....TCATGGATGAGTTGACTCTATTACACCATTTGCCAAACT 378
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
418 SPPIRTHSERRTPRHSPPROASPHRPHARGPROSERATRPHLEU 434
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
379 CAGATTGTCCTCCAGAA 396
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
435 GLUPROGLYVALPROASP 440
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
```

seq_name: p1r2:T04239

seq_documentation_block:
hypothetical protein F14M19.130 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
C:Accession: T04239
R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Hohenseel, J.
submitted to the Protein Sequence Database, March 1999
A:Reference number: 215262
A:Accession: T04239
A:Molecule type: DNA
A:Residues: 1-378 <BEV>
A:Cross-references: EMBL:AL049480
A:Experimental source: cultivar Columbia; BAC clone F14M19
C:Genetics:
A:Map position: 4
A:Introns: 47/3; 130/3; 163/1; 262/2
A>Note: F14M19.130

alignment_scores:
Quality: 82.50 Length: 111
Ratio: 1.269 Gaps: 6

Percent Similarity: 58.559 Percent Identity: 29.730

Alignment_block:

US-09-240-675-1_copy_27_427 x T04239

Align seg 1/1 to: T04239 from: 1 to: 378

```
73 GCAGGTGGAATAAATCTAAATCTCTCA.....AAAGTAGAGT 113
||||| .....||| |||:| .....|||:|
205 AlagLysValLysIleLysCysProGluThrAspLeuAlaGluLe 221
|||:| .....|||:| .....|||:|
114 CGACATCATGATGACAACTTTATCTGAGGTG.....AACA 151
:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
221 uHsIleuIleSerAspSerPheIleGluArgPheArgGlyAsnAsnAsnA 238
152 GGAGC.....GATGAGTCTGCGGAATGTGACTTT 183
||||| .....||| |||:| .....|||:|
238 rGserIleLysGlyLysIlePheGluSerSerGlyAsnGlnLeuTyr 254
184 TCATTC.....GATTATCAAAAACTGGATGGATAATTGATAAATT 227
:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
255 AsnIlePheGlyHsIleTrpAspArgThrValMetAlaLysAsnIleLysTh 271
228 GTCGTGGGTGCAGAAATATTAAGTACCAAAATGCACTTTCTTCACTCA 277
:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
271 rGlyGluLeuGluValIleTyrAsnAlaLysGluAsnIlePheGlyLeuL 288
278 AG.....CTGATGTTTATGAGAAATTAATTCGATTAAGAGCA 318
|| .....|||:| .....|||:|
288 ysProPheThrValLysAsnLeuGluGluVal.....Thr 299
319 GAAAAAGAAACACTTCTTCATGATGAGGT 351
||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
300 GluSerGluSerThrMetValTrpSerGluVal 310
```

OM of: US-09-240-675-1_COPY_27_427 to: SwissProt_38.* out-format: pfs
 Date: Jun 1, 2000 12:37 AM

About: Results were produced by the Gencore software, version 4.5,
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Command line parameters:

-MODEL=frame+12P_model -DEV=xlp
 -O=/gen2_1/USP001/US09240675/runat.30052000.164313.24686/app_query.fasta.1
 -DB=SwissProt_38 -OFMT=fasta -SUFFIX=modif.rsp -GAPOP=12.000
 -CAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000 -LOOPEXT=0.000
 -OGAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blsum62
 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pc
 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
 -MAXLEN=1000000 -USER=US09240675 -NCPU=6 -ICPU=3 -NO_XLPHY -WAIT
 -THREADS=1

Search information block:

Query: US-09-240-675-1_COPY_27_427
 Query length: 401
 Database: SwissProt_38.*
 Database sequences: 83857
 Database length: 30454973
 Search time (sec): 45.030000

score_list:

Sequence	Strid Orig	Zscore	Escore	Len	Documentation
SwissProt_38:INRI_HUMAN	692.00	1368.21	2.3e-69	557	P17181 homo sapiens (human).
SwissProt_38:INRI_BOVIN	454.00	891.17	8.6e-43	560	O04790 bos taurus (bovine).
SwissProt_38:INRI_SHEEP	439.00	861.11	4.0e-41	560	O28589 ovis aries (sheep).
SwissProt_38:INRI_MOUSE	366.50	715.34	5.0e-33	590	P33896 mus musculus (mouse).
SwissProt_38:CRF4_HUMAN	136.50	259.66	2.2e-07	325	O08334 homo sapiens (human).
SwissProt_38:INRS_HUMAN	104.50	195.20	0.0008	337	P38484 homo sapiens (human).
SwissProt_38:INRS_HUMAN	85.50	153.83	0.1151	489	P15260 homo sapiens (human).
SwissProt_38:K18_YEAST	83.50	153.97	0.1808	306	P06242 saccharomyces cerevisiae
SwissProt_38:CP84_YEAST	83.00	148.28	0.2207	520	O42600 arabidopsis thaliana
SwissProt_38:IL1B_RAT	79.50	136.24	0.5854	918	P40100 rattus norvegicus (rat)
SwissProt_38:IL1OR_HUMAN	78.00	137.32	0.8091	578	O13651 homo sapiens (human).
SwissProt_38:6DCS_SOYBN	76.50	139.68	1.10	315	P26690 glycine max (soybean)
SwissProt_38:11OR_MOUSE	76.50	134.36	1.19	575	O61727 mus musculus (mouse).
SwissProt_38:IL1B_HUMAN	76.50	130.23	1.27	918	P40189 homo sapiens (human).
SwissProt_38:11R_HUMAN	75.50	131.11	1.57	662	P43701 homo sapiens (human).
SwissProt_38:VNS3_ROTUN	75.50	127.83	3.25	486	P35424 human rotavirus (sero
SwissProt_38:K1CH_YEAST	71.00	123.23	4.90	582	P20485 saccharomyces cerevisiae
SwissProt_38:CA01_HUMAN	70.50	125.41	5.31	406	P15907 homo sapiens (human).
SwissProt_38:P37_MYCGE	70.00	125.28	5.95	368	O49410 mycoplasma genitalium.
SwissProt_38:SC230_PLAFO	70.00	106.34	7.93	3135	O08372 plasmodium falciparum
SwissProt_38:CONA_BPT4	69.50	132.76	5.96	141	O01438 bacteriophage t4, com
SwissProt_38:NGAL_HUMAN	69.50	129.76	6.23	198	P80188 homo sapiens (human).
SwissProt_38:YDGP_HAEIN	69.50	129.36	6.27	207	P46291 haemophilus influenzae
SwissProt_38:RRA_CWJH	69.50	102.17	9.46	4488	P19751 murine coronavirus m
SwissProt_38:VE2_HPV42	68.50	121.58	8.85	398	P27223 human papillomavirus t
SwissProt_38:TYO3_RAT	68.50	114.57	9.84	880	P55166 rattus norvegicus (rat)
SwissProt_38:YD83_SCHPO	67.50	111.40	12.95	1004	O10408 schistosomacanthomyces
SwissProt_38:VE2_HPV23	67.00	117.87	13.15	431	P50769 human papillomavirus t
SwissProt_38:HPRI_YEAST	67.00	112.95	14.17	752	P17629 saccharomyces cerevisiae
SwissProt_38:VPH2_NPVAC	66.50	121.61	13.92	252	P24728 autographa californica
SwissProt_38:ICED_HUMAN	66.50	118.05	14.69	377	P49662 homo sapiens (human).
SwissProt_38:CA01_RAT	66.50	117.46	14.82	403	P13721 rattus norvegicus (rat)
SwissProt_38:YCF0_MARPO	66.50	108.85	16.88	1068	P12221 marichantia polymorpha
SwissProt_38:Y060_MYCGE	66.00	119.16	16.18	297	P43306 mycoplasma genitalium
SwissProt_38:Y107_METJA	66.00	114.12	17.46	525	O57571 methanococcus jannasch
SwissProt_38:PD12_MOUSE	66.00	111.93	18.05	673	O08642 mus musculus (mouse).
SwissProt_38:PHLC_PSEAE	66.00	111.21	18.25	730	P06200 pseudomorus aeturgus
SwissProt_38:CTFD_STRMT	66.00	105.07	20.02	1462	P49331 streptococcus mutans
SwissProt_38:KRYL_DICDI	66.00	104.36	20.24	1584	P18160 dictyostellium disco
SwissProt_38:IDPOE_YEAST	65.50	100.37	24.08	2222	P21951 saccharomyces cerevisiae

SwissProt_38:N358_HUMAN + 65.50 97.08 25.31 3224 P49792 homo sapiens (human)
 SwissProt_38:YFE2_YEAST + 65.00 109.91 23.34 674 P43560 saccharomyces cerevisiae
 SwissProt_38:VILI_DICDI + 65.00 106.79 24.47 959 P36418 dictyostellium discoideum
 SwissProt_38:N153_HUMAN - 65.00 102.99 25.92 1475 P49790 homo sapiens (human)

seq_name: SwissProt_38:INRI_HUMAN

seq_documentation_block:

ID	INRI_HUMAN	STANDARD:	PRT:	557 AA.
AC	P17181			
DT	01-AUG-1990 (rel. 15)	Created		
DT	01-AUG-1990 (rel. 15)	Last sequence update		
DT	15-FEB-2000 (rel. 39)	Last annotation update		
DE	INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).			
GN	IFNAR1 OR IFNAR			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
RP	SEQUENCE FROM N.A.			
RP	USE G., Lutfalla G., Gresser I.;			
RA	USE G., Lutfalla G., Gresser I.;			
RT	"Genetic transfer of a functional human interferon alpha receptor			
RT	into mouse cells: cloning and expression of its cDNA."			
RT	Cell 60:225-234(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	USE G., Lutfalla G., Gresser I.;			
RT	"The structure of the human interferon alpha/beta receptor gene."			
RT	J. Biol. Chem. 267:2802-2809(1992).			
RN	[3]			
RP	PHOSPHORYLATION BY TYK2.			
RA	Colmanick O., Van H., Domanski P., Handa R., Smalley D.,			
RA	Mullersman J., Witte W., Krishnan K., Krolewski J.;			
RT	"Direct binding to and tyrosine phosphorylation of the alpha subunit			
RT	of the type I interferon receptor by p135tyk2 tyrosine kinase."			
RT	Mol. Cell. Biol. 14:8133-8142(1994).			
CC	- FUNCTION: RECEPTOR FOR INTERFERON ALPHA AND BETA. BINDING TO TYPE			
CC	I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS			
CC	INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-			
CC	SUBUNITS THEMSELVES.			
CC	- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	- TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALL TISSUES AND			
CC	EVEN ON THE SURFACE OF MOST IFN-RESISTANT CELLS.			
CC	- PTM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYK2 TYROSINE KINASE.			
CC	- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.			
CC	- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.			
CC	-----			
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CC	entities requires a license agreement (see http://www.isb-sdb.ch/announce/			
CC	or send an email to license@sdb.ch).			
CC	-----			
DR	EMBL: J03171; AA52730.1; -			
DR	EMBL: X60459; CA942992.1; -			
DR	PIR: A32694; A32694.			
DR	PIR: S17112; S17112.			
DR	MIM: 107450; -			
KW	Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism;			
FT	Phosphorylation.			
FT	SIGNAL	1	27	POTENTIAL.
FT	CHAIN	28	557	INTERFERON-ALPHA/BETA RECEPTOR ALPHA
FT	DOMAIN	28	436	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	437	457	POTENTIAL.
FT	DOMAIN	458	557	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	79	87	BY SIMILARITY.
FT	DISULFID	199	220	BY SIMILARITY.


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54 ATGGGTCTTCCGCGAGCCGAGTGGAAAAATCTAAATCTCCCTCAAA 103
16 gtrpvalleuproalaalaserglyualaasleuyls...ProGluA 32
104 AAGTAGAGTCGACATCATGATGACACTTATCCGAGGTGGAGACAG 153
32 snvalgluilehsllelaspaspasphepuleuylstrpanser 48
154 AGCGATGAGTCTGTGCGGAGTGTGACTTTTTCATTCGATTATCAAAAAC 203
49 SerSerGluSerVallylsasnvalThrPheserAlaAspTyrGlnIlele 65
204 TGGCATGATTAATGATTAATGATTTGCTGGGTGTCAGAAATTAAGTA 253
65 ucllythraspansrplyslyseuserglycysglnhsllethrsert 82
254 CCAATGCACTTTCTTCTACCTCAAGCTG...AATGTTTGAAGAAAT 300
82 hrlscysasnpheserSerValgluLeuGlnasnvalPheglulysile 98
301 AATTCGCTTAAGACAGCAAAAA...GAACAACCTTCTCATGATGATGA 347
99 GluleuarglilearglaleagluluglyAsnAsnthserthrtptyrG1 115
348 GGTGACTCATTTACACCACTTTCGCAAGCTCAGATTGCTCCAGAGAG 397
115 uvalgluprophevalpropheleuGlnalaglnlleglyProphroAspy 152
398 TA 399
132 al 132

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seq_name: SwissProt_38:INRL_SHEEP

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seq_documentation_block:
ID INRL_SHEEP STANDARD: PRT: 560 AA.
AC 028589; 095206;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-BEC)
DE (INTERFERON ALPHA/BETA RECEPTOR-1).
GN IFNARI OR IFNAR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OC (1)
RN RN
RP SEQUENCE FROM N.A.
RC TISSUE-ENDOMETRIUM;
RX MEDLINE: 97135690.
RA Kaluz S., Fisher P.A., Kaluzova M., Sheldrick E.L., Flint A.P.F.;
RT "Structure of an ovine interferon receptor and its expression in
RT endometrium."
RT J. Mol. Endocrinol. 17:207-215(1996).
RL (2)
RN RN
RP SEQUENCE FROM N.A.
RC TISSUE-ENDOMETRIUM;
RX MEDLINE: 98006426.
RA Han C.-S., Machalagan N., Klemann S.W., Roberts R.M.;
RT "Molecular cloning of ovine and bovine type I interferon receptor
RT subunits from uteri, and endometrial expression of messenger
RT ribonucleic acid for ovine receptors during the estrous cycle and
RT pregnancy."
RL Endocrinology 138:4757-4767(1997).
CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
CC I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
CC SUBUNITS THEMSELVES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT
CC CONCEPTUS AT DAY 15 OF PREGNANCY.

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```

CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X95939; CA65183.1; -
DR EMBL; U65978; AAB84231.1; -
DR PIRAM; PF00041; fn3; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 560
FT FT
FT DOMAIN 25 437
FT TRANSMEM 438 458
FT DOMAIN 459 560
FT DISULFD 76 84
FT DISULFD 199 220
FT CARBOHYD 47 47
FT CARBOHYD 55 55
FT CARBOHYD 85 85
FT CARBOHYD 108 108
FT CARBOHYD 109 109
FT CARBOHYD 122 122
FT CARBOHYD 222 222
FT CARBOHYD 285 285
FT CARBOHYD 313 313
FT CARBOHYD 359 359
FT CARBOHYD 377 377
FT CARBOHYD 434 434
FT CONFLICT 352 522
FT CONFLICT 522 522
SQ SEQUENCE 560 AA; 63918 MW; E7198A1905D4805C CRC64;

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alignment_scores: Quality: 439.00 Length: 134
Ratio: 3.851 Gaps: 4
Percent Similarity: 85.075 Percent Identity: 67.910

alignment_block:

US-09-240-675-1_COPY_27_427 x INRL_SHEEP ..

Align seg 1/1 to: INRL_SHEEP from: 1 to: 560

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4 ATGGTGTCTCTCTGCGCGAGCCGAGTGGCGGCGGCGGCGCC 53
||||| ||||||| ||||||| ||||||| |||
1 MetLeuSerLeuLeuGlyAlaThrThrLeuMetLeuValAla...GlyAsr 16
54 ATGGGTGTCTCTGCGCGAGCCGAGTGGCGGCGGCGGCGGCGCC 53
||||| ||||||| ||||||| ||||||| |||
16 gtrpvalleuproalaalaserglyualaasleuyls...GluA 32
104 AAGTAGAGTCGACATCATGATGACACTTATCCGAGGTGGAGACAG 153
||||| ||||||| ||||||| ||||||| |||
32 snvalgluilehsllelaspaspasphepuleuylstrpanser 48
154 AGCGATGAGTCTGTGCGGAGTGTGACTTTTTCATTCGATTATCAAAAAC 203
||||| ||||||| ||||||| ||||||| |||
49 SerSerGluSerVallylsasnvalThrPheserAlaAspTyrGlnIlele 65
204 TGGCATGATTAATGATTAATGATTTGCTGGGTGTCAGAAATTAAGTA 253
||||| ||||||| ||||||| ||||||| |||
65 ucllythraspansrplyslyseuserglycysglnhsllethrsers 82
254 CCAATGCACTTTCTTCTACCTCAAGCTG...AATGTTTGAAGAAAT 300
||||| ||||||| ||||||| ||||||| |||
82 erlyscysasnpheserSerValgluLeuGlnalaglnlleglyProphroAspy 98

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301 AAATTGCGTATTAAGCAGAAAAA...GAAACACTTCTTCATGATGCA 347
...:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
99 GlutENaArg1leArg1ag1ug1ug1yasnasnTrIrrSerTrIrrPTyG1 115
348 GGTGACGATCATTTACACCATTTGCGAAAGCCAGATGTGTCCTCAGAG 397
115 uValGluPrOpheValPrOpheLeuLysAlaGlnIleGlyPrOpAspV 132
398 TA 399
11
132 al 132
seq_name: SwissProt_38:INRL_MOUSE
seq_documentation_block:
ID INRL_MOUSE STANDARD; PRT; 590 AA.
P33896;
DC 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 13-FEB-2000 (Rel. 39, Last annotation update)
DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
GN IFNARI OR IFNAR OR IFAR.
OS MUS MUSCULUS (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN
[1]
SEQUENCE FROM N.A.
RP MEDLINE: 92262522.
RX Use G., Lutfalla G., Bandu M.T., Proudhon D., Mogensen K.E.;
RA "behavior of a cloned murine interferon alpha/beta receptor expressed
in homosppecific or heterosppecific background.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4774-4778(1992).
CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
SUBUNTS THEMSELVES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC
-----
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-----
CC CC
DR EMBL; M89641; AAA37890.1; -.
DR PIR; A45283; A45283.
DR MGD; MGI:107658; IFNAR.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 590
FT
FT
FT DOMAIN 27 429
FT TRANSMEM 430 449
FT DOMAIN 450 590
FT DISULFD 78 86
FT DISULFD 199 220
FT CARBOHYD 43 43
FT CARBOHYD 109 109
FT CARBOHYD 181 181
FT CARBOHYD 214 214
FT CARBOHYD 314 314
FT CARBOHYD 370 370
FT CARBOHYD 409 409
FT CARBOHYD 413 413
FT CARBOHYD 590 AA; 65776 MW; 7EC6DEF370185D3A CRC64;
SQ SEQUENCE
alignment_scores:

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Quality: 366.50 Length: 133
Ratio: 3.524 Gaps: 1
Percent Similarity: 78.195 Percent Identity: 52.632

alignment_block:
US-09-240-675-1_COPY_27_427 x INR1_MOUSE ..

Align seg 1/1 to: INR1_MOUSE from: 1 to: 590

      4 ATGTCGTCTCCTGGGCGGACGACCACTTATGCTGCTGCCCGTGAGCC 53
        |||.....|||.....|||.....|||.....|||.....|||.....|||
      1 MetleuAlaValAlglYAlaAlaAlaLeuValLeuValAlaGlYAla 17
      54 ATGGGTGTGTCCCGCACCCGACGGTGGAAAAAATCTAAATCTCCCTCAA 103
        |||.....|||.....|||.....|||.....|||.....|||.....|||
      17 OTTValLeuProSerAlaAlaglyGlyGUAsnLeuLysProGluA 34
      104 AAGTAGAGATGCATCATAGATACACAACCTTATCTCGAGGTGGAAAGC 153
        |||.....|||.....|||.....|||.....|||.....|||.....|||
      34 snlleAspValTYrllelEAspsrnsnyrrhlEulsSTPSeSer 50
      154 AGCGATGAGTGTGTGGGAATGTGACTTTTCATTGCATTATCAAAAAC 203
        |||.....|||.....|||.....|||.....|||.....|||.....|||
      51 HIsglyIuseMetgLyseValThPheserAlaglunryAdghly 67
      204 TGGGATGGATAATTGGATAAATGTCTGGGTGCACAAATTAATCTAGA 253
        |||.....|||.....|||.....|||.....|||.....|||.....|||
      67 saspDuaLaLysSTPLeuLysValProGUcYsGlnHIsThrThrt 84
      254 CCAATATGCAACTTTTCTCACTCAAGCGATGATTTTGAAGAAATAAA 303
        |||.....|||.....|||.....|||.....|||.....|||.....|||
      84 hLYsCYsGLuPheserleuLusphrhAsnValTYrlleLysThGln 100
      304 TTGCCTATAGACGAGAAAAAGAAAAC...ACTTCTTCATGGTATGAGT 350
        |||.....|||.....|||.....|||.....|||.....|||.....|||
      101 PheargValArGalaglUGlUGlYAsnserThrserserrTPAsngLUva 117
      351 TGACTCATTTACACCATTTGCCAAAGTCACATGTGTCCTCCAAAGTA 399
        |||.....|||.....|||.....|||.....|||.....|||.....|||
      117 lAspropheIllepOpheryrrhAlAHIsMeSerProProGUlval 133

seq_name: SwissProt_38:CRF4_HUMAN

seq_documentation_block:
ID_CRF4_HUMAN STANDARD; PRT; 325 AA.
AC Q08334;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE CYTOKINE RECEPTOR CLASS-II CRF2-4 PRECURSOR.
DE CRFB4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
NC [1]
RN SEQUENCE FROM N.A.
RP TISSUE=FETAL BRAIN;
RC MEDLINE; 93300510.
RA Lutfalla G., Gardiner K., Uze G.;
RT "A new member of the cytokine receptor gene family maps on chromosome
RT 21 at less than 35 kb from IRMAR."
RL Genomics 16:366-373(1993).
RN [2]
RP SEQUENCE FROM N.A.
RP MEDLINE; 96054036.
RA Lutfalla G., McInnis M.G., Antonarakis S.E., Uze G.;
RT "Structure of the human CRFB4 gene: comparison with its IFNAR
RT neighbor."
RL J. Mol. Evol. 41:338-344(1995).
CC -1- FUNCTION: IS PROBABLY INVOLVED IN THE INTERFERON SYSTEM.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS
```

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CC CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; Z11727; CAAT8933.1; -.
CC DR EMBL; U08988; AAA86872.1; -.
CC DR PIR; A47003; A47003.
CC DR HSSP; p13726; 1DAN.
CC DR MIM; 123889; -.
CC KW Receptor; Transmembrane; Glycoprotein; Signal.
CC FT SIGNAL 1 19 POTENTIAL.
CC FT CHAIN 20 325 CYTOKINE RECEPTOR CLASS-II CRF2-4.
CC FT DOMAIN 20 220 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 221 249 POTENTIAL.
CC FT DOMAIN 250 325 CYTOPLASMIC (POTENTIAL).
CC FT DISULFID 66 74 BY SIMILARITY.
CC FT DISULFID 188 209 BY SIMILARITY.
CC FT CARBOHYD 49 49 POTENTIAL.
CC FT CARBOHYD 49 68 POTENTIAL.
CC FT CARBOHYD 102 68 POTENTIAL.
CC FT CARBOHYD 161 161 POTENTIAL.
CC FT CONFLICT 124 124 A -> D (IN REF. 2).
CC FT CONFLICT 269 273 FLAGHP -> VGRME (IN REF. 2).
CC FT CONFLICT 274 325 MISSING (IN REF. 2)
CC FT CONFLICT 325 AA: 37011 MW: 66706C79F8514B23 CnC6d;
CC SEQUENCE

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alignment_scores:
  Quality: 136.50      length: 121
  Ratio: 1.896        Gaps: 5
  Percent Similarity: 59.504      Percent Identity: 33.058

alignment_block:
US-09-240-6755-1_COPY_27_427 x CRF4_HUMAN ..

Align seg 1/1 to: CRF4_HUMAN from: 1 to: 325

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[illegible]

seq_name: SwissProt_38:INGS_HUMAN

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seq_documentation_block:
ID      INGS_HUMAN      STANDARD:      PRT:      337 AA.
AC      P38484:
DT      01-OCT-1994 (Rel. 30, Created)
DT      01-OCT-1994 (Rel. 30, Last sequence update)
DT      01-NOV-1997 (Rel. 35, Last annotation update)
DE      INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (INTERFERON-GAMMA
GN      RECEPTOR ACCESSORY FACTOR-1) (AF-1) (INTERFERON-GAMMA TRANSDUCER-1).
OS      HOMO SAPIENS (HUMAN).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC      Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE-LUNG FIBROBLAST;
RX      MEDLINE: 94170380.
RA      Soh J., Donnelly R.J., Kolenko S., Mariano T.M., Cook J.R.,
RA      Wang N., Emanuel S.L., Schwartz B., Miki T., Pestka S.,
RT      "Identification and sequence of an accessory factor required for
RT      activation of the human Interferon gamma receptor.";
RL      Cell 76:793-802(1994).
CC      -1- FUNCTION: PART OF THE RECEPTOR FOR INTERFERON GAMMA. REQUIRED FOR
CC      SIGNAL TRANSDUCTION. THIS ACCESSORY FACTOR IS AN INTEGRAL PART OF
CC      THE IFN-GAMMA SIGNAL TRANSDUCTION PATHWAY AND IS LIKELY TO
CC      INTERACT WITH GAF, JAK1, AND/OR JAK2.
CC      -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC      -1- SIMILARITY: CONTAINS 2 FIBROBLAST TYPE III-LIKE DOMAINS.
CC      -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC      CC
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announcement).
CC      or send an email to license@isb-sib.ch).
CC      CC
DR      EMBL: U05875; AAA16955.1; -.
DR      EMBL: U05877; AAA16956.1; -.
DR      MIM: 147569; -.
DR      PFM: PF00041; In3. 1.
DR      Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FW      SIGNAL
FT      CHAIN 1 27 POTENTIAL.
FT      DOMAIN 28 337 INTERFERON-GAMMA RECEPTOR BETA CHAIN.
FT      TRANSMEM 28 247 EXTRACELLULAR (POTENTIAL).
FT      DOMAIN 248 268 POTENTIAL.
FT      DOMAIN 269 337 CYTOPLASMIC (POTENTIAL).
FT      CARBOHYD 56 56 POTENTIAL.
FT      CARBOHYD 85 85 POTENTIAL.
FT      CARBOHYD 110 110 POTENTIAL.
FT      CARBOHYD 137 137 POTENTIAL.
FT      CARBOHYD 219 219 POTENTIAL.
FT      CARBOHYD 231 231 POTENTIAL.
FT      VARIANT 64 64 R -> O.
FT      SEQUENCE 337 AA: 37834 MM: 18C61B10AD90E309 CRC64:
FO      /FTID=VAR_002718

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alignment_scores:
  Quality: 104.50
  Ratio: 1.393
  Percent Similarity: 51.724
  Length: 145
  Gaps: 7
  Percent Identity: 25.517
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Alignment_block:
US-09-240-675-1_COPY_27_427 x INGS_HUMAN ..
Align seg 1/1 to: INGS_HUMAN from: 1 to: 337
34 GTCGTCGTCGCCGAGGCCCATGGGTGTTGCCCGCAGCCGACAGTGA... 81
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201 AACTGGATGATATGATATAATGCTGCGCTGCACATATTTCTA 250
 : ||||| :
 : ||||| :
 65 ntjrglyvallysanssercglutrpilaealacysileasnilleser 82
 : ||||| :
 251 GTACCAATATGCACTTTCTTCTCACTCAAGCTGAATGTTATGAAGAAT 300
 : ||||| :
 82 ishlstlrcysasnliiseraspHisValGlyaspProserasnSerleu 98
 : ||||| :
 301 AATTCGCGATATAAGCA.....GAAAAAAGAAACACTTCTTCATG 341
 : ||||| :
 99 TrpValArgValylsAlaArgValGlyGlnlySglu.....SerIatry 113
 : ||||| :
 342 GATGAGGTTGACTCATTTACACCATTTCCCAAGCTCAGATGGCTCTC 351
 : ||||| :
 113 rAlaLysSerGluGluPheAlaValGlyArgaspGlyLysileGlyProp 130
 : ||||| :
 392 CACAGATG 399
 : ||||| :
 130 rOlySleu 132

seq_name: SwissProt_38:K128_YEAST

seq_documentation_block:

ID K128_YEAST STANDARD: PRT: 306 AA.

AC P06242; 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE SERINE/THREONINE-PROTEIN KINASE KIN28 (EC 2.7.1.-).

CN KIN28 OR YDL108W OR D2330.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;

OC Saccharomycetaceae; Saccharomyces.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE: 87053839.

RA Simon M., Seraphin B., Faye G.;

RT "KIN28, a yeast split gene coding for a putative protein kinase

homologous to CDC28."

RL EMBO J. 5:2697-2701(1986).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-S288C / FY1679;

RX MEDLINE: 97051597.

RA Satz J.E., Buitrago M.J., Garcia R., Revuelta J.L., del Rey F.;

RT "The sequence of a 20.3 kb DNA fragment from the left arm of

Saccharomyces cerevisiae chromosome IV contains the KIN28, MSS2,

PHO2, POL3 and DUN1 genes, and six new open reading frames."

RL Yeast 12:1077-1084(1996).

RN [3]

RP ASSOCIATION WITH CCL1.

RX MEDLINE: 94047081.

RA Valay J.G., Simon M., Faye G.;

RT "The kin28 protein kinase is associated with a cyclin in

Saccharomyces cerevisiae."

RL J. Mol. Biol. 234:307-310(1993).

CC -1- FUNCTION: PROTEIN KINASE ESSENTIAL FOR CELL PROLIFERATION.

CC FUNCTION IN ASSOCIATION WITH CYCLIN CCL1.

CC -1- SIMILARITY: BELONGS TO THE CDC2/CDC28 SUBFAMILY OF SER/THR

CC PROTEIN KINASES.

CC -----

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entities requires a license agreement (see <http://www.isb-sib.ch/announce/>

DR HSPB; P24941; 1A01.
 DR TRANSFAC; T02194; -.
 DR SGD; L0000905; KIN28.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 DR PROSITE; PS50011; PROTEIN KINASE-DOM; 1.
 DR PFAM; PF00069; PKinase; 1.
 DR Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Cell division.
 FT DOMAIN 7 290 PROTEIN KINASE.
 FT NP_BIND 13 21 ATP (BY SIMILARITY).
 FT BINDING 36 36 ATP (BY SIMILARITY).
 FT ACT_SITE 129 129 BY SIMILARITY.
 SQ SEQUENCE 306 AA; 35247 MW; 763A5720A1D9ACF3 CRC64;

alignment_scores:

Quality: 83.50 Length: 102
 Ratio: 1.606 Gaps: 4
 Percent Similarity: 50.980 Percent Identity: 26.471

alignment_block:

US-09-240-675-1_COPY_27_427 x K128_YEAST ..

Align seg 1/1 to: K128_YEAST from: 1 to: 306

115 GACATCATAGATGACACACTTATCTCGAGGTGGACAGGAGATGATC 164
 :|||: :
 :|||: :
 159 GUILIELEthSerAsnValAlaThrArgTlpyrArgAlaProGlu.. 174
 :|||: :
 165 TCTCGGGAATGTGACTTTTTCATTCGATTATCAAAAACCTGGAGATG 214
 :|||: :
 175LeuIlePheGlyAlaLysIleThrSerAlaIleAspI 188
 :|||: :
 215 ATTGATTAATTTGCTGCGCTCAGAAATATACAGTACCAAAATGCAC 264
 :|||: :
 188 lerrp.....SerValIleValIle 194
 :|||: :
 265 TTTTCTTCATCAGCTG.....AATGTTTA 290
 :|||: :
 195 PheAlaGluLeuMetLeuArgIleProTyrLeuProGlyGlnAsnAsp 211
 :|||: :
 291 TGAAGAAATTAATTCGTATTAAGAGCAAGAAAAGAACTCTT...T 337
 :|||: :
 211 laspGlnMetGluValThrPheArgAlaLeuGlyThrProThrAspArg 228
 :|||: :
 338 CATGATATAGTTGATGATTTACACCATTTCCGAAAGCTAGATGTGT 387
 :|||: :
 228 spTrpProGluValIleSerPheMetThrTyrAsnLysLeuGlnIleTyr 244
 :|||: :
 388 CCTCCA 393
 :|||: :
 245 ProPro 246

seq_name: SwissProt_38:CP84_ARATH

seq_documentation_block:

ID CP84_ARATH STANDARD: PRT: 520 AA.

AC Q42600; 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE CYCROCHROME P450 84A1 (FERULATE-5-HYDROXYLASE) (EC 1.14.-.-) (F5H).

CN CY84A1 OR F4H1 OR F23B13.110.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;

OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;

OC Arabidopsis.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-CV. COLUMBIA.

RX MEDLINE: 96293440.

RA Meyer K., Cusumano J.C., Somerville C.R., Chapelle C.C.S.;
 RT "Ferulate-5-hydroxylase from Arabidopsis thaliana defines a new
 family of cytochrome P450-dependent monooxygenases";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:6869-6874(1996).
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, COLUMBIA;
 RA Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
 RA Hohnselt J., Jesse T., Heijnen L., Vos P., Mewes H.-W., Mayer K.,
 RA Scheller C.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- PATHWAY: GENERAL PHENYLPROPANOIC PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U38416; AAC49389.1; ..
 DR EMBL: AL022141; CA18128.1; ..
 DR PRINTS: PR00385; P450.
 DR PROSITE: PS00086; CYTOCHROME_P450; 1.
 DR PFAM: PF00067; P450; 1.
 KM Oxidoreductase; Monooxygenase; Membrane; Heme.
 FT BINDING 458 458 HEME (By SIMILARITY).
 SO SEQUENCE 520 AA; 58720 MW; E81279AF5BF01BC CRC64;

alignment_scores:

Quality: 83.00 Length: 156
 Ratio: 1.137 Gaps: 6
 Percent Similarity: 46.795 Percent Identity: 21.154

alignment_block:

US-09-240-675-1_COPY_27_427 x CP84_ARATH ..

Align seg 1/1 to: CP84_ARATH from: 1 to: 520

```

1 ATGATGTCGTCCTCTCGGCGGCGACCCCTAGTCTGTCGGCGGCGG 50
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
313 Ilemetaspvalmetpheglyglythrglutthralaalserralle.. 328
51 CCCATGGGTGTTGCCGACGCGGAGTGGAATAAATTAATCTCTC 100
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
329 Gluttrpalaletthr..... glutdeuauryserrprog 340
101 AAAAAGTAGAGGTGCATCATATAGTACAACTTATCTGAGTGAAC 150
  :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
340 luaspleuyls..... 343
151 AGGACGAGTGTCTGTGCGGAATGCTTTTCATTCGATTATCAAAA 200
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
344 Argvalinglingluleualagluval..... 352
201 AACTGGGATGATTAATGATTAATTTGTCTGGGTGTCAGAAATATCTA 250
  ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
353 Valgluleuysparargvaligluiseraprllegiuleutrit 369
251 GTACCAATGCAACTTCTTCACCAAGCTGAAGTTATGACGAATTT 300
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
369 ytleuylscysthrleuylsglu... thrlleuylgmehisprofolle 384
301 AAATGCGTATAGAGAGCAAGAAAAACAATCTCT..... 336
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
385 Protleuileuileuileuileuileuileuileuileuileuileu 401
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
336 ..... 336
401 elleprolylsysetargvalmetileuileuileuileuileuileu 418

```

337TCATGATGAGTGTGACTCATTTACACCATTCGCAAACT 378
 418 spProthrseritpthrpproaspthrPheargProserargpheleu 434
 379 CAGATTGCTCTCCAGAA 396
 435 Gluproglyvalproasp 440
 seq_name: SwissProt_38:IL6B-RAT

seq_documentation_block:
 ID IL6B-RAT STANDARD; PRT; 918 AA.
 AC P40190;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN
 DE 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130).
 GN IL6ST.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE: 93052397.
 RA Wang Y., Nesbitt J.E., Fuentes N.L., Fuller G.M.;
 RT Molecular cloning and characterization of the rat liver IL-6 signal
 transducing molecule, gp130.
 RL Genomics 14:666-672(1992).
 CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
 IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
 SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6R (ALPHA CHAIN) COMPLEX,
 RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES.
 AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
 EMBRYONIC DEVELOPMENT (By SIMILARITY).
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS
 AND ENDOTHELIAL CELLS.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M92340; -; NOT_ANNOTATED_CDS.
 DR PIR: A44257; A44257.
 DR HSSP: P40189; 1B0U.
 DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 DR PFAM: PF00041; fn3; 3.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
 Repeat.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 918 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
 FT DOMAIN 23 618 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 619 640 POTENTIAL.
 FT DOMAIN 641 918 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 26 120 IG-LIKE C2-TYPE DOMAIN.
 FT DOMAIN 124 221 FIBRONECTIN TYPE-III.
 FT DOMAIN 222 323 FIBRONECTIN TYPE-III.
 FT DOMAIN 324 422 FIBRONECTIN TYPE-III.
 FT DOMAIN 423 516 FIBRONECTIN TYPE-III.
 FT DOMAIN 517 612 FIBRONECTIN TYPE-III.
 FT DOMAIN 724 754 SER-RICH.
 FT DISULFID 134 144 BY SIMILARITY.


```

154 AGCGATGACTCTGCGGATGATGACTTTTCATTCGATTATCAAAAAC 203
      ::::: ::::: :::::
48 ILeProAnaNGlnSerGlnSerThrCysArgValAlaLeuLeuArgTy 64
      ::::: ::::: :::::
204 TGGCATGATTAATGATATAATTTCTGCGGTGATCAATATTACTAGT 253
      ||::: ||::: ||:::
64 rGlyLeuSerThrPAsnSerIleSerAsnGlySerGlnThrLeuSer 80
      ::::: ::::: :::::
254 CCAATGCACTTTCTCAGTCAGCAATGCTTATGAGAA..... 297
      ::::: ::::: ||:::
81 .... TyrAspLeuThrAlaValThrLeuAspLeuThrHisSerGly 95
      ::::: ::::: ||:::
298 ATTAATTCGCTATAAGACA...GAAAAAGAAACACTTCTTCATG... 342
      ::::: ||::: ||:::
96 TyrArgAlaArgValArgAlaValAspGlySerArgHisSerAsnTrpH 112
      ::::: ||::: ||:::
343 .....TATGAGCTTGACTACTTTACA 363
      ::::: ||::: ||:::
112 rValThrAsnThrArgPheSerValAspValThr 124
      ::::: ||::: ||:::

seq_name: SwissProt_38:6DCS_SOYBN

seq_documentation_block:
ID 6DCS_SOYBN STANDARD: PRT: 315 AA.
AC P26690;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE NAD(P)H DEPENDENT 6'-DEOXYCHALCONE SYNTHASE (EC 1.-.-.-).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
  core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
  Glycine.
OC [1]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP STRAIN-CV. HAROSY 63;
RX MEDLINE: 91177016.
RA Welle R., Schroeder G., Schlitz E., Grisebach H., Schroeder J.;
  "Induced plant responses to pathogen attack. Analysis and
  heterologous expression of the key enzyme in the biosynthesis of
  phytoalexins in soybean (Glycine max L. Merr. cv. Harosy 63).";
  Eur. J. Biochem. 196:423-430(1991).
RL -1- FUNCTION: CO-ACTS WITH CHALCONE SYNTHASE IN FORMATION OF
  4,2',4'-TRIHYDROXYCHALCONE, INVOLVED IN THE BIOSYNTHESIS OF
  GLYCETOLIN TYPE PHYTOALEXINS.
CC GLYCETOLIN TYPE PHYTOALEXINS.
CC -1- PATHWAY: THIS IS THE KEY ENZYME IN THE BIOSYNTHESIS OF
  PHYTOALEXINS IN SOYBEAN.
CC -1- SUBUNIT: MONOMER.
CC -1- INDUCTION: BY PATHOGEN ATTACK.
CC -1- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE FAMILY.
CC -----
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  or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X55730; CA39261.1;
DR PIR: S14222; S14222.
DR HSP: P14550; 2ALR.
DR PRINTS: PR00069; ALDKETRDZASE.
DR PROSITE: PS00062; ALDO-KETO-REDUCTASE_2; 1.
DR PROSITE: PS00063; ALDO-KETO-REDUCTASE_3; 1.
DR PROSITE: PS00798; ALDO-KETO-REDUCTASE_1; 1.
DR PFAM: PF00248; aldo_red_1.
DR Flavonoid biosynthesis; Oxidoreductase; NADP.
KW SEQUENCE 315 AA; 35490 MW; C3A6BE07EF330F47 CRC64;

```

```

Quality: 76.50 Length: 132
Ratio: 1.048 Gaps: 8
Percent Similarity: 55.303 Percent Identity: 23.485

alignment_block:
US-09-240-675-1_COPY_27_427 x 6DCS_SOYBN ..
Align seg 1/1 to: 6DCS_SOYBN from: 1 to: 315

82 AAAAACTAAATCTCTCAAAAAGTAGAGTGACATCATAGATGACA 131
      ||::: ||::: ||:::
105 LysSerLeuYsrThrLeuGlnLeuGluTyrLeuAspLeu..... 117
      ::::: ||::: ||:::
132 CTTATCTGAGTGAGCAAGACGATGATGTCGGAATGATGACTN 181
      ::::: ||::: ||:::
118 .TyrLeuIleHisTrpProLeuSerSerGlnPro..GlyLysPheSer 133
      ::::: ||::: ||:::
182 TTTCATTCGAT.....TATCAAAAAGCTGGATGAT 213
      ::::: ||::: ||:::
133 heProIleGluValGluAspLeuProPheAspValLysGlyVal... 148
      ::::: ||::: ||:::
214 AATGATTAATATGCTGGTGTGATGATATTAATGATGACCAATGC.. 261
      ||::: ||::: ||:::
149 ...TrpGluSerMetGluGluCysGlnLysLeuGlyLeuThrLysAlaI 164
      ::::: ||::: ||:::
262 .....AAGTTTCTTCACTCAAGCTGAAT..... 285
      ::::: ||::: ||:::
164 eGlyValSerAsnPheSerValLysLysLeuGlnAsnLeuSerValA 181
      ::::: ||::: ||:::
286 .....GTTATGACAAATTAATTCGCTTAAGACGCAAA 321
      ::::: ||::: ||:::
181 IatHrIleArgProValAlaValAspValAlaGluMetAsnLeuAlaTrpGln 197
      ::::: ||::: ||:::
322 AAGAAAGCACTTCTCATGATGATGAG.....GTTGACTC 356
      ::::: ||::: ||:::
198 GlnLysLysLeuArgGluPheCysLysGluAsnGlyIleLeuValThrAl 214
      ::::: ||::: ||:::

357 ATTACACCATTTGCAAA...GCTCAGATTGGTCTCTCAGAACTA 399
      ||::: ||::: ||:::
214 aphSerProLeuArgLysGlyAlaSerArgGlyProAsnGluVal 229
      ::::: ||::: ||:::

seq_name: SwissProt_38:IL10R_MOUSE

seq_documentation_block:
ID IL10R_MOUSE STANDARD: PRT: 575 AA.
AC 061727;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE INTERLEUKIN-10 RECEPTOR PRECURSOR (IL-10R).
GN IL10RA OR IL10R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
  Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-C57BL/6 X AJ F1; TISSUE=HEMATOPOIETIC;
RX MEDLINE: 94068585.
RA Ho A.S.-Y., Liu Y., Khan T.A., Hsu D.-H., Bazan J.F., Moore K.W.;
  "A receptor for Interleukin 10 is related to interferon receptors.";
  Proc. Natl. Acad. Sci. U.S.A. 90:11267-11271(1993).
RL "A. FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -----
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  or send an email to license@isb-sib.ch).
CC -----

```


alignment_scores: Length: 152
Quality: 76.50
Ratio: 1.077
Percent Similarity: 46.711 Percent Identity: 21.711

alignment_block:
US-09-240-675-1_COPY_27_427 x IL6B_HUMAN ..

Align seg 1/1 to: IL6B_HUMAN from: 1 to: 918

```
25 ACGACCGCTAGCGTCGCGCGCGCCATGGGTGTGTCGCGACGCC 74
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
187 SerThrValIyrPheValAsnIleGluValIyrValGluAlaGluAsnAl 203
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
75 AGGTGCAAAA.....AATCTAAATCTCTCAAAAAG 106
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
203 AleuGlyValThrSerAspHisIleAsnPheAspProValIyrLysV 220
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
107 TAGAG.....CTGCACATCATAGATGACAACTTATC 138
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
220 AllysProAsnProProHisAsnLeuSerValIleAsnSerGluGluLeu 236
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
139 .....CTGAGGTG...AACAGACGATGAGTCTGTGG 170
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
237 SerSerIleLeuLysLeuThrThrThrAsnProSerIleLysSerValI 253
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
171 GAATGTGACTTTTCATTCATTCATTCATCAAAAAGTGGATGATATGGA 220
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
253 eileLeuLysTyrAsnIleGlnTyrArgThrLysAspLaserThrTrps 270
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
221 TAAATGTCTGGGTGCAGATATCTACTACCAATGCAACTTTCT 270
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
270 ergInIleProPro...GluAspThrAlaSerThrArgSerSerPheThr 285
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
271 TCACCTCAAGCTGAATGTTATGAAGAATTAATTCCTATACAGACAGA 320
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
286 ValGlnAspLeuLysProPheThrGluTyrValPheArgIleAlyGlyMe 302
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
321 AAAAGAAAAC..... 330
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
302 tlyGlnAspGlyLysGlyTyrTyrPheSerAspTrpSerGluAlaLaserG 319
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
331 .....ACTCTTCATGCTATGATGAG 348
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
319 IylleThrTyrgluAspArgProSerLysAlaProSerPheThrTyrLys 335
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
349 GTTGAC 354
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
336 IleAsp 337
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

seq_name: SwissProt_38:IL2R_HUMAN

seq_documentation_block:
ID IL2R_HUMAN STANDARD: PRT; 662 AA.
AC PA2701:
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INTERLEUKIN-12 RECEPTOR BETA-1 CHAIN PRECURSOR (IL-12R).
GN IL12RB1 OR IL12RB OR IL12R.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94267217.
RA Chua A.O., Chizzonite R., Desai B.B., Trullitt T.P., Nunes P.,
RA Minetti L.J., Warriner R.R., Presky D.H., Levine J.F., Gately M.K.,
RA Gubler U.;
RT *Expression cloning of a human IL-12 receptor component. A new member
of the cytokine receptor superfamily with strong homology to gp130.*;

```
RL J. Immunol. 153:128-136(1994).  
CC -1- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION.  
CC -1- SUBUNIT: MAY FORM DIMERS OR OLIGOMERS. REQUIRES AN UNIDENTIFIED  
CC SUBUNIT TO GENERATE A HIGH AFFINITY IL-12R COMPLEX.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- ALTERNATIVE PRODUCTS: ALTERNATIVE SPLICING MAY GIVE RISE TO A  
CC SECOND PROTEIN 2 AMINO ACIDS SHORTER.  
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.  
CC  
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CC  
CC EMBL: U03187; AAA21340.1; -.  
CC MIM: 601604; -.  
CC DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.  
CC DR PFM: PFM0041; fn3; 1.  
CC KM Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing;  
CC Repeat.  
CC FT SIGNAL 1 23 POTENTIAL.  
CC FT CHAIN 24 662 INTERLEUKIN-12 RECEPTOR BETA-1 CHAIN.  
CC FT DOMAIN 24 545 EXTRACELLULAR (POTENTIAL).  
CC FT TRANSMEM 546 570 POTENTIAL.  
CC FT DOMAIN 571 662 CYTOPLASMIC (POTENTIAL).  
CC FT DOMAIN 43 133 FIBRONECTIN TYPE-III.  
CC FT DOMAIN 143 236 FIBRONECTIN TYPE-III.  
CC FT DOMAIN 237 337 FIBRONECTIN TYPE-III.  
CC FT DOMAIN 338 444 FIBRONECTIN TYPE-III.  
CC FT DOMAIN 445 540 FIBRONECTIN TYPE-III.  
CC FT DISULFD 52 62 BY SIMILARITY.  
CC FT CARBOHYD 121 121 POTENTIAL.  
CC FT CARBOHYD 329 329 POTENTIAL.  
CC FT CARBOHYD 346 346 POTENTIAL.  
CC FT CARBOHYD 352 352 POTENTIAL.  
CC FT CARBOHYD 442 442 POTENTIAL.  
CC FT CARBOHYD 456 456 POTENTIAL.  
CC FT VARSPIC 659 662 KAKM -> DE (IN A SHORTER FORM).  
CC SQ SEQUENCE 662 AA; 73108 MW; 541ADA60F62DA1EF CRC64.
```

alignment_scores: Length: 140
Quality: 75.50
Ratio: 1.020
Percent Similarity: 52.857 Percent Identity: 27.143

alignment_block:
US-09-240-675-1_COPY_27_427 x IL2R_HUMAN ..

Align seg 1/1 to: IL2R_HUMAN from: 1 to: 662

```
34 GTGCTCGTCGCGCGCGCCATGGGTGTGTCGCGACGCCAGTGGAAA 83
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
107 ValLeuThrValThrLeuThrPheValGluSerThrPheArg...AsnG 122
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
84 AATCTAAATCTCTCA..... 102
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
122 nThrGluLysSerProGluValThrLeuGlnLeuTyrAsnSerValIysT 139
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
103 .....AAGTAGAGTCGACATCATGATGACAACTT 135
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
139 yrgLupProPheGluGlyAspIleLysValSerLysLeuAlaGlyGlnLeu 155
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
136 ATCTGAGTGGAGAACAGACGATGACTGTGCGG...AATGTACTTT 162
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
156 ArgMetGluThrPheThrProAspAsnGlnValGlyLacIuValGlnPhe 172
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
183 TTCATTGATTTATCAAAAAGTGGATGATTAATGTGATAAATCTCTG 232
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

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172 eArg.....HisArgThrProSerSerProTIP..LysLeuGIYA 185
233 GGTGT.....CAGAAATATTACTAGTACCAATGCAACTTTCTCTCACTC 276
    |||      |||:::      ::      |||      |||
185 sPCysGIYProGInAspAspThrGluSerCys..LeuCysProLeu 200
277 AAGCTGAATGTTATGAGAAATTAATTGCGTATAGAGCAGAAAAAGA 326
    :::::|||||      ::|||:::|||||      |||
201 GluMetAsnValAlaGInGInLupheGInLeuValArgArgGInLeuGIYse 217
327 AACCACTTCTTCATGGTATGAGGTGACCTCATTTACACCATTCGCCAAG 376
    :::::|||||      ::      ::|||      |||
217 rGInGIYSerSerTIPSerTIPSerSer.....ProValCysValP 232
377 CTCAGATTGGTCCCTCCAGAA 396
    ::|||      |||:::
232 roProGInuAsnProProGIn 238

```



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seq_documentation_block:
ID 061190 PRELIMINARY: PRT: 349 AA.
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE CYTOKINE RECEPTOR FAMILY 2, MEMBER 4 (CLASS II CYTOKINE RECEPTOR 4).
GN IL10RB OR CRFB4 OR CR2-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97199375.
RA GIBBS V.C., PENNICA D.:
RT "CRF2-4: Isolation of cDNA clones encoding the human and mouse
RT proteins."
RL Gene 186:97-101(1997).
DR EMBL: U53696; AAC53062.1; -.
DR MGD: MGI:109380; Il10rb.
PRFAM: PF00041; fn3; 1.
SQ SEQUENCE 349 AA; 39774 MW; AAC1802A CRC32:

Alignment_scores:
Quality: 127.00 Length: 121
Ratio: 1.693 Gaps: 6
Percent Similarity: 61.983 Percent Identity: 30.579

alignment_block:
US-09-240-675-1_COPY_27_427 x 061190 ..
Align seg 1/1 to: 061190 from: 1 to: 349 .
46 GTGGGCCCATGGGTGTTCGCCGACGCCGAGTGAATAATCTAAATC 95
   ::::: |||
   9 LeuGlyAlaAlaIleSerProAspSerGlnLeuAlaIlePr 23
   ::::: |||
   96 TCCTCAAAAGTAGAGTCGACATCATAGTCACTTATCCCGAGGT 145
   ||::: |||
   23 oProGluLysValArgMetAsnSerValAsnPhelYsaSnIleLeuGln 40
   ||::: |||
   146 GGAACAGCAGCGATGAGTCTGTGCGAATGAGTCTTTCATCGATTAT 195
   ||::: |||
   40 rProIuValProAlaPheProLysThrAsnLeuThrPheThrAlaGlnTr 56
   ::::: |||
   196 CAA.....AAACTGGGATGATTAATGGATTAATTTGCTGGGTGCA 239
   ::::: |||
   57 GluSerTyrArgSerPheGlnAspHis.....CysIly 67
   ::::: |||
   240 GAATATTACTACTACCAATGCAATTTCTTCTACTCAAGCTGAAGTTT 289
   ::::: |||
   67 sArgThrAlaSerThrGlnCysAspPheSer.....HisLeuSerLysT 82
   ::::: |||
   290 ATGAGAAATTAATTCGCTATAGAGCAGAA...AAGAGAAACACTTCT 336
   ||::: |||
   82 yrcIyAspTyrThrValArgValArgAlaGluLeuAlaAspGluHisSer 98
   ::::: |||
   337 TCATGCTAGAGGTGACTATTACACCATTTTCGCAAAAGCTCAGATTGG 386
   ::::: |||
   99 GluTrpValAlaSnVal...ThrPheCysProValAlaAspThrIleIleG 114
   ||::: |||
   387 TCCTCCAGAGTA 399
   ||::: |||
   114 yProProGluMet 118
seq_name: sp_r0dent:063953

seq_documentation_block:
ID 063953 PRELIMINARY: PRT: 332 AA.
AC 063953:
DT 01-NOV-1996 (TREMBlrel. 01, Created)

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DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE INTERFERON GAMMA RECEPTOR 2 (INTERFERON GAMMA RECEPTOR BETA SUBUNIT).
GN IFNGR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94170381.
RA HEMMI S., BOHNI R., STARK G., DI MARCO F., AGUET M.:
RT "A novel member of the interferon receptor family complements
RT a functionality of the murine interferon gamma receptor in human
RT cells."
RL Cell 76:803-810(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-129SV/J;
RX MEDLINE: 97128072.
RA EBENSBERGER C., RHEE S., MUTTHUKUMARAN G., LEMBO D., DONNELLY R.,
RA PESTKA S., DEMBIC Z.:
RT "Genomic organization and promoter analysis of the gene Ifngr2
RT encoding the second chain of the mouse interferon-gamma receptor."
RL Scand. J. Immunol. 44:599-606(1996).
DR EMBL: U69599; AAC52938.1; -.
DR EMBL: U69594; AAC52938.1; JOINED.
DR EMBL: U69595; AAC52938.1; JOINED.
DR EMBL: U69596; AAC52938.1; JOINED.
DR EMBL: U69597; AAC52938.1; JOINED.
DR EMBL: U69598; AAC52938.1; JOINED.
DR MGD: S69336; AAB30165.1; -.
DR MGD: MGI:107654; Ifngr2.
PRFAM: PF00041; fn3; 1.
SQ SEQUENCE 332 AA; 37471 MW; 0BF24E9E CRC32:

Alignment_scores:
Quality: 120.00 Length: 130
Ratio: 1.500 Gaps: 8
Percent Similarity: 61.538 Percent Identity: 30.769

alignment_block:
US-09-240-675-1_COPY_27_427 x 063953 ..
Align seg 1/1 to: 063953 from: 1 to: 332
61 TTGTCGCGAGCGCGAGTGA.....AAATCTAAATCTCC 98
   ||::: |||
   16 LeuGlyAlaAlaIleSerProAspSerPheSerGlnLeuAlaIlePr 32
   ::::: |||
   99 TCATAAAGTAGAGTCGACATCATAGTCACTTATCTCTGAGGTGA 148
   ||::: |||
   32 oLeuAsnProArgLeuHisLeuTyrAsnAspGlnIleLeuThrTrp 49
   ::::: |||
   149 ACAGAGCGATGACTCT.....GTGGGAATGTGACT 180
   ::::: |||
   49 lUpProSerProSerSerAsnAspProArgProValIleTyrGluValGlu 65
   ||::: |||
   181 TTTTCATCGATTATCAAAAAAGCGATGAT...AATGATATAAAT 227
   ::::: |||
   66 TyrSerPhe.....IleAspGlySerThrPheAspArgLe 76
   ::::: |||
   228 G.....TCTGCTGTCAGAAATATTACTAGTACCAATGCAACTTTCTT 271
   ||::: |||
   76 uLeuGluProAsnGlyThrAspIleThrGluThrLysCysAspLeuThrG 93
   ::::: |||
   272 CA.....CTCAAGCTGAATGTTTATGAA...GAATTAATTTGGCT 309
   ::::: |||
   93 lYcIyGlyArgLeuLysLeuPheProHisProPheThrValAlaPheLeuArg 109
   ::::: |||
   310 ATTAAGAGCAAAAGAAAGAAC...ACTCTTCATGCTGATGAGGTGATC 356
   ::::: |||
   110 ValArgAlaLysArgGlyAsnLeuThrSerLysThrValGlyLeuGluPr 126

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99 TrpValArgValLysAlaArgValGlyInLysGlu.....SerAlaTy 113
 342 GTAGAGCTTACATTCATTACACATTTCCGAAAGCTCAGATGCTCTC 391
 113 TAlAlSercrIngluPheAlaValCysArgAspGlyLysIleGlyProP 130
 392 CAGAAGTA 399
 130 TOLysLeu 132

seq_name: sp_invertebrate:Q23020

seq_documentation_block:

ID Q23020 PRELIMINARY; PRT: 6048 AA.
 AC Q23020: Q27232 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DE TWITCHIN.
 GN UNC-22 OR ZK617.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
 OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE: 90044042.
 RA BENJAN G.M., KIFF J.E., NECKELMANN N., MOERMAN D.G., WATSON R.H.;
 RT "Sequence of an unusually large protein implicated in regulation of
 RT myosin activity in C. elegans."
 RL Nature 342:45-50(1989).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE: 93387664.
 RA BENJAN G.M., L'HERNAULT S.W., MORRIS M.E.;
 RT "Additional sequence complexity in the muscle gene, unc-22, and its
 RT encoded protein, twitchin, of Caenorhabditis elegans."
 RL Genetics 134:1097-1104(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA HARRIS B.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: X15423; CAA33463.1; -.
 DR EMBL: Z73899; CAA98081.1; ALT_INT.
 DR EMBL: Z73897; CAA98081.1; JOINED.
 DR HSSP: Q63450; 1A06.
 DR PFAM: PF00041; fn3; 31.
 DR PFAM: PF00047; 1g; 13.
 DR PFAM: PF00069; PKinase; 1.
 DR PRINTS: PR00014; FNTYPEIT.
 KW Myosin; Kinase.
 SQ SEQUENCE 6048 AA: 668449 MW: 19770602 CRC32;

alignment_scores:

Quality: 84.00 Length: 117
 Ratio: 1.151 Gaps: 8
 Percent Similarity: 62.393 Percent Identity: 26.496

alignment_block:

US-09-240-675-1_COPY_27_427 x Q23020 ..

Align seg 1/1 to: Q23020 from: 1 to: 6048

88 CTAATAATCTCCTCAAAA.....GTAGAGCTC...GACATCAT 122
 113 TAlAlSercrIngluPheAlaValCysArgAspGlyLysIleGlyProP 1089
 1073 LeuAspArgProSerLysProAsnGlyProLeuGluValSerAspValPh 1089
 123 AGATGACACTTTATCTGAGCTGGAACGAGAGCATGAGTCTGCGGGA 172
 1089 eGluAspAsnLeuAsnLeuSerTrpLysProAspAspAspGlyGlyG 1106

173 ATGTGACTTTTCATTCGATTATCAAAA.....ACTGGATGATTAAT 216
 1106 LuProIleGluTyrTrpGluValGluLysLeuAspThrAlaThrGlyArg 1122
 217 TGGATTAATTTGCTGGGTGTCAGAAATATTACTAGTACCAATGCAACT 266
 1123 TrpValPro.....CysAlaLysValLysAspThrLysAlaHisI 1136
 267 TTCTTCACCTCAAGCTGAATGTTATGAGAAATTAATTCGCTATAGAG 316
 1136 eAspGlyLeuLysLysGly.....GlnThrTrpGlnPheArgValLysA 1151
 317 CA...GAAAAGAAAACACTTCTTCATGTGATGAGCTGACATTTACA 363
 1151 lAlAlSsnLysGluGlyAlaSerAspAlaLeuSerThrAspLysAspThr 1167
 364CCATT...CGCAAAGCTCAGATTGGTCTCCACAAAGT 398
 1168 LysAlaLysAsnProGlyTrpAspGluProGlyLysThrGlyThrProAspVa 1184
 399 A 399
 1184 I 1184

seq_name: sp_invertebrate:Q23550

seq_documentation_block:

ID Q23550 PRELIMINARY; PRT: 6831 AA.
 AC Q23550:
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
 DE UNC-22 PROTEIN.
 GN UNC-22.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
 OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA WHITE S.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Z73897; CAA98064.1; -.
 DR EMBL: Z73899; CAA98064.1; JOINED.
 DR HSSP: P02751; 1FNA.
 DR PFAM: PF00041; fn3; 31.
 DR PFAM: PF00047; 1g; 17.
 DR PFAM: PF00069; PKinase; 1.
 DR PRINTS: PR00014; FNTYPEIT.
 SQ SEQUENCE 6831 AA: 752579 MW: 0A66C338 CRC32;

alignment_scores:

Quality: 84.00 Length: 117
 Ratio: 1.151 Gaps: 8
 Percent Similarity: 62.393 Percent Identity: 26.496

alignment_block:

US-09-240-675-1_COPY_27_427 x Q23550 ..

Align seg 1/1 to: Q23550 from: 1 to: 6831

88 CTAATAATCTCCTCAAAA.....GTAGAGCTC...GACATCAT 122
 113 TAlAlSercrIngluPheAlaValCysArgAspGlyLysIleGlyProP 1872
 1856 LeuAspArgProSerLysProAsnGlyProLeuGluValSerAspValPh 1872
 123 AGATGACACTTTATCTGAGCTGGAACGAGAGCATGAGTCTGCGGGA 172
 1872 eGluAspAsnLeuAsnLeuSerTrpLysProAspAspAspGlyGlyG 1889
 173 ATGTGACTTTTCATTCGATTATCAAAA.....ACTGGATGATTAAT 216
 1889 LuProIleGluTyrTrpGluValGluLysLeuAspThrAlaThrGlyArg 1905

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217 TCGATAAAATGCTGGGTGTCAGAAATATTAAGTACCAATGCAACTT 266
|||||
1906 TrpValPro.....CysAlaLysValLysAspThrLysAlaHisI1 1919
267 TTCTTCACCTAGCTGAATGTTATGAAGAATTAATTCGCTAAGAG 316
|||||
1919 eaSPGlyLeuLysLysGly.....GlnThrTyGlnPheArgValLysA 1934
317 CA...GAAAAAGAAACACTTCTTCATGATGATGAGTGAAGTCAATTACA 363
|||
1934 laValAsnLysGluGlyAlaSerAspAlaLeuSerThrAspLysAspThr 1950
364 .....CCATTTCGCAAGCTCAGATTGGTCTCTCCAGAAAGT 398
|||||
1951 LysAlaLysAsnProTyrAspGluProGlyLysThrGlyThrProAspVa 1967
399 A 399
1967 1 1967
seq_name: sp_invertebrate:Q23551

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seq_documentation_block:
ID Q23551 PRELIMINARY; PRT: 7160 AA.
AC Q23551;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE ZK617.18 PROTEIN.
GN ZK617.18.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
Rhabditina; Rhabditioidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RA HARRIS B.;
RL Submitted (May-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BOFIELD J., BURTON J., CONNELL M., CORSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans".
RL Nature 368:32-38(1994).
RN [3]
RP SEQUENCE FROM N.A.
RA WHITE S.;
RL Submitted (May-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z73899; CA98082.1; -.
DR EMBL: Z73897; CA98082.1; JOINED.
DR EMBL: Z73897; CA98065.1; -.
DR EMBL: Z73899; CA98065.1; JOINED.
DR HSSP: P02751; 1FNA.
DR PFAM: PF00041; fn3; 31.
DR PFAM: PF00047; 1g; 17.
DR PFAM: PF00069; Pkinase; 1.
DR PRINTS: PR00014; ENTPERT11.
SO SEQUENCE 7160 AA; 789211 MW; EDD567FE CRC32;

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alignment_scores:
Quality: 84.00 Length: 117
Ratio: 1.151 Gaps: 8
Percent Similarity: 62.393 Percent Identity: 26.496

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alignment_block:
us-09-240-675-1_COPY_27_427 x Q23551 ..
Align seg 1/1 to: Q23551 from: 1 to: 7160

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```

88 CTAAATCTCTCAAAA.....GTAGAGTC...GACATCAT 122
|||||
2185 LeuAspArgProSerLysProAsnGlyProLeuGluValSerAspValPh 2201
123 AGATGACAACTTTATCCTGAGTGCAGACAGAGATGATGTCGCGA 172
|||||
2201 eGluAspAsnLeuAsnLeuSerThrLysProProAspAspAspGlyG 2218
173 ATGTGACTTTTCATTCGATTATCAAAA.....ACTGGAGATGATAT 216
|||||
2218 LysProLeuGlyTyrGlyGluValGlyLysLeuAspThrAlaThrGlyArg 2234
217 TCGATAAAATGCTGGGTGTCAGAAATATTAAGTACCAATGCAACTT 266
|||||
2235 TrpValPro.....CysAlaLysValLysAspThrLysAlaHisI1 2248
267 TTCTTCACCTAGCTGAATGTTATGAAGAATTAATTCGCTAAGAG 316
|||||
2248 eaSPGlyLeuLysLysGly.....GlnThrTyGlnPheArgValLysA 2263
317 CA...GAAAAAGAAACACTTCTTCATGATGATGAGTGAAGTCAATTACA 363
|||
2263 laValAsnLysGluGlyAlaSerAspAlaLeuSerThrAspLysAspThr 2279
364 .....CCATTTCGCAAGCTCAGATTGGTCTCTCCAGAAAGT 398
|||||
2280 LysAlaLysAsnProTyrAspGluProGlyLysThrGlyThrProAspVa 2296
399 A 399
2296 1 2296
seq_name: sp_vertebrate:O13048

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seq_documentation_block:
ID O13048 PRELIMINARY; PRT: 402 AA.
AC O13048;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE XNR4.
GN XNR4.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipridae; Xenopodinae;
Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97278865.
RA JOSEPH E.M., MELTON D.A.;
RT "Xnr4, a Xenopus nodal-related gene expressed in the Spemann
organizer".
RL Dev. Biol. 184:367-372(1997).
CC -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR EMBL: U79162; AAC60127.1; -.
DR HSSP: P18075; 1BWP.
DR PROSITE: PS00250; TGF-BETA; 1.
DR PFAM: PF00019; TGF-beta; 1.
DR PRINTS: PR00438; GRCYSNOT.
KW Glycoprotein.
SO SEQUENCE 402 AA; 46271 MW; 039E7186 CRC32;

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alignment_scores:
Quality: 80.00 Length: 112
Ratio: 1.404 Gaps: 5
Percent Similarity: 50.893 Percent Identity: 23.214

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10881 rArpPheArVAllysalagluasnlleValglYleuGlYleuProAspt 10998

356 CATTACACATTCGC...AAAGCTGATGTCCTCCAGAGTA 399
10998 hTrrIleProIleGlucylsclngluYleuValProProSerVal 11013

seq_name: sp_fungi:006349

seq_documentation_block:
ID 006349 PRELIMINARY; PRT: 442 AA.
AC 006349:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE CHROMOSOME IV COSMID 9481.
GN D9481.14.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C (AB972);
RA Ding H.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C (AB972);
RA JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DU Z.,
RA FAVELLO A., FULTON L., GATTUNG S., GRECO T., KIRSTEN J., KUCABA T.,
RA HALSMORTH K., HARKINS J., HILLIER L., JIER M., JOHNSON D.,
RA JOHNSTON L., LANGSTON Y., LATREILLE P., LE T., MARDIS E., MENEZES S.,
RA MILLER N., NHAN M., PAULEY A., PELUSO D., RIFKEN L., RILES L.,
RA TAICH A., TREVASKIS E., VIGNATI D., WILCOX L., WOHLMAN P., VAUDIN M.,
RA WILSON R., WATERSTON R.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C (AB972);
RA WATERSTON R.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C (AB972);
RA JIA Y., CHERRY J.M.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U28373; AAB64806.1; -;
SQ SEQUENCE 442 AA; 50492 MW; 5073BC0A CRC32;

alignment_scores:

Quality: 79.00 Length: 117
Ratio: 1.162 Gaps: 7
Percent Similarity: 58.120 Percent Identity: 25.641

Alignment_block:

US-09-240-675-1_COPY_27_427 x 006349 ..

Align seg 1/1 to: 006349 from: 1 to: 442

25 AGACCCCTAGTGTGCTGCGCCCTGGCCCATGGGTTCCTCCGACGCC 74
|||||
208 ThirSerLeuIleValThirYrMetGlYalglYleuLeuSerPhcys.. 223
75 AGGTGGAATAAATCTAAATCTCCCAAAAGTAGAGTCGACATCATAG 124
|||||
224 ..ArgasValLysLysAspSerLmetSerLysglYglYIleT 238
125 ATGACAACCTTATCTGAGTGTGAACAGGACGATGAGTCTCGGGAAT 174
|||||
238 YrSerAsn.....AspProAsnMetLysLys 246
175 GTGACTTTTCA...TTGCATTATCAAAAAAAGTGGATGATTAATTGAT 221
|||||

247 IleCysTyrSerGlYpHeGluphe.....GluAsnTrpVa 258

222 A...AAATTCCTGGTGTGAGATATATTACTAGCAAAATGCAAC...T 265
258 lThngluAsnSerLysValalAspLeuThngLysSerLysCysProIle 275
266 TTCTCTCAGTCAGAGCTGATGTTATGAGAAATTAATTCGCTATPAGA 315
275 hSerLeuValglYserLysLeuSerGlngluYleuIleLeuIleArg 291
316 GCAGAAAAGAAAAAAGACTTCTCATGTGATGAGGTGATTCATACAC 365
292 Cys.....GluMetAspAlaPheAsnPr 299
366 A 366
299 o 299

seq_name: sp_invertebrate:045604

seq_documentation_block:
ID 045604 PRELIMINARY; PRT: 1083 AA.
AC 045604: 045724;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE T01G1.3 PROTEIN.
GN T01G1.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditiia; Rhabditida;
OC Rhabditiina; Rhabditioidea; Rhabditidae; Peloderiinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RA KERSHAW J.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94150718.
RA WILSON R., AINSWORTH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HARKINS T., HILLIER L., JIER M., JOHNSON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCWORTHY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SPALDON N., SMITH A., SONNHAMMER E., STADEN R., STURTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
RL Nature 368:32-38(1994).
RN [3]
RP SEQUENCE FROM N.A.
RA MCLAY K.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z62811; CAB07274.1; -;
DR EMBL: Z92789; CAB07274.1; JOINED.
DR EMBL: Z92789; CAB07223.1; -;
DR EMBL: Z92811; CAB07223.1; JOINED.
DR PRAM: PR00400; W400; 1.
SQ SEQUENCE 1083 AA; 119604 MW; 23EC3C85 CRC32;

alignment_scores:

Quality: 78.00 Length: 128
Ratio: 1.068 Gaps: 7
Percent Similarity: 57.031 Percent Identity: 24.219

Alignment_block:

US-09-240-675-1_COPY_27_427 x 045604 ..

Align seg 1/1 to: 045604 from: 1 to: 1083

```

126 spfyttysercylmethrhnsmsercylulyservalgluvalasp... 141
121 atrnagatgacactttatctctgaggtgcgaacgagcagatcgtctgcg 170
142 ...hhsaspsrleuvalleuphetrpsncluglyserthrlnaleuse 157
171 gatcgacattttctcatcgcattacaaaaaactcggatgatgaattgca 220
157 rsnlysvallleasnpheserttrpsnvalcglycylval...leu 172
221 taaaattg...tcgggtgtcag 240
172 leysleuthrsersnthrargileaspilcysmetalaasmetasp 188
241 aatattactagacacaaatgcacatttct... 270
189 asnphepthrsersaspsrphesanttrpoclunltrprhthlsanphep 205
271 ...tcactcaagctgaattgtttatgaaagaattaaattg... 306
205 oargseralasermetasniletythrpsptyrtylleualaservala 222
307 .....cgmtaagacagacaaaaaagaaacactgtcttcagtgtat 345
222 spptrysercintlleargalaleuqngninprolllethrthval 238
346 gaggttgactcatttacacacatttgcgaaagctcagattggtctccaga 395
239 glumetylmetvalylvalylsargluclyserilleasvalaspgl 255
396 agta 399
355 val 256 .

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seq.name: sp_fungi:008773

seq_documentation_block:
ID      008773      PRELIMINARY;      PRT;      1120 AA.
AC      008773;
DT      01-NOV-1996 (TREMBLrel. 01, Created)
DT      01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT      01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE      CHROMOSOME XV READING FRAME ORF YOR304W.
OS      Saccharomyces cerevisiae (Baker's yeast).
OC      Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomyc
OC      Saccharomycetaceae; Saccharomyces.
RN      [1]
RP      SEQUENCE FROM N.A.
RA      CIEPLEDUC C., JAUVINUX J.C., KORDES E., POIREY R., PUJOL A
RA      TOBIASCH E.;
RN      Submitted (JUL-1996) to the EMBL/Genbank/DBJ databases.
[2]
RP      SEQUENCE FROM N.A.
RA      MRPS;
RL      Submitted (JUL-1996) to the EMBL/Genbank/DBJ databases.
DR      EMBL: 275212; CAA99622.1; -.
DR      PEFAM: PEF00271; helicase_C; 1.
DR      PEFAM: PEF00176; SMT2_N; 1.
SO      SEQUENCE      1120 AA; 130326 MW; 51FCFF47 CRC32;

Alignment_scores:
      Quality:      77.50      Length:      125
      Ratio:      1.123      Gaps:      4
Percent Similarity:      55.200      Percent Identity:      23.200

Alignment_block:
US-09-240-675-1-COPY.27_427 x 008773      ..

Align seg 1/1      to: 008773      from: 1      to: 1120

76 GGTGGAATAATCTA.....AAATCTCCCTCAAAAGTAGAGTCGACAT 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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664 G1yAlAlAlAsmMetPheGluLysAlaSerLysValThrValAspAl 660
120 CATAGATGACAACTTATCTGAGTGCAGACAGAGAGATGCTGCTG 169
    |||:|||||: |||:|||||: |||:|||||: |||:|||||:
680 AspIleAspAlaPheLysGluLysGluLysGluLysGluLysGluLys 696
170 GCATATGACTTTTTCATTCATTCATTCATTCATTCATTCATTCAT 219
    |||:|||||: |||:|||||: |||:|||||: |||:|||||:
697 .....AsnAlaLysTyrGlnSerLeuGlyLeuAspAspLeu 708
220 ATAAATGTCGTGCTGCTGATATTCATTCATTCATTCATTCATTC 269
    |||:|||||: |||:|||||: |||:|||||: |||:|||||:
709 GlnLysPheAsnGlyLysGlnLysGlnLysGlnLysGlnLysGln 725
270 TTCACCTCAAGCTGATGTTATTCAGAAATTAATTCGCTATA..... 312
    |||:|||||: |||:|||||: |||:|||||: |||:|||||:
725 sSerPheGlnLysLysSerAsnAspLysValAlaGluTrpIleAsnPro 742
313 ..AGACGACAAAAAAGAAACACTTCTTCATGATGATGATGATGAT 360
    |||:|||||: |||:|||||: |||:|||||: |||:|||||:
742 eTArgTgTgTgTgTgTgTgTgTgTgTgTgTgTgTgTgTgTgTgT 758
361 .....ACACC 365
759 TyrLysGluIleIleGlyGlySerLysSerAlaSerLysGlnThr 775
366 ATTCGCAAGCTCAGATTCGCTCT 390
    |||:|||||: |||:|||||: |||:|||||: |||:|||||:
775 GlnProLysAlaProArgAlaPro 783

```

seq_name: sp_invertebrate:Q20930

```

seq_documentation_block:
AC Q20930 PRELIMINARY: PRT: 508 AA.
ID Q20930:
AC Q20930:
DT 01-NOV-1996 (TREMBLER. 01, Created)
DT 01-NOV-1996 (TREMBLER. 01, Last sequence update)
DT 01-MAY-1999 (TREMBLER. 10, Last annotation update)
DE F5787.4 PROTEIN.
GN F5787.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabdita; Rhabditida;
OC Rhabditina; Rhabditidae; Rhabditidae; Pelodierinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RA LENNARD N.:
RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94150718.
RA WILSON R., AINSWORTH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAYTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAKINS T., HILLIER L., JER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIEKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIRRY-MING J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPOAT J., WOHLDMAN P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RT Nature 368:32-38(1994).
DR EMBL: Z74037; CAA98493.1.
DR PFAM: PF01421. ReproLysIn: 1.
SO SEQUENCE 508 AA; 57789 MW; B49E91AE CRC32;

```

Alignment_scores:
Quality: 75.50 Length: 148
Ratio: 1.079 Gaps: 5
Percent Similarity: 47.297 Percent Identity: 22.297

alignment_block:
US-09-240-675-1_COPY_27_427 x Q20930 ..

Align seg 1/1 to: Q20930 from: 1 to: 508

```

10 GTCCTCCCTGCGCGGCGAGACACCTAGTGCCTGCGCGCGGCGCCATGGGT 59
    |||:|||||: |||:|||||: |||:|||||: |||:|||||:
118 ILeSerPheGlyAsnGluThrLeuIleMetValPheAlaGlyThrTrpI 134
60 GTTGTCGCCGCGCCGAGP..... 78
134 eAlaThrGlnGluArgAspCysProLeuTrpIleSerTrpAlaGluGlu 151
79 .....GGAATAATCTAAATCTCCCTCAAAAGTAGAG 111
151 LuGluGluArgValLeuAsnGluGluIleArgArgLeuGluGluLysGlu 167
112 CTCGACATC.....ATAGATGACACTTATTCGATGAGTGGA 149
    |||:|||||: |||:|||||: |||:|||||: |||:|||||:
168 ArgAspLeuAsnSerThrPheValAspAspIlePhePheMetAsnSerTh 184
150 CAGGACCGATGAGTCTGTCGGAATGTCATTTTCATTCATTCATTCATA 199
    |||:|||||: |||:|||||: |||:|||||: |||:|||||:
184 rAspSerAspAsnSerSerThrAspAlaLeuIleSerSerAspMetPro 201
200 AAACCTGGGATGGATTAATTCGATTAATTCGCTGCGGTGCAGAAATTA 249
    |||:|||||: |||:|||||: |||:|||||: |||:|||||:
201 ys.....LysLeuArgLysPheValAspIleThr 210
250 AGTACCAATGCAACTTCTTCACACGACGATGATGTTATGAGAAAT 299
    |||:|||||: |||:|||||: |||:|||||: |||:|||||:
211 .....LeuGluGluMetGlnGluAsnAsnSerThrGlu 222
300 TAAATGCGTATAGAGCAAGAAAAAACAATCTTCATGATGATGAG 349
    |||:|||||: |||:|||||: |||:|||||: |||:|||||:
222 tThrLeuLysIleAspSerLysLys.....AlaI 232
350 TTGACTCATTTACACCATTTCCCAAGCTCAGATTCGCTCCCA 393
    |||:|||||: |||:|||||: |||:|||||: |||:|||||:
232 leAspLysPheThrIleThrLeuLysGluGluThrGlyLeuPro 246

```

227 A 227
67 s 67

seq_name: A_Geneseq_36:R14487

seq_documentation_block:

ID R14487 standard; Protein: 436 AA.
AC R14487;
DT 16-JAN-1992 (first entry)
DE Soluble Interferon-alpha/beta receptor.
KW IFN; autoimmune disease; graft rejection; histocompatibility.
OS Homo sapiens.
PN FR2657881-A.
PD 09-AUG-1991.
PF 05-FEB-1990; FR-001298.
PR 05-FEB-1990; FR-001298.
PA (EUBI-) LAB EURO BIOTECHNO.
PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,
PT Toyey MG, Uze G;
DR WPI; 91-319778/44.
DR N-PSDB; 014239.
PT New water-soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus, Bence's disease, aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.
PS Claim 2; Page 45; 52pp; French.
CC The transmembrane and cytoplasmic domains of the native IFN receptor have been deleted to obtain a soluble, circulating form of the receptor. Potentially immunogenic epitopes have thus been eliminated. CC derivatives obtained by substitution or deletion of this sequence are also claimed as are hybrid molecules comprising the soluble CC receptor (or deriv.) and an immunoglobulin such as IgG1.
CC See also 014240.
SO Sequence 436 AA;

Alignment_scores:

Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

Alignment_block:

US-09-240-675-1_COPY_1_229 x R14487 ..

Align seg 1/1 to: R14487 from: 1 to: 436

27 ATGATGCTGCTCTCTGGCGCGAGACCCCTAGTCTGCTGCGCCGTGGG 76
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValAla 17
77 CCCATGGTGTGTGCCGACGCCGAGGTGGAATAAATCTAAATCTCCTC 126
|||||
17 yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
127 AAAAAGTAGAGTGCACATCATGATGACAACTTTATCTGAGAGTGAAC 176
|||||
34 InLysValGluValAspIleIleAspAspAsnPhelLeuArgTrpAsn 50
177 AGGAGCGATGAGTCTGTCGGGAATGCACTTTTTCATTGATTATCAAAA 226
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLys 67
227 A 227
67 s 67

seq_name: A_Geneseq_36:R28495

seq_documentation_block:

ID R28495 standard; Protein: 436 AA.
AC R28495;
DT 31-MAR-1993 (first entry)
DE Sequence of a soluble form of the Interferon (IFN) receptor

DE With a high affinity for IFN-alpha and -beta.
KW Interferon receptor; alpha-Interferon; beta-Interferon.
OS Synthetic.
PN W09218626-A.
PD 29-OCT-1992.
PF 17-APR-1991; F00318.
PR 17-APR-1991; WO-F00318.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,
PT Toyey M, Uze G;
DR WPI; 92-382110/46.
DR N-PSDB; Q30532.
PT Water soluble polypeptide(s) strongly bind Interferon(s) alpha and beta - useful as immunosuppressants, for treating auto-immune diseases and transplant rejection
PS Claim 2; Fig 1; 58pp; English.
CC DNA encoding the water-soluble polypeptide with a high affinity for IFN-alpha and -beta is isolated by PCR, using appropriate oligonucleotides as primers and cloned cDNA as template. For example, CC bacteriophage lambda ZAP, containing the entire coding sequence of CC the IFN-alpha and -beta receptor (Q30533), was incubated with oligos Q30534 and Q30535. R28496 represents the complete receptor. R28495 CC lacks the transmembrane and cytoplasmic domains. Both forms bind CC IFN in the same way as antibodies so are immunosuppressants e.g. for treating autoimmune diseases and graft rejection. They lack the CC toxic side-effects of known immunosuppressants such as steroids.

Sequence 436 AA;

Alignment_scores:

Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

Alignment_block:

US-09-240-675-1_COPY_1_229 x R28495 ..

Align seg 1/1 to: R28495 from: 1 to: 436

27 ATGATGCTGCTCTCTGGCGCGAGACCCCTAGTCTGCTGCGCCGTGGG 76
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValAla 17
77 CCCATGGTGTGTGCCGACGCCGAGGTGGAATAAATCTAAATCTCCTC 126
|||||
17 yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
127 AAAAAGTAGAGTGCACATCATGATGACAACTTTATCTGAGAGTGAAC 176
|||||
34 InLysValGluValAspIleIleAspAspAsnPhelLeuArgTrpAsn 50
177 AGGAGCGATGAGTCTGTCGGGAATGCACTTTTTCATTGATTATCAAAA 226
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLys 67
227 A 227
67 s 67

seq_name: A_Geneseq_36:R71723

seq_documentation_block:

ID R71723 standard; Protein: 436 AA.
AC R71723;
DT 16-OCT-1995 (first entry)
DE IFN receptor extracellular domain.
KW IFN receptor; Interferon receptor; Interferon-alpha; Interferon-beta; monoclonal antibody; immunomodulator; AIDS.
OS Homo sapiens.
PN W09507716-A.
PD 23-MAR-1995.
PF 16-SEP-1994; E03114.
PR 17-SEP-1993; EP-402279.

PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
 PI Benizri EJ, Tovey MG;
 DR WPI: 95-11187/17.
 DR N-PSDB: 086457.
 PT Compn. of monoclonal antibodies against Interferon receptor -
 PT useful as immuno-modulator, eg. for treating AIDS
 PS Disclosure: Fig. 2A-2B; 105pp; English.
 CC A recombinant soluble form of the human interferon class I receptor
 CC protein extracellular domain, given in R71723, was expressed in
 CC either E. coli or COS cell hosts. The protein was used to raise
 CC immunomodulatory monoclonal antibodies.
 SO Sequence 436 AA;

alignment_scores: Length: 67
 Quality: 340.00 Gaps: 0
 Ratio: 5.075
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-240-675-1_COPY_1_229 x R71723

Align seg 1/1 to: R71723 from: 1 to: 436

```

27 ATGATGTCGTCCTCCTGGCGCGAGACCCCTAGTCTGCTCCGCGGTGG 76
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValAl 17
77 CCCATGGGTGTGTCCGACGCCGAGTGGAATAATCTAAATCTCTC 126
|||||
17 yProTPrValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerPro 34
127 AAAAAGTAGAGTCGACATCATGATGACAACTTATCTGAGGTGGAAC 176
|||||
34 InlysvAlaIuValAspIleIleAspAspAsnPhelLeuValArgTTPAsn 50
177 AGGAGCGATGAGTCTGTCCGGAATGTGACTTTTCATTGCATTATCAAA 226
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnly 67
227 A 227
67 s 67

```

seq_name: A_Geneseq_36:W21806

seq_documentation_block:

ID W21806 standard; Protein: 496 AA.
 AC W21806;
 DT 23-SEP-1997 (first entry)
 DE Spliced-deleted interferon alpha-receptor form 2.
 OS Interferon alpha-receptor; IFNAR.
 KW Homo sapiens.
 FH Key Location/Qualifiers
 FT domain 1..419
 FT /label= Extracellular domain
 FT /note= "comprises amino acid residues 1-413 and
 FT 422-427 of transmembrane IFNAR"
 FT 420..496
 FT domain /label= Intracellular domain
 FT /note= "comprises amino acids 481-557 of
 FT transmembrane IFNAR"
 PN AU9475977-A.
 PD 11-MAY-1995.
 PF 20-OCT-1994; 075977.
 PR 24-OCT-1993; IL-107378.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PA (ABRA/) ABRAMOVICH C.
 PI Abramovich C, Ratovitski E, Revel M;
 DR WPI: 95-200634/27.
 PT New mammalian soluble interferon alpha-receptor forms - used for
 PT inhibiting, modulating or modifying the activities of interferon(s)
 PS Example 3; Fig 7; 46pp; English.

CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 2
 CC (W21806) is characterised by a double deletion when compared to
 CC transmembrane IFNAR (W21804). The extracellular domain is
 CC shortened by 6 amino acid residues and is followed by a truncated
 CC intracellular domain. There is no transmembrane region. The amino
 CC acid sequence is predicted from a cDNA clone (see also T73521) obtd.
 CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR
 CC splice-deleted forms 1 (see also W21805) and 2 may regulate the
 CC response of human cells to IFNs, either by acting as IFN
 CC antagonists or by regulating IFN activities. They can be expressed
 CC in host cells and used to inhibit, modulate or modify the
 CC activities of IFNs alpha and beta in cells, tissues and organisms,
 CC or for diagnostic purposes.
 SO Sequence 496 AA;

alignment_scores: Length: 67
 Quality: 340.00 Gaps: 0
 Ratio: 5.075
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-240-675-1_COPY_1_229 x W21806

Align seg 1/1 to: W21806 from: 1 to: 496

```

27 ATGATGTCGTCCTCCTGGCGCGAGACCCCTAGTCTGCTCCGCGGTGG 76
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValAl 17
77 CCCATGGGTGTGTCCGACGCCGAGTGGAATAATCTAAATCTCTC 126
|||||
17 yProTPrValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerPro 34
127 AAAAATAGAGTCGACATCATGATGACAACTTATCTGAGGTGGAAC 176
|||||
34 InlysvAlaIuValAspIleIleAspAspAsnPhelLeuValArgTTPAsn 50
177 AGGAGCGATGAGTCTGTCCGGAATGTGACTTTTCATTGCATTATCAAA 226
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnly 67
227 A 227
67 s 67

```

seq_name: A_Geneseq_36:R11958

seq_documentation_block:

ID R11958 standard; Protein: 557 AA.
 AC R11958;
 DT 18-JUL-1991 (first entry)
 DE Human alpha-interferon receptor protein.
 KW Human alpha IFN; IFN agonists; antiviral; anti tumour agent;
 KW drug targeting.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT peptide 1..27
 FT /label= signal peptide
 PN WO9105862-A.
 PD 02-MAY-1991.
 PF 19-OCT-1990; F00758.
 PR 20-OCT-1989; FR-013770.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 PA Mogensen KE, Uze G, Lutfalla G, Gresser I;
 DR WPI: 91-148740/20.
 DR N-PSDB: Q11701.
 PT New human alpha-interferon receptor protein - useful for testing
 PT interferon agonists and in treatment or diagnosis
 PS Disclosure: fig 4; 30pp; French.
 CC This recombinant human alpha interferon (IFN) receptor protein is
 CC useful for the testing of IFN agonists and for treatment and diag-
 CC nosis of viral diseases and tumours. Antibodies raised against

CC this protein can be used for blocking the receptor when required,
 CC eg where overexpression of alpha-IFN is harmful. The Abs are
 CC also useful for eg drug targeting. Variants of the protein,
 CC having residue 164 (Thr) replaced by Arg and an Asp inserted
 CC between residues 479 and 480, are also useful.
 SQ Sequence 557 AA;

alignment_scores:
 Quality: 340.00 Length: 67
 Ratio: 5.075 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_1_229 x R11958

Align seg 1/1 to: R11958 from: 1 to: 557

```

27 ATGATGTCGTCCTCGGCGCGACGACCTAGTCTGTCGCCCTGGG 76
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValAl 17
77 CCCATGGGTGTCGCCGACCCGACGAGTGAATAAATCTCCTC 126
|||||
17 yProTIPValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerPro 34
127 AAAAAGTAGAGTCGACATCATAGATGACACTTATCCTGAGGTGAC 176
|||||
34 InLysValGluValAspIleIleAspAspAsnPhelIleLeuArgTyrP 50
177 AGGAGCGATGAGTCTCGGGAATGTGACTTTTCATTCGATTATCAAA 226
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGln 67

```

227 A 227

67 s 67

seq_name: A_Geneseq_36:R14488

seq_documentation_block:

ID R14488 standard; Protein: 557 AA.
 AC R14488;
 DT 16-JAN-1992 (first entry)
 DE Complete interferon-alpha/beta receptor.
 KW IFN; autoimmune disease; graft rejection; histocompatibility.
 OS Homo sapiens.
 FT Key Location/Qualifiers
 FT domain 437..457
 FT /label= transmembrane
 FT 458..557
 FT /label= cytoplasmic
 FT FR2657881-A.
 PN 09-FEB-1991.
 PD 05-FEB-1990; 001298.
 PR 05-FEB-1990; FR-001298.
 PA (EUBR-) LAB EURO BIOTECHNO.
 PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE;
 PI Tovey MG, Uze G;
 PI WPI: 91-319778/44.
 DR N-PSDB: Q14240.
 PT New water-soluble polypeptide(s) with affinity for IFN-alpha and
 PT beta - used to treat e.g. lupus erythematosus, Behcet's disease,
 PT aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.
 PS Disclosure: Page 47: 52pp; French.
 CC The invention covers derivatives of the interferon-alpha and/or beta
 CC receptor obtained by deleting the transmembrane and cytoplasmic domains
 CC of the native receptor or by substitution. Potentially immunogenic
 CC epitopes are eliminated and the deriv. can be secreted from
 CC transformed cells. Soluble deriv.s block the activity of IFN alpha/beta
 CC and can be used to treat autoimmune diseases or to inhibit graft
 CC rejection. See also Q14239.
 SQ Sequence 557 AA;

alignment_scores:
 Quality: 340.00 Length: 67
 Ratio: 5.075 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_1_229 x R14488

Align seg 1/1 to: R14488 from: 1 to: 557

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27 ATGATGTCGTCCTCGGCGCGACGACCTAGTCTGTCGCCCTGGG 76
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValAl 17
77 CCCATGGGTGTCGCCGACCCGACGAGTGAATAAATCTCCTC 126
|||||
17 yProTIPValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerPro 34
127 AAAAAGTAGAGTCGACATCATAGATGACACTTATCCTGAGGTGAC 176
|||||
34 InLysValGluValAspIleIleAspAspAsnPhelIleLeuArgTyrP 50
177 AGGAGCGATGAGTCTCGGGAATGTGACTTTTCATTCGATTATCAAA 226
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGln 67

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227 A 227

67 s 67

seq_name: A_Geneseq_36:R28496

seq_documentation_block:

ID R28496 standard; Protein: 557 AA.
 AC R28496;
 DT 31-MAR-1993 (first entry)
 DE Sequence of a soluble form of the interferon (IFN) receptor
 DE with a high affinity for IFN-alpha and -beta.
 KW Interferon receptor; alpha-interferon; beta-interferon.
 OS Synthetic.
 PN WO9218626-A.
 PD 29-OCT-1992.
 PF 17-APR-1991; F00318.
 PR 17-APR-1991; WO-F00318.
 PA (EUBR-) LAB EURO BIOTECHNOLOGIE.
 PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,
 PI Tovey M, Uze G;
 PI WPI: 92-382110/46.
 DR N-PSDB: Q30533.
 PT Water soluble polypeptide(s) strongly bind interferon(s) alpha
 PT and beta - useful as immunosuppressants, for treating auto-immune
 PT diseases and transplant rejection
 PS Claim 3; Fig 2; 58pp; English.
 CC DNA encoding the water-soluble polypeptide with a high affinity for
 CC IFN-alpha and -beta is isolated by PCR, using appropriate
 CC oligonucleotides as primers and cloned cDNA as template.
 CC bacteriophage lambda ZAP, containing the entire coding sequence of
 CC the IFN-alpha and -beta receptor (Q30533), was incubated with oligos
 CC Q30534 and Q30535. R28496 represents the complete receptor. R28495
 CC lacks the transmembrane and cytoplasmic domains. Both forms bind
 CC IFN in the same way as antibodies so are immunosuppressants e.g. for
 CC treating autoimmune diseases and graft rejection. They lack the
 CC toxic side-effects of known immunosuppressants such as steroids.
 SQ Sequence 557 AA;

alignment_scores:
 Quality: 340.00 Length: 67
 Ratio: 5.075 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-240-675-1_COPY_1_229 x R28496 ..

Align seg 1/1 to: R28496 from: 1 to: 557

```

27 ATGATGCTGCTCTCTCGGCGCGAGACCCCTAGTGTCTGCTGCCGTGGG 76
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValAl 17
77 CCCATGGGTGTGTCGCCAGCCGAGGTGGAATAATCTAAATCTCCTC 126
|||||
17 yProtrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
127 AAAAAAGTAGAGTCGACATCATAGATGACAACTTATCCTGAGGTGGAA 176
|||||
34 InlyValGluValAlaSplilelleAspAspAsnPhelLeuArgTrpAsn 50
177 AGGAGCGATGAGTCTGCGGGAATGTGACTTTTCATTGATTAACA 226
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnly 67
227 A 227
|
67 s 67

```

seq_name: A_Geneseq_36:R42635

seq_documentation_block:

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ID R42635 standard; Protein; 557 AA.
AC R42635;
DT 20-APR-1994 (first entry)
DE Human interferon receptor.
KW IFN-R; extracellular domain; monoclonal antibody; viral infection;
KW cell proliferation; allograft rejection; systemic lupus erythematosus;
KW psoriasis; multiple sclerosis; Behcet's disease; aplastic anaemia;
KW immunodeficiency; measles virus; interferon alpha-beta.
OS Homo sapiens.
FT domain 1..436
FT key /label= extracellular domain
FT /note= "soluble, immunogenic form of IFN-R"
PN EP-563487-A.
PD 06-OCT-1993.
PE 31-MAR-1992; 400902.
PR 31-MAR-1992; EP-400902.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
PI Benoit P, Maguire D, Meyer F, Plavec I, Tovey MG;
DR WPI: 93-312951/40.
DR P-PSDB: R42635.
PT Monoclonal antibody to human interferon type-I receptor - having
PT neutralising activity against human type I interferon, used for
PT therapy and diagnosis
PS Disclosure: Fig.3; 21pp; English.
CC Monoclonal antibodies produced against soluble forms of the human
CC interferon alpha-beta receptor based on the full-length human IFN-R
CC sequence are claimed. The antibodies are useful for treatment and
CC prophylaxis of disorders involving cell proliferation and/or viral
CC infection.
SO Sequence 557 AA;

```

alignment_scores:

Quality:	340.00	Length:	67
Ratio:	5.075	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

alignment_block:

US-09-240-675-1_COPY_1_229 x R42635 ..

Align seg 1/1 to: R42635 from: 1 to: 557

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27 ATATGCTGCTCTCTCGGCGCGAGACCCCTAGTGTCTGCTGCCGTGGG 76
|||||

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1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValAl 17
77 CCCATGGGTGTGTCGCCAGCCGAGGTGGAATAATCTAAATCTCCTC 126
|||||
17 yProtrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
127 AAAAAAGTAGAGTCGACATCATAGATGACAACTTATCCTGAGGTGGAA 176
|||||
34 InlyValGluValAlaSplilelleAspAspAsnPhelLeuArgTrpAsn 50
177 AGGAGCGATGAGTCTGCGGGAATGTGACTTTTCATTGATTAACA 226
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnly 67
227 A 227
|
67 s 67

```

seq_name: A_Geneseq_36:R75356

seq_documentation_block:

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ID R75356 standard; Protein; 557 AA.
AC R75356;
DT 16-OCT-1995 (first entry)
DE Human IFN receptor.
KW IFN receptor; interferon receptor; interferon-alpha;
KW interferon-beta; monoclonal antibody; immunomodulator; AIDS.
OS Homo sapiens.
FT key Location/Qualifiers
FT domain 1..436
FT /label= Extracellular domain
PN W09507716-A.
PD 23-MAR-1995.
PE 16-SEP-1994; E03114.
PR 17-SEP-1993; EP-402279.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
PI Benizri EJ, Tovey MG;
DR WPI: 95-131187/17.
DR N-PSDB: Q86458.
PT Compn. of monoclonal antibodies against interferon receptor -
PT useful as immunomodulator, eg. for treating AIDS
PS Disclosure: Fig.3A-2B; 105pp; English.
CC The amino acid sequence of human interferon class I receptor is
CC given in R75356. A recombinant soluble form of the extracellular
CC domain of this receptor (R71723) has been used to raise
CC immunomodulatory monoclonal antibodies.
SO Sequence 557 AA;

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alignment_scores:

Quality:	340.00	Length:	67
Ratio:	5.075	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

alignment_block:

US-09-240-675-1_COPY_1_229 x R75356 ..

Align seg 1/1 to: R75356 from: 1 to: 557

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27 ATGATGCTGCTCTCTCGGCGCGAGACCCCTAGTGTCTGCTGCCGTGGG 76
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValAl 17
77 CCCATGGGTGTGTCGCCAGCCGAGGTGGAATAATCTAAATCTCCTC 126
|||||
17 yProtrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
127 AAAAAAGTAGAGTCGACATCATAGATGACAACTTATCCTGAGGTGGAA 176
|||||
34 InlyValGluValAlaSplilelleAspAspAsnPhelLeuArgTrpAsn 50
177 AGGAGCGATGAGTCTGCGGGAATGTGACTTTTCATTGATTAACA 226
|||||

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FT	modified_site	120. .125	/note="unique phosphorylation site"
FT	modified_site	135. .140	/note="common phosphorylation site"
FT	modified_site	180. .185	/note="unique phosphorylation site"
FT	modified_site	499. .504	/note="common phosphorylation site"
FT	modified_site	535. .540	/note="unique phosphorylation site"
FT	modified_site	537. .542	/note="common phosphorylation site"
FT	modified_site	593. .598	/note="common phosphorylation site"
FT	modified_site	623. .628	/note="common phosphorylation site"
FT	modified_site	627. .632	/note="common phosphorylation site"
FT	modified_site	648. .653	/note="unique phosphorylation site"
FT	modified_site	670. .675	/note="common phosphorylation site"
FT	modified_site	733. .738	/note="common phosphorylation site"
FT	modified_site	757. .762	/note="unique phosphorylation site"
FT	modified_site	813. .818	/note="common phosphorylation site"
FT	modified_site	899. .903	/note="unique phosphorylation site"
FT	modified_site	910. .915	/note="unique phosphorylation site"
FT	modified_site	969. .974	/note="common phosphorylation site"
FT	modified_site	1031. .1036	/note="common phosphorylation site"
FT	modified_site	1060. .1065	/note="unique phosphorylation site"
FT	modified_site	1241. .1246	/note="unique phosphorylation site"
FT	modified_site	1302. .1307	/note="common phosphorylation site"
FT	modified_site		/note="common phosphorylation site"
PN		NO9610629-A1.	
PD	11-APR-1996.		
PF	03-OCT-1995; U13041.		
PR	03-OCT-1994; US-317310.		
PA	(JOSL-) JOSLIN DIABETES CENT INC.		
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.		
PI	Pierce JH, Sun XJ, White MF;		
DR	WPI: 96-209351/21.		
NR	N-PSDB: T28293.		
PT	New Insulin receptor substrate polypeptide and corresp. nucleic acid		
PT	- vectors, antibodies etc., useful for diagnosis, treatment and		
PT	assessing risk of diabetes etc., also for drug screening		
PS	Disclosure: Page 47-53: 105pp; English.		
CC	Mouse insulin receptor substrate-2, or IRS-2 (R96999), is a		
CC	substrate for the insulin receptor, interleukin-4 receptor and		
CC	interleukin-15 receptor, and can be phosphorylated by these		
CC	receptors. It contains a number of phosphorylation sites in		
CC	common with IRS-1, showing the 2 proteins to be related. IRS-2		
CC	can be obt'd, e.g. by affinity purification from insulin-stimulated		
CC	PC-12 cells using immobilized SH2 domains of p85, or can		
CC	be expressed in transformed host cells carrying an encoding cDNA		
CC	sequence (T78293). Cells or animals having the IRS-2 transgene		
CC	can be used to study insulin-related disorders, e.g. type II		
CC	diabetes. IRS-2 can be used to raise antibodies and for drug		
CC	screening. 1321 AA;		
CC	Sequence		

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Percent Similarity: 44.444      Percent Identity: 29.167

alignment_block:
US-09-240-675-1_COPY_1_229/rev x R96994  ..

Align seg 1/1 to: R96994 from: 1 to: 1321

124 GGAGATTATAGATTTTTCACCTGGCGGGGGGAGACAACCCATGGGCC 75
|||||: :|||:|||||: :|||:|||||: :|||:|||||:
1029 GYAspIeNtYrYArgLeuProProlAsaSerAlaIaIaThSerGInGlyPr 1045
|||||: |||: :|||:|||||: :|||:|||||:
74 CACGGCGAGCAGCACACTAGGTCGTCTCGCCGCCAGA..... 40
|||||: |||: :|||:|||||: :|||:|||||:
1045 cYhrIaGlySerSerMet.SerSerGluProGlyspaSngIAspTyr 1061
40 ..... 40

1062 ThrGluMetAlaPheGlyValAlaAlaIaThrProProGlnProIleValAl 1078
39 .....GACGACCATCATCTGGGAGCC 18
: :|||:|||||: :
1078 aProProlYsProGluGlyAlaIaArgValAlaSerProThrSerGlyLeuL 1095
74 GCCGCAGATCCCTG 4
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1095 ySaArgLeuSerLeu 1099

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alignment_scores:      63.50      Length:      72
                    Quality:      Caps:      2
                    Ratio:      1.984
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34 IntysValGIuValaspIlelleaspaspaspheilleuArgTrpAsn 50

177 AGGAGCATGAGTCTCGGAAATGACTTTTTCATTTCATTAACAAA 226

51 ArgSeraspGluSerValGIyAsnValThrPheSerPheAspTyrGlnly 67

227 A 227

67 s 67

seq_name: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:US-08-307-588-2

seq_documentation_block:

; Sequence 2, Application US/08307588

; Patent No. 5919453

; GENERAL INFORMATION:

; APPLICANT: BENOIT, Patrick

; APPLICANT: MEYER, Francois

; APPLICANT: MAGUIRE, Deborah

; APPLICANT: PLAVEC, Ivan

; APPLICANT: TOVEY, Michael G.

; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON

; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington

; STATE: D.C.

; ZIP: 20007

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/307,588

; FILING DATE: 05-DEC-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/EP93/00770

; FILING DATE: 30-MAR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 92400902.0

; FILING DATE: 31-MAR-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Saxe, Bernhard D.

; REGISTRATION NUMBER: 28,665

; REFERENCE/DOCKET NUMBER: 17283/117/GUPL

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)672-5300

; TELEFAX: (202)672-5399

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 436 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-307-588-2

alignment_scores:

Quality: 340.00

Ratio: 5.075

Percent Similarity: 100.000

Length: 67

Gaps: 0

Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_1_229 x US-08-307-588-2 ..

Align seg 1/1 to: US-08-307-588-2 from: 1 to: 436

27 ATGATGCTGCTCCTCGGCGGACGACCCGTAGTGTGCTGCGCGTGG 76

|||||

1 MetMetValValIleuLeuClYAlaThrThrLeuValIleuValAlaValGI 17

77 CCCATGGGTGTTGTCGCCAGCCGACAGTGAAGAAAAATCTAAATCTCTC 126

17 yPrOTpValIleuSerAlaAlaIleGlyLysAsnLeuYsSerProG 34

127 AAAAAAGTAGAGTCCGACATCATGATGACACCTTATCTGAGGTGAGC 176

34 IntysValGIuValaspIlelleaspaspaspheilleuArgTrpAsn 50

177 AGGAGCATGAGTCTCGGAAATGACTTTTTCATTTCATTAACAAA 226

51 ArgSeraspGluSerValGIyAsnValThrPheSerPheAspTyrGlnly 67

227 A 227

67 s 67

seq_name: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:US-08-328-256-12

seq_documentation_block:

; Sequence 12, Application US/08328256

; Patent No. 5643749

; GENERAL INFORMATION:

; APPLICANT: REVEL, Michel

; APPLICANT: ABRAMOVICH, Carolina

; APPLICANT: RATOVIJSKI, Edward

; TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W., Suite 300

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/328,256

; FILING DATE: 24-OCT-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: IL 107378

; FILING DATE: 24-OCT-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: BROWDY, Roger L.

; REGISTRATION NUMBER: REVEL-13

; REFERENCE/DOCKET NUMBER: 25,618

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; INFO: 248633

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 496 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-328-256-12

alignment_scores:

Quality: 340.00

Ratio: 5.075

Percent Similarity: 100.000

Length: 67

Gaps: 0

Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_1_229 x US-08-328-256-12 ..

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Align seg 1/1 to: US-08-328-256-12 from: 1 to: 496

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27 ATATGATGCTCTCTCCGCGGCGGACACCGCTAGTCTGCTCCGCGG 76
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValAl 17
77 CCCATGGGTGTGTCGCGACCCGACAGTGGAATAAATCTAAATCTCTC 126
|||||
17 yProTPrValLeuSerAlaAlaIaGlyGlyLysAsnLeuLysSerPro 34
34 InLysValGluValAspIleIleAspAspAsnPhelIleLeuArgTrp 50
127 AGAGCGATAGCTCTCGGAATGTGACTTTTCATCGATATCAAAA 226
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheserPheAspTyrGln 67
227 A 227
67 s 67
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seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-328-256-10

seq_documentation_block:

Sequence 10, Application US/08328256

Patent No. 5643749

GENERAL INFORMATION:

APPLICANT: REVEL, Michel

APPLICANT: ABRAMOVICH, Carolina

APPLICANT: RATOVIKSKI, Edward

TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS

TITLE OF INVENTION: PREPARATION AND USE

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/328,256

FILING DATE: 24-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 11,107,378

FILING DATE: 24-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: REVEL-13

REFERENCE/DOCKET NUMBER: 25,618

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 557 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-328-256-10

alignment_scores: Quality: 340.00 Length: 67

Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_1_229 x US-08-328-256-10 ..

Align seg 1/1 to: US-08-328-256-10 from: 1 to: 557

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27 ATATGATGCTCTCTCCGCGGCGGACACCGCTAGTCTGCTCCGCGG 76
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValAl 17
77 CCCATGGGTGTGTCGCGACCCGACAGTGGAATAAATCTAAATCTCTC 126
|||||
17 yProTPrValLeuSerAlaAlaIaGlyGlyLysAsnLeuLysSerPro 34
34 InLysValGluValAspIleIleAspAspAsnPhelIleLeuArgTrp 50
127 AGAGCGATAGCTCTCGGAATGTGACTTTTCATCGATATCAAAA 226
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheserPheAspTyrGln 67
227 A 227
67 s 67
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seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-471-454-2

seq_documentation_block:

Sequence 2, Application US/08471454

Patent No. 5731169

GENERAL INFORMATION:

APPLICANT: MOGENSEN, Knud E.

APPLICANT: UZE, Gilles

APPLICANT: LUTFALLA, Georges

APPLICANT: GRESSER, Ion

TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR

TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE

TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,454

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/900,642

FILING DATE: 15-JUN-1992

APPLICATION NUMBER: FR 89/13770

FILING DATE: 20-OCT-1989

ATTORNEY/AGENT INFORMATION:

NAME: BRINE, THOMAS E.

REGISTRATION NUMBER: 32,205

REFERENCE/DOCKET NUMBER: 960-7

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

TELEX: 200797 NIXN UR

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-454-2

alignment_scores:
Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-240-675-1_COPY_1_229 x US-08-471-454-2 ..

Align seg 1/1 to: US-08-471-454-2 from: 1 to: 557

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27 ATGATGTCCTCTCTGCGCGCAGACCTAGTCCTGCGCGG 76
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1 Metetvalvalleuleuglyalathrthrleuvalalavalgl 17
77 CCATGGGTGTTCGCCGAGCCGAGTGAAAAATCTAAATCTCCTC 126
|||||
17 yprotipvalleuseralaaalaglyglylsasnleuylsserproG 34
127 AAAAGTAGAGTCGACATCATAGATGACAATTATCTGAGGTGGAAC 176
|||||
34 lnlysvaigluvalaspllelleaspaspasnphelleuargtrpsn 50
177 AGGAGCGATGAGTCCTGCGGGAATGTGACTTTTCATTCGATTATCAAAA 226
|||||
51 Argseraspgluservalgllyasnvalthrpheserpheasptyrglnly 67
227 A 227
67 s 67
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seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-466-974-2

seq_documentation_block:

Sequence 2, Application US/08466974
Patent No. 5861258
GENERAL INFORMATION:
APPLICANT: MOGENSEN, Knud E.
APPLICANT: UZE, Gilles
APPLICANT: LUTFALLA, Georges
TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHUYE P. C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,974
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989

ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-466-974-2

alignment_scores:
Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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US-09-240-675-1_COPY_1_229 x US-08-466-974-2 ..

Align seg 1/1 to: US-08-466-974-2 from: 1 to: 557

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27 ATGATGTCCTCTCTGCGCGCAGACCTAGTCCTGCGCGG 76
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1 Metetvalvalleuleuglyalathrthrleuvalalavalgl 17
77 CCATGGGTGTTCGCCGAGCCGAGTGAAAAATCTAAATCTCCTC 126
|||||
17 yprotipvalleuseralaaalaglyglylsasnleuylsserproG 34
127 AAAAGTAGAGTCGACATCATAGATGACAATTATCTGAGGTGGAAC 176
|||||
34 lnlysvaigluvalaspllelleaspaspasnphelleuargtrpsn 50
177 AGGAGCGATGAGTCCTGCGGGAATGTGACTTTTCATTCGATTATCAAAA 226
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51 Argseraspgluservalgllyasnvalthrpheserpheasptyrglnly 67
227 A 227
67 s 67
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seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-471-453-2

seq_documentation_block:

Sequence 2, Application US/08471453
Patent No. 586153
GENERAL INFORMATION:
APPLICANT: MOGENSEN, Knud E.
APPLICANT: UZE, Gilles
APPLICANT: LUTFALLA, Georges
TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHUYE P. C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,453
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-453-2

alignment_scores:
Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-240-675-1_COPY_1_229 x US-08-471-453-2 ..

Align seg 1/1 to: US-08-471-453-2 from: 1 to: 557

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77 CCATGGGTGTGTCCGCGAGCGAGTGAATAAATCTCAATCTCTC 126
|||||
17 yProTrrValLeuSerAlaAlaAlaGlyGlyAsnLeuLysSerPro 34
127 AAAAGTAGAGGTGACATCATAGATGACAACTTATCTGAGTGAAC 176
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34 InLysValGluValAlaSpIleIleAspAspAsnPhelLeuArgTrpAsn 50
177 AGAGCGATGAGTCTGCGGGAATGACTTTTCATTGATTCATAAA 226
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51 ArgSerAspLysSerValGlyAsnValThrPheSerPheAspTrpGln 67
227 A 227
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67 s 67
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seq_documentation_block:
Sequence 4, Application US/08307588
Patent No. 5919453

GENERAL INFORMATION:
APPLICANT: BENOIT, Patrick
APPLICANT: MEYER, Francois
APPLICANT: MAGUIRE, Deborah
APPLICANT: PLAVEC, Ivan
APPLICANT: TOVEY, Michael G.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
TITLE OF INVENTION: INTERFERON
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
ZIP: 20007

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (ERO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00770
FILING DATE: 30-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92400902.0
FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 17283/117/GUPL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-307-588-4

alignment_scores:
Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-240-675-1_COPY_1_229 x US-08-307-588-4 ..

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77 CCATGGGTGTGTCCGCGAGCGAGTGAATAAATCTCAATCTCTC 126
|||||
17 yProTrrValLeuSerAlaAlaAlaGlyGlyAsnLeuLysSerPro 34
127 AAAAGTAGAGGTGACATCATAGATGACAACTTATCTGAGTGAAC 176
|||||
34 InLysValGluValAlaSpIleIleAspAspAsnPhelLeuArgTrpAsn 50
177 AGAGCGATGAGTCTGCGGGAATGACTTTTCATTGATTCATAAA 226
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51 ArgSerAspLysSerValGlyAsnValThrPheSerPheAspTrpGln 67
227 A 227
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67 s 67
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seq_name: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:PCT-US94-14277-3

seq_documentation_block:
Sequence 3, Application PC/TUS9414277
GENERAL INFORMATION:
APPLICANT: Aguet, Michel
APPLICANT: Bohnl, Ruth

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NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,412A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Mackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 015280-229000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEO ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 543 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
FEATURE:
NAME/KEY: Protein
LOCATION: 1..543
OTHER INFORMATION: /note= "mutine ERF amino acid sequence
OTHER INFORMATION: (first 8 amino acids from first exon not
US-08-469-412A-7 included)"
Alignment_scores:
Quality: 65.00 Length: 32
Ratio: 2.826 Gaps: 1
Percent Similarity: 71.875 Percent Identity: 43.750
Alignment_block:
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Align seg 1/1 to: US-08-469-412A-7 from: 1 to: 543
108 TTCACCTGCGGGCTGCAGCAACCCATGGGCCGAGGAGAGACT 59
||| :::::||::| ||:::||| ||:::|||||
367 PhelyspheylsleuglnpropropoleuglyArgargglnargalaa1 363
58 AGGCGCTGCCCCCGCAGAGA....CGACCATCATCTGGGAGC 19
||||::::| | ||||| |::| ||:::|||||
363 aglyglutysalaproglyglthrapsysserSerglyglYser 398
seq_name: /cgn2_6/ptodata/1/lac/5B-COMB.pep:US-08-317-310A-64
seq_documentation_block:
; Sequence 64, Application US/08317310A
; Patent No. 5858701
GENERAL INFORMATION:
APPLICANT: WHITE, Morris F.
APPLICANT: SUN, Xiao Jian
APPLICANT: PIERCE, Jacalyn H.
TITLE OF INVENTION: THE IRS FAMILY OF GENES
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston

```

```

: GENERAL INFORMATION:
: APPLICANT: Pestka, Sidney
: APPLICANT: Kotenko, Sergei
: TITLE OF INVENTION: CYTOKINE RECEPTOR SIGNAL TRANSDUCTION
: TITLE OF INVENTION: CHAIN
: NUMBER OF SEQUENCES: 25
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: David A. Jackson, Esq.
: STREET: 411 Hackensack Ave, Continental Plaza, 4th
: STREET: Floor

```

```

1 GENERAL INFORMATION:
2
3 APPLICANT: Williamson, Kim C.
4
5 APPLICANT: Kaslow, David C.
6
7 TITLE OF INVENTION: Cloning and Expression of Plasmidum
8
9 TITLE OF INVENTION: Falliciparum Transmission-Blocking Target Antigen, Pfs230
10
11 NUMBER OF SEQUENCES: 4
12
13 CORRESPONDENCE ADDRESS:
14
15 ADDRESSEE: Townsend and Townsend and Crew LLP
16
17 STREET: Two Embarcadero Center, 8th Floor
18
19 CITY: San Francisco
20

```

```
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,170B
FILING DATE: 13-OCT-1994
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/010,409
FILING DATE: 29-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Quine, Jonathan A.
REGISTRATION NUMBER: P-41,261
REFERENCE/DOCKET NUMBER: 015280-113100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-323-170B-2
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alignment_scores:
Quality: 59.00 Length: 51
Ratio: 1.844 Gaps: 3
Percent Similarity: 62.745 Percent Identity: 37.255
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alignment_block:
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Align seg 1/1 to: US-08-323-170B-2 from: 1 to: 3135
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787 serglaspilleglylleleupheprolysasnileyssthrth 803
128 AAAAGTAGAGTCGACATCATAGATGACAACTTATCTCTGAGGGAACA 177
||||| |||||
803 rcyspheglu...glumetilleprotyrAsnLysgluileystpAsnL 819
178 GGAGCGATGACTGTGCGGAAT...GTGACTTTTCATTCGATTATCAA 224
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819 ysgluAsnLysSerleuclLysnleuValAsnSerValValtyrAsn 835
225 AAA 227
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836 Lys 836
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seq_documentation_block:
Sequence 7, Application US/08469427A
Patent No. 5607918
GENERAL INFORMATION:
APPLICANT: Eriksson, Ulf
APPLICANT: Olofsson, Birgitta
APPLICANT: Alltalo, Kari
APPLICANT: Pajusola, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
```

```
CITY: Washington
STATE: DC
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,427A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 41979cp2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 195 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: adult mouse heart
US-08-469-427A-7
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alignment_scores:
Quality: 58.00 Length: 70
Ratio: 1.611 Gaps: 2
Percent Similarity: 51.429 Percent Identity: 24.286
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83 ProAspAspIleuGlucysValProthrglyGlnHisGlnValArgme 99
64 TCGGCGCCGCGGAGCGGCGGTGTGCGGACGCCGAGGTGGAATAAT 113
||||| |||||
99 tGlnValProGlyProMetclGlnIleuMetIleGlnItyrProSer 116
114 CTAATCTCTCTCAAAAGTAGAGTCGACATCATAGATGACAACTTAT 163
||||| |||||
116 erGlnLeuGlyGlnMetSerLeuGlnIleuHisSerGlnGlyProSer 132
164 CCGAGAGTGAACAGAG.....CGATGATCTG 192
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193 TCGGGAATG 202
149 sProProCys 152
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Sequence 7, Application US/08609443B
Patent No. 5840693
GENERAL INFORMATION:
APPLICANT: ERIKSSON, ULF
APPLICANT: OLOFSSON, Birgitta
```

APPLICANT: ALITALO, Karl
 APPLICANT: PAJUSOLA, Katri
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
 TITLE OF INVENTION: DNA CODING THEREFOR
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Evenson, McKown, Edwards & Lenahan, P.L.L.C.
 STREET: 1200 G Street, N.W., Suite 700
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/609,443B
 FILING DATE: 01-MAR-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/397,651
 FILING DATE: 01-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/469,427
 FILING DATE: 06-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/569,063
 FILING DATE: 06-DEC-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: EVANS, Joseph D
 REGISTRATION NUMBER: 26,269
 REFERENCE/DOCKET NUMBER: 1064/41979CP4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 628-8800
 TELEFAX: (202) 628-8844
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 195 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 TISSUE TYPE: adult mouse heart
 US-08-609-443B-7

alignment_scores:
 Quality: 58.00 Length: 70
 Ratio: 1.611 Gaps: 2
 Percent Similarity: 51.429 Percent Identity: 24.286

alignment_block:
 US-09-240-675-1_COPY_1_229 x US-08-609-443B-7 ..

Align seg 1/1 to: US-08-609-443B-7 from: 1 to: 195

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 64 TCGTCCCGCGGCGCATGGCTGTTCGCCGACGCCGAGGTGGAATAAT 113
 |||||
 99 tGlnValProGIyPrometGIyGlnIleuMetIleGlnItyProSerS 116
 114 CTAAATCTCTCTCAAAAAGTAGAGTGCAGACATCATAGATGACAATTAT 163
 |||||
 116 erGlnLeuGIyGlnMetSerLeuGIuGlnHisSerGlnGlnGlnGlnArg 132
 164 CCTGAGGTGAGACAGAG.....CGATGAGTCTG 192

|||||
 133 ProTylsTylsGlnSerAlaValIysProAspSerProArgIleuGly 149
 193 TCGGGAATGT 202
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 149 sProProCys 152

Mon Jun 5 12:51:10 2000

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Date: Jun 1, 2000 12:36 AM

About: Results were produced by the GenCore software, version 4.5.
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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-O/cg2_1/USFTO.spool/US09240675/runat_30052000_164312_24623/app_query.fasta.1
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-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
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Search information block:

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Query length: 229
Database: PIR_63:.*
Database sequences: 168808
Database length: 58629743
Search time (sec): 85.570000

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PIR2:A5283	+	198.00	415.38	5.0e-16	590	interferon alpha/beta receptor
PIR2:S13141	-	77.00	155.07	0.3143	294	hypothetical protein (ribosomal
PIR2:T09357	-	77.00	154.79	0.3151	304	hypothetical protein F33K16.40
PIR2:J05807	-	71.00	133.16	1.85	828	trp3 protein - rat
PIR2:S42718	-	69.00	123.91	3.41	1475	nuclear pore complex protein P
PIR2:T6381	+	68.50	139.87	3.35	194	hypothetical protein Y105CB.0
PIR2:T08930	+	67.50	133.03	5.09	1106	hypothetical protein 119.5K protein (U
PIR2:D00405	+	63.00	123.09	9.78	571	hypothetical protein T15N24.90
PIR2:D2866	+	63.50	126.67	14.00	252	major polyhedral calyx protein
PIR2:T13088	-	63.00	117.73	17.36	640	DNA-packaging protein - phage N
PIR2:A45731	+	62.50	129.36	17.73	141	comt-alpha protein - chicken
PIR2:B42701	+	62.50	125.58	18.37	221	PR264 protein - mouse
PIR2:T02841	+	62.50	122.31	18.95	326	probable membrane protein MTCC
PIR2:T04418	+	62.50	121.43	19.10	361	MHC class I histocompatibility
PIR2:A56391	+	62.00	114.43	23.26	730	phospholipase C (EC 3.1.4.3) -
PIR2:T30255	+	62.00	111.27	23.96	1062	inversin - mouse
PIR2:A42701	+	61.50	123.38	24.36	221	PR264/SC35 protein - human
PIR2:A42634	+	61.50	123.38	24.36	221	splicing factor SC35 - human
PIR2:A47003	+	61.50	121.60	24.77	273	cytokine receptor family II, me
PIR2:S14054	+	61.50	120.13	25.12	325	cytokine receptor family class
PIR2:A70525	-	61.50	115.26	26.30	580	CLN3 protein - yeast (Saccharom
PIR2:A70525	-	61.50	114.70	26.44	620	hypothetical protein RV0312 - M
PIR2:A44831	-	61.50	110.83	27.42	129	phosphoenolpyruvate carboxylase
PIR2:T35511	-	60.50	128.71	30.95	129	hypothetical protein SC1A9.25C
PIR2:T35511	-	60.50	117.56	33.42	340	DNA-directed RNA polymerase alp
PIR2:T35511	-	60.50	117.56	33.42	340	hypothetical protein F08D12.9
PIR2:T35511	-	60.50	109.17	38.27	1880	tractin - medicinal leech
PIR2:T09555	+	60.00	118.39	37.79	270	probable cytochrome P450 monoox
PIR2:T09518	+	60.00	115.54	38.82	379	hypothetical protein T25F10.2
PIR2:T09518	+	60.00	114.78	39.10	415	O-antigen transporter - Escheri
PIR2:J06496	-	60.00	111.45	40.34	616	cytochrome-c oxidase (EC 1.9.3.
PIR2:J06496	-	60.00	110.12	40.85	722	phosphate acetyltransferase - D
PIR2:J06496	-	60.00	107.43	41.90	994	c-mer tyrosine kinase receptor
PIR2:J06496	-	60.00	99.93	44.96	2424	calcium channel BI-2 - rabbit
PIR2:B24853	+	59.50	128.07	39.32	75	hypothetical protein (transducti
PIR2:B24853	+	59.50	125.00	40.47	108	hypothetical protein APE0658 -
PIR2:T24003	+	59.50	115.61	44.21	330	hypothetical protein R07B5.3 -
PIR2:S11143	+	59.50	115.36	44.32	340	class I histocompatibility anti

seq_name: PIR2:A32694
seq_documentation_block:
interferon alpha/beta receptor precursor - human
C:Species: Homo sapiens (man)
C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 22-Oct-1999
C:Accession: A32694; S17112
R:Uze, G., Lutfalla, G., Gresser, I.
Cell 60, 225-234, 1990
A:Title: Genetic transfer of a functional human interferon alpha receptor into mouse
A:Reference number: A32694; MUID:90124632
A:Accession: A32694
A:Molecule type: mRNA
A:Residues: 1-557 <UZE>
A:Cross-references: GB:J03171; NID:g184645; PIDN:AAA52730.1; PID:g306914
A:Submitted to the EMBL Data Library, July 1991
A:Description: The structure of the human interferon alpha/beta receptor gene.
A:Reference number: S17112
A:Accession: S17112
A:Molecule type: DNA
A:Residues: 1-16, 'A', 18-329, 'V', 343-557 <UT>
A:Cross-references: EMBL:X60459; NID:g32671
A:Gene: GDB:IFNAR1; IFNAR: IFRC
A:Cross-references: GDB:120078; OMIM:107450
A:Map position: 21q22.1-21q22.1
A:Intons: 26/1, 67/2, 126/1, 177/3, 225/1, 263/2, 342/1, 381/3, 432/1, 480/3
A:Keywords: cytokine receptor; glycoprotein; transmembrane protein
F:1-21/Domain: transmembrane #status predicted <TRN2>
F:437-455/Domain: transmembrane #status predicted <TRN2>
F:50,58,81,88,110,172,254,313,314,376,416,433,507,518,537/Binding site: carboxydrate

alignment_scores:

Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_1_229 x A32694 ..
Align seg 1/1 to: A32694 from: 1 to: 557

27	ATGATGCGTCGTCCTGCGGCGGAGCCGCTAGTGCCTGCGCGGCGG	76
1	MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG	17
77	CCCATGGGTGTGTCGCGGCGGAGCGGAGTGAATAAATCTAAATCTCTC	126
17	ProTirPAlaLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG	34
127	AAAAAGTAGAGGTGCATCATATGATGCAACTTATCTCTAGGTGGAAC	176
34	InLysValGLeuValAlaSplLeuLeuAspAsnPhelLeuAlaGlyTyrP	50
177	AGGACGATGAGTCTGTCGGGAATGTGACTTTTCATCGATTATCAAAA	226
51	AGGSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnL	67
227	A 227	
67	S 67	
seq_name: PIR2:S27387		
seq_documentation_block:		
interferon alpha receptor type 1 precursor - bovine		

C:Species: Bos primigenius taurus (cattle)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C:Accession: S27387; S33770
 R:Mouchel-Vielh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G.
 FEBS Lett. 313, 255-259, 1992
 A:Title: Specific antiviral activities of the human alpha interferons are determined at
 A:Reference number: S27387; MUID:93076908
 A:Accession: S27387
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-560 <MOU>
 A:Cross-references: EMBL:X68443; NID:9431; PIDN:CAA48484.1; PID:9432
 R:Experimental source: MDBK cells
 R:Lim, J.K.; Langer, J.A.
 Biochim. Biophys. Acta 1173, 314-349, 1993
 A:Title: Cloning and characterization of a bovine alpha interferon receptor.
 A:Reference number: S33770; MUID:93305725
 A:Accession: S33770
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-421, 'V', 423-560 <LIM>
 A:Cross-references: EMBL:L06320; NID:9163187; PIDN:AAA02571.1; PID:9163188
 A:Experimental source: Lung
 C:Keywords: antiviral; cytokine receptor; transmembrane protein
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-560/Product: Interferon alpha receptor type 1 #status predicted <MAT>

alignment_scores: Quality: 209.00 Length: 65
 Ratio: 3.800 Gaps: 2
 Percent Similarity: 84.615 Percent Identity: 69.231

alignment_block:
 US-09-240-675-1_COPY_1_229 x S27387

Align seg 1/1 to: S27387 from: 1 to: 560

```

30 ATGGTGCCTCTCTGGCGGCGAGCAGCCTAGTGTCTGCGCGCCGCGGCC 79
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 MetleuAlaValValGlyAlaAlaSerGlyGluAlaAsnLeuLys...GlyAr 16
80 ATGGGTGTTGCCGAGCCGCGAGGTGGAATAAATCTAAATCTCTCTCAA 129
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
16 gtrPvalLeuProAlaAlaSerGlyGluAlaAsnLeuLys...ProGluA 32
130 AAGTAGAGTCGACATCATAGACAACTTATCTGAGGTGGAACAGG 179
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
32 snValGluIleHisIleIleAspAsnPhenLeuLysTyrPnsSer 48
180 AGCGATGAGTCTGTGGGAATGTGACTTTTCATTCGATTATCAA 224
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
49 SerSerGluSerValLysAsnValThrPheSerAlaAspTyrGln 63

```

seq_name: plr2:AA5283

seq_documentation_block:
 Interferon alpha/beta receptor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
 C:Accession: A45283; I48423; I48424; I48425; I48426; I48427; I48428; I48429
 R:Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudoun, D.; Mogensen, K.E.
 Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992
 A:Title: Behavior of a cloned murine interferon alpha/beta receptor expressed in homospere
 A:Reference number: A45283; MUID:92262522
 A:Accession: A45283
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-590 <UZE>
 A:Cross-references: GB:M89641; NID:9194111; PIDN:AAA37890.1; PID:9194112
 R:Lutfalla, G.; Uze, G.
 A:Note: sequence extracted from NCBI backbone (NCBIN:102354, NCBIPI:102357)
 Gene 148, 343-346, 1994

A:Title: Structure of the murine interferon alpha/beta receptor-encoding gene: high-1
 A:Reference number: I48423; MUID:95047447
 A:Accession: I48423
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 118-125 <RES>
 A:Cross-references: EMBL:U06237; NID:9497103; PIDN:AAA65003.1; PID:9755810
 A:Accession: I48424
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 127-224 <RE2>
 A:Cross-references: EMBL:U06238; NID:9497104; PIDN:AA01749.1; PID:9755811
 A:Accession: I48425
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 243-264 <RE3>
 A:Cross-references: EMBL:U06239; NID:9497106; PIDN:AAA65004.1; PID:9755812
 A:Accession: I48426
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 397-424 <RE5>
 A:Cross-references: EMBL:U06241; NID:9497110; PIDN:AAA65006.1; PID:9755812
 A:Accession: I48428
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 426-445 <RE6>
 A:Cross-references: EMBL:U06242; NID:9497112; PIDN:AAA65007.1; PID:9755813
 A:Accession: I48429
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 473-590 <RE7>
 A:Cross-references: EMBL:U06244; NID:9497114; PIDN:AAA65008.1; PID:9755815
 C:Genetics:
 A:Gene: IFNAR
 A:Introns: 177/3; 331/1
 C:Keywords: cytokine receptor; transmembrane protein

alignment_scores: Quality: 198.00 Length: 65
 Ratio: 3.536 Gaps: 0
 Percent Similarity: 86.154 Percent Identity: 55.385

alignment_block:
 US-09-240-675-1_COPY_1_229 x A45283

Align seg 1/1 to: A45283 from: 1 to: 590

```

30 ATGGTGCCTCTCTGGCGGCGAGCAGCCTAGTGTCTGCGCGCCGCGGCC 79
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 MetleuAlaValValGlyAlaAlaSerGlyGluAlaValLeuValAlaGlyAla 17
80 ATGGGTGTTGCCGAGCCGCGAGGTGGAATAAATCTAAATCTCTCTCAA 129
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 oTrPvalLeuProSerAlaAlaGlyGlyGluAlaAsnLeuLysProProGluA 34
130 AAGTAGAGTCGACATCATAGACAACTTATCTGAGGTGGAACAGG 179
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 snIleAspValTyrIleIleAspAsnTyrThrLeuLysTyrPnsSer 50
180 AGCGATGAGTCTGTGGGAATGTGACTTTTCATTCGATTATCAA 224
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51 HisGlyGluSerMetGlySerValThrPheSerAlaGluTyrArg 65

```

seq_name: plr2:SI3141

seq_documentation_block:
 hypothetical protein (ribosomal RNA repeat region) - Giardia lamblia

seq_name: pir2:S42718

seq_documentation_block:

nuclear pore complex protein nup153 - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S42718; S37477
R:McMorrow, I.; Bastos, R.; Horton, H.; Burke, B.
Biochim. Biophys. Acta 1217, 219-223, 1994
A:Title: Sequence analysis of a cDNA encoding a human nuclear pore complex protein, hnpf
A:Reference number: S42718; MUID:94154002
A:Accession: S42718
A:Molecule type: mRNA
A:Residues: 1-1475 <MCM>
A:Cross-references: EMBL:Z25535; NED:g406224; PIDN:CAAB0982.1; PID:g406225

alignment_scores:

Quality:	69.00	Length:	77
Ratio:	1.683	Gaps:	3
Percent Similarity:	53.247	Percent Identity:	33.766

alignment_block:

US-09-240-675-1_COPY_1_229/rev x S42718 ..

Align seg 1/1 to: S42718 from: 1 to: 1475

```
193 ACAGCATCAGCTCCTGTCACACCCAGGATTAATGTCATCATATGAT 144
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1248 ThSerGIserLeuPheSerGlnAspSerLysLeuAlaThrThrSer 1264
143 GTGCACCTCTACTTTTGGAGAGATTTCATCCACCTCGCGCTG 94
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1264 rSerThrGlyThrAlaValThrProPheValPheGlyProGlyAlaSerS 1281
93 CGACACACACC.....CATGGCCCGACGGCAGCAGC 62
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1281 eTrAsnAsnThrThrThrSerGlyPheGlyPheGlyAlaThrThrThrSer 1297
61 .....ACTAGGCTGCTCGCGCCAG 42
|||||:|||||:|||||:|||||:|||||:|||||:
1298 SerSerAlaGlySerSerPheValPheGlyThr.GlyProSerAlaProS 1314
41 GAGGAGCAGCATCATCTGGAGCCGCCGC 13
|||||:|||||:|||||:|||||:|||||:|||||:
1314 eTrAlaSerProAlaPheGlyAlaAsnGln 1323
```

seq_name: pir2:T26391

seq_documentation_block:

hypothetical protein Y105C5B.o - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T26391
R:McMurray, A.
Submitted to the EMBL Data Library, September 1999
A:Reference number: Z20208
A:Accession: T26391
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-194 <WIL>
A:Cross-references: EMBL:AL110479; NID:e1542153; PIDN:CA854363.1; CESP:Y105C5B.o
A:Experimental source: clone Y105C5B
C:Genetics:
A:Gene: CESP:Y105C5B.o
A:introns: 13/1: 56/3: 155/2

alignment_scores:

Quality:	68.50	Length:	56
Ratio:	1.756	Gaps:	2
Percent Similarity:	69.643	Percent Identity:	32.143

alignment_block:

US-09-240-675-1_COPY_1_229 x T26391 ..

Align seg 1/1 to: T26391 from: 1 to: 194

```
36 GTCTCCTGGGCGGAGACCTAGTGTCTGCTCCGCGGCGCCATGGT 85
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MetLeuLeuArgAlaAlaLeuLeuIlePheIleSer...AlaProTyrPva 16
86 GTTGCCCGCAGCCGCGAGTGGAAAAATCTAAATCTTCCTCAAAAAGTAG 135
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
16 IleuSerValThrValAllyAsnMetThrGlyTyrGlnIleuIlySileH 33
136 AGGTGCATCATAGATGACCACTTATCTGAGGTGGACAGAGCGAT 185
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
33 IStleAsnLeuLeu.....AsnGlyIleArgGlnIlyAsnAlaIleAsp 47
186 GAGTCTGTGGGAAATGTG 203
|||||:|||||:|||||:|||||:|||||:|||||:
48 GluGlnValAlaAlaAsnMet 53
```

seq_name: pir2:J00405

seq_documentation_block:

hypothetical 119.5K protein (uvra region) - Micrococcus luteus
N:Alternate names: ORF 1 protein
C:Species: Micrococcus luteus, Micrococcus lysodeikticus
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 18-Jun-1993
R:Shiota, S.; Nakayama, H.
Mol. Gen. Genet. 217, 332-340, 1989
A:Title: Micrococcus luteus homolog of the Escherichia coli uvra gene: identification
A:Reference number: S04781; MUID:89364717
A:Accession: J00405
A:Molecule type: DNA
A:Residues: 1-1106 <SHI>
A:Cross-references: EMBL:X15867
A:Note: all the codons between two in-frame stop codons are translated; the translate
A:Note: the gene encoding this protein overlaps uvra gene

alignment_scores:

Quality:	67.50	Length:	78
Ratio:	1.875	Gaps:	3
Percent Similarity:	46.154	Percent Identity:	30.769

alignment_block:

US-09-240-675-1_COPY_1_229/rev x J00405 ..

Align seg 1/1 to: J00405 from: 1 to: 1106

```
204 TCACATTCGCCGACAGACATCGCTCCTGTCACACCTCAGATAAAGTTG 155
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
36 SerProInnGlyGlnThrProValSerCysPro..... 46
154 TCATCTATGATGTGCACTCTACTTTTGGAGAGATTTTACATTTTTC 105
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
47 .....CysProProLeuCysTyrProArgArgAlaGlnIleuLeuH 60
104 ACCTCGGCGCTG.....CGACACACCCATGGGC 76
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
60 IShIsArgLeuLeuValArgArgArgGlyProArgArgArgProArgLeuArg 76
75 CCAGCGCAGCAGCAGCTAGGTGCGCGGCCCA.....GGAGGAGC 35
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
77 ProArgArgArgAlaLeuGlyArgAlaGlyProHisArgArgProGlyArg 93
34 ACCATCATCTGGAGCCGCCGAGATCCCTGCAG 1
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
93 gProArgAlaGlnProGlnGlyArgGlyCysGln 104
```

seq_name: pir2:T08930

```

seq_documentation_block:
  hypochemical protein T15N24.90 - Arabidopsis thaliana
  C:Species: Arabidopsis thaliana (mouse-ear cress)
  C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999
  C:Accession: T08930
  R:Bevan, M.; Zimmermann, W.; Gruenewald, A.; Mambuti, R.; Bancroft, I.; Mewes, H.W.; May
  submitted to the Protein Sequence Database, May 1999
  A:Reference number: Z16518
  A:Accession: T08930
  A:Molecule type: DNA
  A:Residues: 1-571 <BEV>
  A:Cross-references: EMBL:AL078465; GSPDB:GN00062; ATSP:T15N24.90
  A:Experimental source: cultivar Columbia; BAC clone T15N24
  C:Genetics:
  A:Gene: ATSP:T15N24.90
  A:Map position: 4
  A:Introns: 76/3; 90/3; 142/3; 311/1; 363/2; 415/2

alignment_scores:
  Quality: 65.00      Length: 68
  Ratio: 1.711        Gaps: 5
  Percent Similarity: 55.882  Percent Identity: 33.824

alignment_block:
  US-09-240-675-1_COPY_1_229 x T08930 ..

Align seg 1/1 to: T08930 from: 1 to: 571

23 CCAGATGATGCTGCTCTCTGCGCCGACGACCTAGTCTGTCGCCG 72
   |||||
353 ProAspPSP.....AspAspProPheSerLysArg 363
73 TCGGCCCATGGGT.....GTTCTCGCAGCGCGAGGT 104
   ||||
363 GARGMETGUGLYALAMETGLULETHRPROLEUVALYSPROILEARG 380
105 GGAATAAATCTAAATCTCTCTCAAAAAGTAGAGTGCATCATAGATGA 154
   |||||
380 LUPROARGVALVALGINTHRLSESR.GLUVALASPILEUUNSPAS 396
155 CAACITTTATCTGAGGTGACAGAGCATGAGTCTC.....GGCA 198
   |||||
396 polytyr.....ArgTTPARGLYSTYGLYGLYVALVALARGGLYA 411
199 AT 200
   ||
411 sn 411

seq_name: p1r2:D72866

seq_documentation_block:
  major polyhedral calyx protein - Autographa californica nuclear polyhedrosis virus
  C:Species: Autographa californica nuclear polyhedrosis virus, AcNPV
  A:Note: dsDNA virus
  C:Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 24-Nov-1999
  R:Avyres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
  Virology 202, 586-605, 1994
  A:Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.
  A:Reference number: A72850; MUID:94303173
  A:Accession: D72866
  A:Status: preliminary
  A:Molecule type: DNA
  A:Residues: 1-252 <AYR>
  A:Cross-references: GB:U22858; NID:9510708; PIDN:AAA66761.1; PID:9559200
  R:O'Neill, C.; Hupp, B.; Mueller, T.; Doerfler, W.
  J. Virol. 61, 3048-3057, 1987
  A:Title: Overlapping sets of viral RNAs reflect the array of polypeptides in the ECORI J
  A:Reference number: A43679; MUID:87311863
  A:Accession: C43679
  A:Status: preliminary
  A:Molecule type: DNA

```

```

A:Residues: 1-252 <DEL>
A:Cross-references: GB:M17548; NID:9808747; PIDN:AAA66805.1; PID:9808750
C:Genetics:
A:Gene: Ac-PE/pp14

alignment_scores:
  Quality: 63.50      Length: 73
  Ratio: 1.924        Gaps: 2
  Percent Similarity: 45.205  Percent Identity: 31.507

alignment_block:
  US-09-240-675-1_COPY_1_229/rev x D72866 ..

Align seg 1/1 to: D72866 from: 1 to: 252

228 TTTTGTGATATCGATGAAAAAGTCACATTCGCCAGCACTCATCGTC 179
   |||||
96 PheTYARGARGARGSERARGSERARGSERARGSERARGSERArgSe 112
178 CTGTCACACTCAGATAAGTTGCATCTATGATGACCTCTACTTT 129
   ||||
112 rargserProHts.....CysArgPro..... 119
128 TTGAGGAGATTTTACATTTTTCACCTCGCGCTGCGGACACACCCATG 79
   ||||
120 .....ArgserArgserProHtsCys 126
78 GGCCACGCGCGACGACACTAGGCTGTCGCGCCGACGACGACGACATC 29
   |||||
127 ArgProArgSerArgSerArgSerArgSerArgSerArgSerArgSer 143
28 ATCTGGAGCGCGCGCAGCA 10
   ||||
143 rserProArgArgGLYArg 149

seq_name: p1r2:T13088

seq_documentation_block:
  DNA-packaging protein - phage N15
  N:Alternate names: terminase large chain gp2
  C:Species: phage N15
  C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999
  C:Accession: T13088
  R:Hendrix, R.W.; Ravin, V.K.; Castjens, S.R.; Ford, M.E.; Ravin, N.V.; Smirnov, I.K.
  submitted to the EMBL Data Library, May 1998
  A:Reference number: Z17603
  A:Accession: T13088
  A:Status: preliminary; translated from GB/EMBL/DBJ
  A:Molecule type: DNA
  A:Residues: 1-640 <HEN>
  A:Cross-references: EMBL:AF064539; NID:93192683; PID:93192685; PIDN:AMC19038.1
  C:Genetics:
  A:Note: gene 2
  C:Superfamily: phage lambda DNA packaging protein A
  C:Keywords: DNA packaging

alignment_scores:
  Quality: 63.00      Length: 99
  Ratio: 1.340        Gaps: 4
  Percent Similarity: 47.475  Percent Identity: 26.263

alignment_block:
  US-09-240-675-1_COPY_1_229 x T13088 ..

Align seg 1/1 to: T13088 from: 1 to: 640

8 GATCTGCGCGCGCTCCAGATGATGATG..... 34
   |||||
101 GluLeuLeuTTPleuProThrAspGlyAspAlaAspAspMetLysSe 117
35 .....CGTCTCTGCGCGCGGACGACCTAGTCTGTCGCGCGTGGCC 77

```

```

117 rHsValGluProThrIleArgAspAlaProSerLeuLeuSerLeuAla 133
78 CCATCG.....GTGTGTCCGCA.....95
134 ProTrpTyrGlyLysLysHisArgAspAsnThrLeuSerMetLysArgPh 150
96 .....GCCCGAGGTGGAAAAAATCTAAATCTC 123
150 ethraSnglyArgGlyPheTrpCysLeuGlyLysAlaAlaLysAsn 167
124 CTCMAAAGTAGAGTCGACATCATAGACACTTATCTGAGAGTGG 173
167 yArgGluLysSerValAspValValGlyTyrAspGluLeuAlaAlaPha 183
174 MACAGAGCGCATGATCTGCGGAATGACCTTTTCATTCAT 218
184 AspAlaAspIleGluLysGluLysSerProThrPheLeuGlyAsp 198

```

seq_name: p1r2:A45731

seq_documentation_block:

```

comC: alpha protein - phage T4
N: Alternate names: gp comC alpha
C: Species: phage T4
A: Note: host Escherichia coli
C: Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 08-Oct-1999
C: Accession: A45731
R: Sanson, B.; Uzan, M.
J. Bacteriol. 174, 6539-6547, 1992
A: Title: Sequence and characterization of the bacteriophage T4 comCalpha gene product, a
A: Reference number: A45731; MUID:93015705
A: Accession: A45731
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-141 <SAS>
A: Cross-references: GB:M89919; NID:9215829; PIDN:AAA32485.1; PID:9215832
C: Genetics:
A: Gene: comC alpha
A: Map position: 5.848-6.274
C: Superfamily: phage T4 comC-alpha protein
C: Keywords: transcription regulation

```

```

alignment_scores:
  Quality: 62.50      Length: 50
  Ratio: 2.155        Gaps: 3
  Percent Similarity: 58.000  Percent Identity: 34.000

```

alignment_block:

US-09-240-675-1_COPY1_1_229 x A45731 ..

```

Align seg 1/1 to: A45731 from: 1 to: 141
42 CTGGGCGCGACCCCTAGTGTCTGTCGCGCGCCATGGGTGTGTC 91
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||
49 LeuGlyArgProThrLysIleMetThrSerIleGly.....ValLeuLys 63
92 CGCAGCCCGCGAGGTGGAAAAATCTAAATCTCTCAAAAAAGTAGAGTGC 141
:  |||  |||  |||  |||  |||  |||  |||  |||  |||
63 sArgCysAlaGlyGly.....A 69
142 ACATCATAGATGACACTTATCTGATGAGAGAGAGAGATGACTCT 191
|||||  |||  |||  |||  |||  |||  |||  |||  |||
69 sPleLeuAspGluAsnPhelle.....TrpLeuSerThrAsnGluAla 83

```

seq_name: p1r2:B42701

seq_documentation_block:

```

PR264 protein - chicken
C: Species: Gallus gallus (chicken)
C: Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 24-Sep-1999
C: Accession: B42701; S17327

```

```

R: Vellard, M.; Sureau, A.; Soret, J.; Martinerie, C.; Perbal, B.
Proc. Natl. Acad. Sci. U.S.A. 89, 2511-2515, 1992
A: Title: A potential splicing factor is encoded by the opposite strand of the trans-
A: Reference number: A42701; MUID:92212859
A: Accession: B42701
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-221 <VEL>
A: Cross-references: EMBL:X62446; NID:963751; PIDN:CAA44306.1; PID:963752
C: Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleopri
F: 15-82/Domain: ribonucleoprotein repeat homology <RRM2>

```

```

alignment_scores:
  Quality: 62.50      Length: 55
  Ratio: 2.083        Gaps: 3
  Percent Similarity: 54.545  Percent Identity: 38.182

```

alignment_block:

US-09-240-675-1_COPY1_1_229 x B42701 ..

Align seg 1/1 to: B42701 from: 1 to: 221

```

5 AGGATCTGCGG...CGGCTCCAGATGATGTCGTCCT.....43
|||||  |||  |||  |||  |||  |||  |||  |||  |||
83 ArgGluLeuArgValGlnMetAlaArgTyrGlyArgProAspSerH1 99
44 ....GGCGCGCGACCCCTAGTGTCTGTCGCGCGCCATGGTGTG 89
:  |||  |||  |||  |||  |||  |||  |||  |||
99 sHisSerArgArgGlyArgProArgArgArgTyrGlySerSerGlyTyrG 116
90 TCCGC.....AGCGCAGGTGGAAAAATCTAAATCTGCCA 127
|||  |||  |||  |||  |||  |||  |||  |||
116 LysArgSerArgSerProArgArgArgArgArgSerArgSerArgSer 132
128 AAAAGTAGAGTCTGA 142
|||  |||  |||  |||  |||  |||  |||  |||
133 ArgSerArgSerArg 137

```

seq_name: p1r2:T02841

seq_documentation_block:

```

probable membrane protein MTCC - Leishmania major
C: Species: Leishmania major
C: Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 10-Dec-1999
C: Accession: T02841
R: Myler, P.J.
submitted to the EMBL Data Library, May 1998
A: Description: The nucleotide sequence of Leishmania major Friedlin chromosome 1.
A: Reference number: 214740
A: Accession: T02841
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 1-326 <MYL>
A: Cross-references: EMBL:AE001274; NID:93264850; PID:91617564
C: Genetics:
A: Gene: MTCC
A: Map position: 1
C: Superfamily: Saccharomyces probable membrane protein YOR271c

```

```

alignment_scores:
  Quality: 62.50      Length: 66
  Ratio: 1.645        Gaps: 3
  Percent Similarity: 57.576  Percent Identity: 30.303

```

alignment_block:

US-09-240-675-1_COPY1_1_229 x T02841 ..

Align seg 1/1 to: T02841 from: 1 to: 326

```

12 TGGCGGCTCCAGATGATGTCGTCCTCG.....CG 46
|||||  |||  |||  |||  |||  |||  |||  |||

```

```

156 CysGcGlySerLeuLeuAlaIleThrMetTrpLeuLysArgIleProThrG 172
47 GCGCAGCAACCTAGTGCCTGC...GCCGTGGCCCATGGGTGTCCG 93
   ::::||||| ::::||||| :|||:::
172 yThrThrHisSerThrIleuIleArgAlaThrValProPheLeuAlaValS 189
94 CAGCCGCGAGGTGGAAAAATCTTAAATCTCCGCAAAAGTAGAG..... 137
   ::::|||||::: ||||| ||| ::::||| |||
189 eRcysAlaIleAlaThrValAsnLeuAlaSerMetCysArgAsnGluTrpLeu 205
138 .....GTGCACATCATAGATCAACAATTACTCTGAG 170
   ::::|||||::: ::::|||||::: :|||
206 SerSerGlyGlnGlyIleLeuArgValValaAspAspAspGlyValIleThrArg 221

```

OM of: US-09-240-675-1_COPY_1_229 to: SwissProt_38:.* out-format : pfs

Date: Jun 1, 2000 12:37 AM

About: Results were produced by the Gencore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL=frame+2p.model -DEV=xlp
-O=/cgn2_1/USPRO.spool/US09240675/runat_30052000_16413_24686/app-query.fasta.1
-DB=SwissProt_38 -OFMT=fasta -SUFFIX=modif -RSP -GAPOP=12.000
-GAPERT=0.000 -MINMATCH=0.100 -LOOPEL=0.000 -XGAPEXT=0.000
-GAPOP=4.500 -XGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-GAPOP=6.000 -XGAPEXT=7.000 -XGAPOP=10.000 -XGAPEXT=0.500
-DELDP=6.000 -DELDP=7.000 -STAR=1 -MATRIX=blomsum62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR_SCORE=pcr
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=1000000 -USER=US09240675 -NCPU=6 -ICPU=3 -NO_XLPRY -MATT
-THREADS=1

Search information block:

Query: US-09-240-675-1_COPY_1_229
Query length: 229
Database: SwissProt_38:.*
Database sequences: 83857
Database length: 30454973
Search time (sec): 45.030000

score_list:

Sequence	Strd Orig	ZScore	EScore	len	Documentation
SwissProt_38:INRI_HUMAN	340.00	695.87	6.5e-32	557	P17181 homo sapiens (human)
SwissProt_38:INRI_BOVIN	209.00	421.06	1.3e-16	560	O04790 bos taurus (bovine)
SwissProt_38:INRI_SHEEP	204.00	410.57	5.0e-16	560	O28589 ovis aries (sheep)
SwissProt_38:INRI_MOUSE	198.00	397.55	2.5e-15	590	P38996 mus musculus (mouse)
SwissProt_38:INRI_HUMAN	69.00	119.30	3.20	1475	P45790 homo sapiens (human)
SwissProt_38:INRI_HUMAN	68.00	121.79	4.02	854	O34971 ratthayabacter ratthayabacter
SwissProt_38:INRI_HUMAN	67.00	115.66	5.45	1382	O14152 homo sapiens (human)
SwissProt_38:INRI_HUMAN	65.50	121.32	7.54	483	O75069 homo sapiens (human)
SwissProt_38:INRI_HUMAN	65.00	119.17	8.71	551	P70459 mus musculus (mouse)
SwissProt_38:INRI_HUMAN	63.50	122.58	12.29	252	P24728 autographa californica
SwissProt_38:INRI_HUMAN	63.50	108.69	13.93	1321	P81122 mus musculus (mouse)
SwissProt_38:INRI_HUMAN	63.00	107.50	15.95	1344	P23116 mus musculus (mouse)
SwissProt_38:INRI_HUMAN	62.50	125.35	15.40	141	O01438 bacteriophage t4. contd
SwissProt_38:INRI_HUMAN	62.50	121.59	15.93	221	P30352 gallus gallus (chicken)
SwissProt_38:INRI_HUMAN	62.00	110.52	19.94	730	P06300 pseudomonas aeruginosa
SwissProt_38:INRI_HUMAN	61.50	119.49	20.84	221	O01130 homo sapiens (human)
SwissProt_38:INRI_HUMAN	61.50	116.26	21.46	325	O08334 homo sapiens (human)
SwissProt_38:INRI_HUMAN	61.50	111.40	22.41	580	P13365 saccharomyces cerevisiae
SwissProt_38:INRI_HUMAN	61.50	106.98	23.32	982	P28594 anabaena sp. (strain)
SwissProt_38:INRI_HUMAN	60.50	113.80	28.17	339	P72404 streptomyces coelicolor
SwissProt_38:INRI_HUMAN	60.00	111.06	32.72	415	P37745 escherichia coli. put
SwissProt_38:INRI_HUMAN	60.00	107.76	33.70	615	P16262 bacillus p33 (thermop)
SwissProt_38:INRI_HUMAN	60.00	96.26	37.37	2424	P27884 oryctolagus cuniculus
SwissProt_38:INRI_HUMAN	59.00	118.07	39.45	140	P23152 homo sapiens (human)
SwissProt_38:INRI_HUMAN	59.00	116.75	39.93	164	P23152 homo sapiens (human)
SwissProt_38:INRI_HUMAN	59.00	108.45	43.02	441	O080910 human papillomavirus t
SwissProt_38:INRI_HUMAN	59.00	107.47	43.40	496	P31360 homo sapiens (human)
SwissProt_38:INRI_HUMAN	59.00	94.23	48.88	2405	O33610 chlamydomonas reinhardtii
SwissProt_38:INRI_HUMAN	59.00	92.01	49.87	3135	O08372 plasmodium falciparum
SwissProt_38:INRI_HUMAN	58.50	98.87	53.13	1220	O15452 homo sapiens (human)
SwissProt_38:INRI_HUMAN	58.00	113.96	52.57	178	O57736 methanococcus jannasch
SwissProt_38:INRI_HUMAN	58.00	111.46	53.77	240	P19664 lotus tetragonolobus (c3.7)
SwissProt_38:INRI_HUMAN	58.00	108.61	55.16	337	P15893 spiroplasma vitruvii
SwissProt_38:INRI_HUMAN	58.00	107.47	55.73	386	P20599 eritricum aestivum (w)
SwissProt_38:INRI_HUMAN	58.00	106.47	56.24	435	P22533 brassica oleracea var
SwissProt_38:INRI_HUMAN	58.00	106.22	56.36	448	P46936 gallus gallus (chicken)
SwissProt_38:INRI_HUMAN	58.00	106.11	56.42	454	O080903 human papillomavirus t
SwissProt_38:INRI_HUMAN	58.00	105.75	56.60	474	O53305 mycobacterium tuberculosis
SwissProt_38:INRI_HUMAN	58.00	103.19	57.92	643	P06440 vaccinia virus (strain)
SwissProt_38:INRI_HUMAN	58.00	96.40	61.56	1446	P33479 pseudorabies virus (
SwissProt_38:INRI_HUMAN	58.00	96.31	61.61	1461	P11675 pseudorabies virus (

SwissProt_38:YAO2_SCHPO + 57.50 110.41 61.51 240 | O08675 schizosaccharomyces
SwissProt_38:SRA_MOUSE + 57.50 109.03 62.28 283 | O60701 mus musculus (mo
SwissProt_38:MMS3_MYCTU + 57.50 108.57 62.54 299 | O10390 mycobacterium tu
SwissProt_38:TAP_DROME + 57.50 106.17 63.90 398 | O16867 drosophila melano-

seq.name: SwissProt_38:INRI_HUMAN

seq-documentation_block:

ID	INRI_HUMAN	STANDARD:	PRT:	557 AA.
AC	P17181			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	15-FEB-2000 (Rel. 39, Last annotation update)			
DE	INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).			
GN	IFNARI OR IFNAR.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Catarrhini; Homnidae; Homo.			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 90124632.			
RA	Uze G., Lutfalla G., Gresser I.;			
RT	"Genetic transfer of a functional human interferon alpha receptor			
RL	into mouse cells: cloning and expression of its cDNA.";			
RL	Cell 60:225-234(1990).			
RN	(2)			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 92129376.			
RA	Lutfalla G., Gardiner K., Proudhon D., Vielh E., Uze G.;			
RT	"The structure of the human interferon alpha/beta receptor gene.";			
RL	J Biol. Chem. 267:2802-2809(1992).			
RN	(3)			
RP	PHOSPHORYLATION BY TYR2.			
RX	MEDLINE: 95059042.			
RA	Colamonici O., Yan H., Domanski P., Handa R., Smalley D.,			
RT	Millerman J., Witte M., Krishnan K., Krolewski J.;			
RL	Direct binding to and tyrosine phosphorylation of the alpha subunit			
RL	of the type I interferon receptor by p135tyk2 tyrosine kinase.";			
RL	Mol. Cell. Biol. 14:8133-8142(1994).			
CC	- FUNCTION: RECEPTOR FOR INTERFERON ALPHA AND BETA. BINDING TO TYPE			
CC	I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS			
CC	INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-			
CC	SUBUNIT THEMSELVES.			
CC	- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	- TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALL TISSUES AND			
CC	EVEN ON THE SURFACE OF MOST IFN-RESISTANT CELLS.			
CC	- PTM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYK2 TYROSINE KINASE.			
CC	- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.			
CC	- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.			
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: J03171; AAA52730.1; -			
DR	EMBL: X60459; CAA42992.1; -			
DR	PIR: A32694; A32694.			
DR	PIR: S17112; S17112.			
DR	MIM: 107450; -			
KW	Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism;			
KW	Phosphorylation.			
FT	SIGNAL 1 27			
FT	CHAIN 28 557			
FT	POTENTIAL INTERFERON-ALPHA/BETA RECEPTOR ALPHA			
FT	CHAIN.			
FT	DOMAIN 28 436			
FT	EXTRACELLULAR (POTENTIAL).			
FT	POTENTIAL.			
FT	CYTOSOLIC (POTENTIAL).			
FT	BY SIMILARITY.			
FT	DISULFID 79 87			
FT	BY SIMILARITY.			
FT	DISULFID 199 220			

```

FT MOD_RES 466 466 PHOSPHORYLATION (BY TYK2) (PROBABLE).
FT MOD_RES 481 481 PHOSPHORYLATION (BY TYK2) (PROBABLE).
FT CARBOHYD 50 50 POTENTIAL.
FT CARBOHYD 58 58 POTENTIAL.
FT CARBOHYD 81 81 POTENTIAL.
FT CARBOHYD 88 88 POTENTIAL.
FT CARBOHYD 110 110 POTENTIAL.
FT CARBOHYD 110 110 POTENTIAL.
FT CARBOHYD 172 172 POTENTIAL.
FT CARBOHYD 254 254 POTENTIAL.
FT CARBOHYD 313 313 POTENTIAL.
FT CARBOHYD 314 314 POTENTIAL.
FT CARBOHYD 376 376 POTENTIAL.
FT CARBOHYD 416 416 POTENTIAL.
FT CARBOHYD 433 433 POTENTIAL.
FT VARIANT 168 168 POTENTIAL.
FT CONFLICT 17 17 /FtId-VAR_002717.
SO SEQUENCE 557 AA: 63525 MW: 06744C8A1ADB73 CRC64:

```

```

Alignment_scores:
Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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Alignment_block:

US-09-240-675-1_COPY_1_229 x INRL_HUMAN

Align seg 1/1 to: INRL_HUMAN from: 1 to: 557

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27 ATGATGTCCTCTCTGCGCGAGACCTAGTCTGTCGCGCGG 76
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValAl 17
77 CCCATGGGCTGTCTGCGCGAGCGCGAGGTAATAATCTCTCTC 126
17 yProTTPValLeuSerAlaAlaAlaGlyLysAsnLeuLysSerProG 34
127 AAAAGTAGAGTCGACATCATAGATGACACTTATCTCTGAGGAGAC 176
34 InLysValGluValAlaAspIleIleAspAspAsnPhelIleLeuArgTrpAsn 50
177 AGGAGGATGAGTCTGTCGGGAGATGACTTTTCATTGATTATCAAA 226
51 ArgSerAspGluSerValGlyLysAsnValThrPheSerPheAspTyrGln 67
227 A 227
67 s 67

```

seq_name: SwissProt_38:INRL_BOVIN

seq_documentation_block:

```

ID INRL_BOVIN STANDARD: PRT: 560 AA.
AC 004790:
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IN-ALPHA-REC).
GN IFNARI OR IFNAR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LUNG:
RX Mouchel-Viehl E., Lutfalia G., Mogensen K.E., Uze G.:
RT "Specific antiviral activities of the human alpha interferons are
RT determined at the level of receptor (IFNAR) structure.",
RL FEBS Lett. 313:255-259(1992).
RN [2]

```

```

RP SEQUENCE FROM N.A.
RX MEDLINE: 93305725.
RA Lin J.-K., Langer J.A.:
RT "Cloning and characterization of a bovine alpha interferon receptor.";
RL Blochim. Biophys. Acta 1173:314-319(1993).
CC -I- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
CC I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
CC SUBUNITS THEMSELVES.
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -I- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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DR EMBL: X68443; CAA8484.1; -
DR EMBL: L06320; AAA02571.1; -
DR PIR: S33770; S33770.
DR PIR: S27387; S27387.
DR PIR: PF00041; fn3; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24 BY SIMILARITY.
FT CHAIN 25 560 INTERFERON-ALPHA/BETA RECEPTOR ALPHA
FT DOMAIN 25 437 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 438 458 POTENTIAL.
FT DOMAIN 459 560 CYTOPLASMIC (POTENTIAL).
FT DISULFID 76 84 BY SIMILARITY.
FT DISULFID 199 220 BY SIMILARITY.
FT CARBOHYD 47 47 POTENTIAL.
FT CARBOHYD 55 55 POTENTIAL.
FT CARBOHYD 85 85 POTENTIAL.
FT CARBOHYD 109 109 POTENTIAL.
FT CARBOHYD 172 172 POTENTIAL.
FT CARBOHYD 254 254 POTENTIAL.
FT CARBOHYD 313 313 POTENTIAL.
FT CARBOHYD 377 377 POTENTIAL.
FT CARBOHYD 434 434 POTENTIAL.
FT CONFLICT 422 422 F -> V (IN REF. 2).
SO SEQUENCE 560 AA: 63818 MW: 66076B72861E1D11 CRC64:

```

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Alignment_scores:
Quality: 209.00 Length: 65
Ratio: 3.800 Gaps: 2
Percent Similarity: 84.615 Percent Identity: 69.231

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Alignment_block:

US-09-240-675-1_COPY_1_229 x INRL_BOVIN

Align seg 1/1 to: INRL_BOVIN from: 1 to: 560

```

30 ATGTCGTCCTCTCTGCGCGAGACCTAGTCTGTCGCGCGGCC 79
1 MetLeuAlaLeuLeuGlyAlaThrThrLeuMetLeuValAla...GlyAr 16
80 ATGGTGTGTCGCGAGCGCGAGTGAATAAATCTAATCTGCTCAA 129
16 gTTPValLeuProAlaAlaSerGlyGluAlaAsnLeuLys...ProGluA 32
130 AAGTAGAGTCGACATCATAGATGACAACTTATCTGAGGTGAGAC 179
32 snValGluIleIleIleIleAspAspAsnPhelLeuLysTrpAsnSer 48
180 AGCGATGAGTCTGTCGGGAGATGACTTTTCATTGATTATCAAA 224
49 SerSerGluSerValLysAsnValThrPheSerAlaAspTyrGln 63

```



```

seq_name: SwissProt_38:INRL_SHEEP
seq_documentation_block:
ID INRL_SHEEP STANDARD: PRT; 560 AA.
AC 028589; 095206;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE INTERFERON ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC)
DE (INTERFERON ALPHA/BETA RECEPTOR-1).
GN IFNARI OR IFNAR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Caprinae; Ovis.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-ENDOMETRIUM.
RX MEDLINE: 97135690.
RA Kaluz S., Fisher P.A., Kaluzova M., Sheldrick E.L., Flint A.P.F.;
RT "Structure of an ovine interferon receptor and its expression in
RT endometrium."
RL J. Mol. Endocrinol. 17:207-215(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-ENDOMETRIUM.
RX MEDLINE: 98006426.
RA Han C.-S., Mathalagan N., Klemann S.W., Roberts R.M.;
RT "Molecular cloning of ovine and bovine type I interferon receptor
RT ribonucleic acid for ovine receptors during the estrous cycle and
RT pregnancy."
RL Endocrinology 138:4757-4767(1997).
CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
CC I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
CC SUBUNITS THEMSELVES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT
CC CONCEPTUS AT DAY 15 OF PREGNANCY.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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CC -----
DR EMBL: X95939; CA65183.1; -
DR EMBL: U65978; AAB84231.1; -
DR PFM: PFD0041; fn3; 1.
KM Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 560
FT DOMAIN 25 437
FT TRANSMEM 438 458
FT DOMAIN 459 560
FT DISULFID 76 84
FT DISULFID 199 220
FT CARBOHYD 47 47
FT CARBOHYD 55 55
FT CARBOHYD 85 85
FT CARBOHYD 108 108
FT CARBOHYD 109 109
FT CARBOHYD 172 172
FT CARBOHYD 222 222
FT CARBOHYD 285 285
FT CARBOHYD 313 313

```

```

FT CARBOHYD 359 359 POTENTIAL.
FT CARBOHYD 377 377 POTENTIAL.
FT CARBOHYD 434 434 POTENTIAL.
FT CONFLICT 352 352 S -> G (IN REF. 2).
FT CONFLICT 522 522 A -> D (IN REF. 2).
SQ SEQUENCE 560 AA; 63918 MW; E7198A1905D4805C CRC64;

alignment_scores:
Quality: 204.00 Length: 65
Ratio: 3.778 Gaps: 2
Percent Similarity: 83.077 Percent Identity: 69.231

alignment_block:
us-09-240-675-1_copy_1_229 x INRL_SHEEP
Align seg 1/1 to: INRL_SHEEP from: 1 to: 560

30 ATGTCGCTCCTCGGCGGAGACCCCTAGTGTCTGCGCCGTCGCGCC 79
||||| ||||||| ||||||| ||||||| |||
1 MetuenseleuenglyAlaThrleuMetleuVala...GIYar 16
80 ATGGGTGTGTCGCCAGCCAGGTGGAATAAATCTAAATCTCTCAAA 129
||||| ||||||| ||||||| |||
16 gtrpvalleuproAlaAlaSerlyguaAlaSerleuLysSer...GIUA 32
130 AAGTAGAGTCGACATCATGACAACTTATCTGTAGTGGAACAGG 179
||||| ||||||| ||||||| ||||||| |||
32 snvalgluilehstlelleapspasnphetheulystripasnSer 48
180 AGCAGTAGTGTGCGGGAATGACATTTTCATTCATATCAAA 224
||||| ||||||| ||||||| |||
49 SersegiusevalArgasnvalthrPheSerAlaAspTyrGln 63

seq_name: SwissProt_38:INRL_MOUSE
seq_documentation_block:
ID INRL_MOUSE STANDARD: PRT; 590 AA.
AC P33896;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE INTERFERON ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
GN IFNARI OR IFNAR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE: 92262522.
RA Uze G., Lutfalla G., Bandu M.T., Proudhon D., Mogensen K.E.;
RT "Behavior of a cloned murine interferon alpha/beta receptor expressed
RT in homospesific or heterospesific background."
RL Proc. Natl. Acad. Sci. U.S.A. 89:4774-4778(1992).
CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
CC I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
CC SUBUNITS THEMSELVES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M89641; AAA37890.1; -
DR PIR: A45283; A45283.
DR MGI: MGI:107658; IFNAR.

```

KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 27 590 INTERFERON-ALPHA/BETA RECEPTOR ALPHA
 FT
 FT DOMAIN 27 429 CHAIN.
 FT TRANSMEM 430 449 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 450 590 POTENTIAL.
 FT DISULFID 78 86 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 199 220 BY SIMILARITY.
 FT CARBOHYD 43 43 POTENTIAL.
 FT CARBOHYD 109 109 POTENTIAL.
 FT CARBOHYD 181 181 POTENTIAL.
 FT CARBOHYD 214 214 POTENTIAL.
 FT CARBOHYD 314 314 POTENTIAL.
 FT CARBOHYD 370 370 POTENTIAL.
 FT CARBOHYD 409 409 POTENTIAL.
 FT CARBOHYD 413 413 POTENTIAL.
 SQ SEQUENCE 590 AA; 65776 MW; 7EC6DF370185D3A CRC64;

alignment_scores:
 Quality: 198.00 Length: 65
 Ratio: 3.536 Gaps: 0
 Percent Similarity: 86.154 Percent Identity: 55.385

alignment_block:

US-09-240-675-1_COPY_1_229 x INR1_MOUSE ..

Align seg 1/1 to: INR1_MOUSE from: 1 to: 590

```

30 ATGTCGTCCTCTGCGCGGAGACCTAGTCTGTCGCGCGGCGCC 79
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MetLeuAlaValAlaValAlaAlaAlaValAlaAlaGlyAlaSer 17
80 ATGGGTGTGTCGCGAGCCGAGGTGGAATAATCTAAATCTCTCAAA 129
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17 CrrpAlaLeuProSerAlaAlaGlyGlyGlnAsnLeuLysProGlnUA 34
130 AAGTAGAGCTGACATGACATGACATTTATCTCTGAGGTGAACAGG 179
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 snilespAlaIyrllelleaspAspAsnTyrThrLeuLysTrpSer 50
180 AGCGATGATGTCGCGAATGCTTTTTCATTTCGATTATCAAA 224
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51 H1SGlyGluSerMetClySerValThrPheSerAlaGluTyrArg 65

```

seq_name: SwissProt_38:N153_HUMAN

seq_documentation_block:

ID N153_HUMAN STANDARD; PRT; 1475 AA.
 AC P49790;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE NUCLEAR PORE COMPLEX PROTEIN NUP153 (NUCLEOPORIN NUP153) (153 KD
 DE NUCLEOPORIN).
 GN NUP153.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94154002.
 RA McMorris I., Bastos R., Horton H., Burke B.;
 RT "Sequence analysis of a cDNA encoding a human nuclear pore complex
 RT protein, hnup153.";
 RL Blochman, Biophys. Acta 1217:219-223(1994).
 CC -1- FUNCTION: POSSIBLE DNA-BINDING SUBUNIT OF THE NUCLEAR PORE
 CC COMPLEX (NPC). THE REPEAT-CONTAINING DOMAIN MAY BE INVOLVED IN
 CC ANCHORING COMPONENTS OF THE PORE COMPLEX TO THE PORE MEMBRANE.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR PORE COMPLEX. LOCATED TO THE
 CC TERMINAL RING STRUCTURE OF THE NUCLEOPLASMIC CAGE.
 CC -1- DOMAIN: CONTAINS X-F-X-F-G REPEATS.

CC -1- SIMILARITY: THE REPEAT REGION COMPOSED OF PENTAPEPTIDE REPEATS
 CC SEPARATED BY SER/THR-RICH DOMAINS IS SIMILAR TO THAT OF YEAST
 CC NUP1, NSP1, POM 121 AND MAMMALIAN P62.
 CC
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 CC
 DR EMBL: Z25535; CAA80982.1; -
 DR IPI: 603948; -
 DR PIR: P00061; zf-RanBP; 4.
 KW Nuclear protein; Transport; Repeat; Zinc-finger; DNA-binding.
 FT DOMAIN 4 14 GLY-RICH.
 FT DOMAIN 443 447 POLY-GLY.
 FT ZN_FING 662 681 C4-TYPE.
 FT ZN_FING 726 745 C4-TYPE.
 FT ZN_FING 797 816 C4-TYPE.
 FT ZN_FING 855 874 C4-TYPE.
 SQ SEQUENCE 1475 AA; 153889 MW; 3CB415A6909DF80E CRC64;

alignment_scores:
 Quality: 69.00 Length: 77
 Ratio: 1.683 Gaps: 3
 Percent Similarity: 53.247 Percent Identity: 33.766

alignment_block:

US-09-240-675-1_COPY_1_229/rev x N153_HUMAN ..

Align seg 1/1 to: N153_HUMAN from: 1 to: 1475

```

193 ACAGATCATGCTCTCTCTTCCACCTCAGATAAGTGTCTCATGAT 144
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1248 ThrSerGlnSerLeuLeuPheSerGlnAspSerLysLeuAlaThrThr 1264
143 CTCGACCTCTACTTTTTCAGAGATTTTGAATTTTTCACCTCGGCTG 94
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1264 rSerThrGlyThrAlaValAlaThrProPheValPheGlyProGlyAlaSer 1281
93 CGGACCAACACC.....CATGGCCACGCGGACGAGC 62
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1281 eraSnaSnThrThrThrSerGlyPheGlyAlaThrThrThrSer 1297
61 .....ACTAGGCTCTGCGCGCCGAG 42
1298 SerSerAlaGlySerSerPheValPheGlyThrGlyProSerAlaPro 1314
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
41 GAGGACGACCATCATCTGGAGCGCGCGC 13
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1314 eraAlaSerProAlaPheGlyAlaAsnGln 1323

```

seq_name: SwissProt_38:KDPD_RATRA

seq_documentation_block:

ID KDPD_RATRA STANDARD; PRT; 854 AA.
 AC O34971;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE SENSOR PROTEIN KDPD (EC 2.7.3.-).
 GN KDPD.
 OS Rathayibacter rathayi (Corynebacterium rathayi).
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Micrococcales; Microbacteriaceae; Rathayibacter.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-25;
 RA Labadie J.C.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM KDPD/KDPE
CC INVOLVED IN THE REGULATION OF THE KDP OPERON. KDPD MAY FUNCTION
CC AS A MEMBRANE-ASSOCIATED PROTEIN KINASE THAT PHOSPHORYLATES KDPE
CC IN RESPONSE TO ENVIRONMENTAL SIGNALS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
CC -1- SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE
CC KINASES.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AJ002069; CAA05169.1; -
CC DR PFM: AF030293; AAB84261.1; -
CC DR PFM: PF00512; signal; 1.
CC KW Sensory transduction; Transferase; Kinase; Phosphorylation;
CC Transmembrane.
CC FT TRANSMEM 35 55 POTENTIAL.
CC FT TRANSMEM 158 178 POTENTIAL.
CC FT TRANSMEM 374 394 POTENTIAL.
CC FT TRANSMEM 409 429 POTENTIAL.
CC FT TRANSMEM 450 470 POTENTIAL.
CC FT DOMAIN 605 854 TRANSMITTER DOMAIN (POTENTIAL).
CC FT MOD_RES 628 628 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
CC SO SEQUENCE 854 AA; 90670 MW; 201867CAFDDB865 CRC64;

alignment_scores:
Quality: 68.00 Length: 45
Ratio: 2.519 Gaps: 2
Percent Similarity: 60.000 Percent Identity: 44.444

alignment_block:

US-09-240-675-1_COPY_1_229 x KDPD_RATRA ..

Align seg 1/1 to: KDPD_RATRA from: 1 to: 854

8 GATCTCGCGCGCTCCACATGATGCTGCTCTCTGGG..... 46
|||||
629 AspleuHARArgProPheaspGlyGlnGlnLysGlyGlyTrpLeuA1 645
47CGGACGACCTAGTGGCTGGCGCGCGCCCGCATGGGTGG 89
|||||
645 AleuHISArgaspPspProValCysArgArg.....ProGlyGlyAlaA 660
90 TCCGACGCCGACGAGTGGAAAAAATCTAAATCTCC 124
:::|||||
660 laArgspArgArgArgLysProAlaHISLeuSer 671

seq_name: SwissProt_38:IF3A_HUMAN

seq_documentation_block:

ID IF3A_HUMAN STANDARD: PRT: 1382 AA.

AC Q14152; 000653;
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 10 (EIF-3 THETA)
DE (EIF3 P167) (EIF3 P180) (EIF3 P185) (KIAA0139).
OS EIF3S10.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BONE MARROW;
RX MEDLINE: 96127530.
RA Nagase T., Seki N., Tanaka A., Ishikawa K.-I., Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. IV.

RT The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by
RT analysis of cDNA clones from human cell line KG-1.";
RL DNA Res. 2:167-174(1995).

RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97294683.
RA Scholler J.R., Kaner S.B.;
RT "The human p167 gene encodes a unique structural protein that contains
RT centrosomin A homology and associates with a multicomponent complex.";
RL DNA Cell Biol. 16:515-531(1997).

RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97207269.
RA Johnson K.R., Merrick W.C., Zoll W.L., Zhu Y.;
RT "Identification of cDNA clones for the large subunit of eukaryotic
RT translation initiation factor 3. Comparison of homologues from human,
RT Nicotiana tabacum, Caenorhabditis elegans, and Saccharomyces
RT cerevisiae.";
RL J. Biol. Chem. 272:7106-7113(1997).

CC -1- FUNCTION: BINDS TO THE 40S RIBOSOME AND PROMOTES THE BINDING OF
CC METHIONYL-TRNAI AND MRNA.

CC -1- SUBUNIT: EIF-3 IS COMPOSED OF AT LEAST 10 DIFFERENT SUBUNITS.

CC -1- SUBCELLULAR LOCATION: CYTOSOLASMIC.

CC -1- PTM: PHOSPHORYLATED.

CC -1- SIMILARITY: BELONGS TO THE EIF3S10 FAMILY.

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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: D50929; BAA09488.1; -
CC DR EMBL: U58046; AAB41584.1; -
CC DR EMBL: U78311; AAB80695.1; -
CC DR MIM: 602039; -
CC KW Initiation factor; Protein biosynthesis; Repeat; Phosphorylation.
CC FT DOMAIN 925 1172 25 X 10 AA TANDEN REPEAT OF D (DE)-D-R-
CC (GP)-(PS)-(RW)-R-(GN)-(AM).
CC SO SEQUENCE 1382 AA; 166568 MW; 485C01B28D67EBBA CRC64;

alignment_scores:
Quality: 67.00 Length: 87
Ratio: 1.634 Gaps: 6
Percent Similarity: 47.126 Percent Identity: 32.184

alignment_block:

US-09-240-675-1_COPY_1_229 x IF3A_HUMAN ..

Align seg 1/1 to: IF3A_HUMAN from: 1 to: 1382

23 CGAGATGATGCTGCTCTCTCT.....GGGCGCGACGACCTAGTCTCG 66
|||||
952 ProAspAspArgValProArgArgLysMetAspAspArgGlyPr 968
67 TCGCGGTGGCGCCATGGGTGTTCGCCGACCGCGAG..... 103
|||||
968 CArgArgGlyProGluGluAspArgPheSerArgArgGlyAlaAspAspA 985
104TGAAAAAATCT.....AAATC 121
|||||
985 SPArgProSerTyrArgAsnThrAspAspArgProProArgArgLile 1001
122 TCCCTCAAAAAGTAGAGT.....CGACATCATAGATGACAACTTATCC 165
|||||
1002 AlaAspGluAspArgGlyAsnTyrArgHis AlaAspAspArgProp 1018
166 TGAGC.....TGAAACAGACGACATAG 188
|||||
1018 roArgArgGlyLeuAspGluAspArgGlySerTyrArgTThrAlaAspLeu 1034

RT "Nucleotide sequence and expression of a phosphate-regulated gene
RT encoding a secreted hemolysin of Pseudomonas aeruginosa."
RL J. Bacteriol. 167:291-298(1986).
RN [2]

RP REVISIONS.

RA Pritchard A.E.;

CC Submitted (AUG-1986) to the EMBL/Genbank/DBJ databases.

CC -1- FUNCTION: HYDROLYSES SPHINGOMYELIN IN ADDITION TO
CC PHOSPHATIDYLCHOLINE.

CC -1- CATALYTIC ACTIVITY: A PHOSPHATIDYLCHOLINE + H(2)O = 1,2-
CC DIACYLGLYCEROL + CHOLINE PHOSPHATE.

CC -1- SIMILARITY: 40% IDENTITY TO NON-HEMOLYTIC PHOSPHOLIPASE C.

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CC -----

DR EMBL: M3047; AA25966.1; -

DR PIR; A26391; A26391.

KW Hemolysis; Toxin; Hydrolase; Signal.

FT SIGNAL 1 38

SO SEQUENCE 730 AA; 82655 MW; F1D3695824445F8F CRC64;

alignment_scores:

Quality:	62.00	Length:	69
Ratio:	1.824	Gaps:	4
Percent Similarity:	49.275	Percent Identity:	26.087

alignment_block:

US-09-240-675-1_COPY_1_229 x PHLC_PSEAE ..

Align seg 1/1 to: PHLC_PSEAE from: 1 to: 730

```
63 CTCGTCGGCGGCGCATGGGTGTTCGCCGCGCCGACGTCGAGAAAAA 112
|||||:|||||:|||||:|||||:|||||:
404 LeuIleAlaIleSerProTIP.....SerLysGlyGly..... 414
113 TCTAAATCTCTCTCAAAAAGTAGAGTCGACATCATAGACAACTTTA 162
|||||:|||||:|||||:|||||:|||||:
415 .....LysValSerAlaGluValPheAspHisThrSerV 426
163 TCCTGAGG..... 170
:::|||||
426 allLeuArgPheLeuGluArgPheGlyLeuValGluGluAsnIleSer 442
171 ...TGGACAGGAGGAGATGAGCTCTCGGGAATGAGACTTTTCATTCGA 217
|||||:|||||:|||||:|||||:|||||:
443 ProTrpArgArgAla.....ValCysGlyAspLeuThrSerLeuPheAs 457
218 TTATCAA 224
|:::||||
457 pPheGln 459
```


KI intestinalis.?"

69 spargProseTTP

```

67  TCGCCCTGGAGCCCAAGGGAGTTGTCGGAGCGGAGG..... 103
      |||||
52  CAGTAAgCgCgTProGluGluAspArgPheSerArgArgGlyAlaAspAspa 69
      |||||
104 .....TGAATAAAATCT.....AAATCT 121
      |||||
69  SPAGProSerTyrPArgSntTrpAspAspAspArgProProTArgArgIle 85
      |||||

```

[illegible]

```

seq_documentation_block:
ID      014152      PRELIMINARY:      PRI:      1382 AA.
AC      014152;      000653;
DT      01-NOV-1996 (TREMBLrel. 01, Created)
DT      01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT      01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE      KIAA0139 PROTEIN.
GN      KIAA0139.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC      Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE; 96127530.
RA      MAGASE T., SEKI N., TANAKA A., ISHIKAWA K., NOMURA N.;
RT      "Prediction of the coding sequences of unidentified human genes. IV.
RT      The coding sequences of 40 new genes (K1A0121-K1A0160) deduced by
RT      analysis of cDNA clones from human cell line KG-1.";
RL      DNA Res. 2:167-174(1995).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE; 90239007.
RA      KANNER S.B., REYNOLDS A.B., VINES R.R., PARSONS J.T.;
RT      "Monoclonal antibodies to individual tyrosine--phosphorylated protein
RT      substrates of oncogene-encoded tyrosine kinases.";
RL      Proc. Natl. Acad. Sci. U.S.A. 87:3328-3332(1990).
RN      [3]
RP      SEQUENCE FROM N.A.
RA      SCHOLLER J.K., KANNER S.B.;
RT      Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
RN      [4]
RP      SEQUENCE FROM N.A.
RX      MEDLINE; 97207269.
RA      JOHNSON K.R., MERRICK W.C., ZOLL W.L., ZHU Y.;
RT      "Identification of cDNA clones for the large subunit of eukaryotic
RT      translation initiation factor 3. Comparison of homologues from human
RT      Nicotiana glauca, Caenorhabditis elegans, and Saccharomyces
RT      cerevisiae.";
RL      J. Biol. Chem. 272:7106-7113(1997).
RN      [5]
RP      SEQUENCE FROM N.A.
RA      ZHU Y., JOHNSON K.R.;
RT      Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; D50929; BAA09488.1; -.
DR      EMBL; U58046; BAB41584.1; -.
DR      EMBL; U78311; AAB80695.1; -.
SQ      Initiation factor.
SQ      SEQUENCE 1382 AA: 166568 MW: AEF0846C CRC32:

```

```
alignment_scores:
  quality: 67.00
  ratio: 1.634
  percent_similarity: 47.126
  length: 87
  caps: 6
  percent_identity: 32.184
```

alignment_block:
US-09-240-675-1_COPY_1_229 x Q14152

Align seg 1/1 to: Q14152 From: 1 to: 1382

[illegible]

```

seq_documentation_block:
ID 076514 PRELIMINARY; PRT: 365 AA.
AC 076514;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE CER-1.
GN CER-1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
OC Rhabditina; Rhabditioidea; Rhabditidae; Peloderinae; Caenorhabditis
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-N2;
RA MORITA K., CHOW K.L., UENO N.;
RT "body Length and Male Tail Ray Pattern Formation of C. elegans are
RT Regulated by a Member of the TGFb Family.";
RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF074395; AAC26791.1; -.
DR HSSP; P18075; 1BMP.
DR PFAM; PF00019; TGF-beta; 1.
DR PRINTS; PRO0438; GFCYSKNT.
SQ SEQUENCE 365 AA; 41781 MM; 54051BEE CRC32;

```

```
alignment_scores:
  Quality: 66.00      Length: 54
  Ratio: 1.941      Gaps: 2
  Percent Similarity: 62.963      Percent Identity: 31.483
```

alignment_block:

Align seg 1/1 to: 076514 from: 1 to: 365

```

53  GACCCTAGTCGTCGTCGCCGTGGGCCCATGGGTGTGTTCGCGACGCCGAG 102
    ::::::::::::::::::::|::::::::::::|
228  GlnPterSerSerValIArgPArg.....LysAsnSerAspGly 239
    ::::::::::::::::::::|::::::::::::|
103  GTGGAAAAATATCAAAATATCTCCTCAAAAAGTAGAGTCGACATATAGAT 152
    ::::::::::::::::::::|::::::::::::|
239  nThGlyAsnSerGluArgLysLysAsnArgLysLysGlyValArgLysHisHis 255
    ::::::::::::::::::::|::::::::::::|
153  GACAACCTTATCTCGAGGTGCAACAGAGCGATGCTGTGCGGAAATGT 202
    ::::::::::::::::::::|::::::::::::|

```

266AsnThrGluAlaGluSerAsnLeuGlyArgThr 267
203 GACTTTTCATT 214
|||||:
268 AspMetGlyVal 271

seq_name: sp_mhc:030849

seq_documentation_block:
ID 030849 PRELIMINARY; PRT: 358 AA.

AC 030849;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE MHC CLASS I ANTIGEN PRECURSOR
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-B/J;
RX MEDLINE: 84290724.
RA "KOCINSKI M.L., MARCHE P.N., MAX E.E., KINDT T.J.;
RT "Rabbit class I MHC genes: cDNA clones define full-length transcripts
RT of an expressed gene and a putative pseudogene."
RL J. Immunol. 133:2261-2269(1984).
DR EMBL: K02442; AAA98731.1; -
DR HSSP: P30460; 1AGE.
DR PRAM: PF00047; 1g; 1.
DR PRAM: PF00129; MHC_I; 1.
KW Signal; MHC.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 358 MHC CLASS I ANTIGEN.
SQ SEQUENCE 358 AA; 39828 MW; 86894130 CRC32.

alignment_scores:
Quality: 63.50 Length: 95
Ratio: 1.296 Gaps: 3
Percent Similarity: 51.579 Percent Identity: 23.158

alignment_block:

US-09-240-675-1_COPY_1_229 x 030849 ..

Align seg 1/1 to: 030849 from: 1 to: 358

12 TGCGGGGCTCCAGATGATGTCCTCCCTGGCGGAGACCCCTACT 61
|||||:
3 CysGlyAla.....LeuLeuLeuLeuAlaGlyAlaLeuThr 17
62 GCTCTGCGCCGTGGCCCATGGGTGTG.....TCCGAGCCGCGAG 102
: : : : :
17 rglurhrarghrghlyserhlsrleuargtyrphethrralalals 34
103 GTGGAATAATCTCTCAAAAAGTAGAGGTGACATCTAAT 152
: : : : :
34 errargprogluLeuProgluProargPhemeSerValGlyTyValasp 50
153 GACACCTTATCTCTGAG..... 170
| : : : :
51 AsprhrglnphevalargPheaspserspalaalaserproargalagl 67
171TGGAACAGCA 180
67 uProargAlaProtrPmetargGluValaspProgluTyrrtrPasparg 84
181 CGGATGACTGTGCGGAATGAGACTTTTCTTTC 215
: : : : :
84 InThrGluArgAlaLysAsnThrAlaLeuSerPhe 95

seq_name: sp_rudent:088970

seq_documentation_block:

ID 088970 PRELIMINARY; PRT: 734 AA.
AC 088970;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE INSULIN RECEPTOR SUBSTRATE-2 (FRAGMENT).
GN IRS2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA XU G., UIMER W.T., WOLF B.A.;
RT "Partial genomic DNA sequence of mouse beta-cell IRS-2."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF090738; AAC61743.1; -
FT NON-TER 1 1
SQ SEQUENCE 734 AA; 75251 MW; B3410CAF CRC32;

alignment_scores:
Quality: 63.50 Length: 72
Ratio: 1.984 Gaps: 2
Percent Similarity: 44.444 Percent Identity: 29.167

alignment_block:

US-09-240-675-1_COPY_1_229/rev x 088970 ..

Align seg 1/1 to: 088970 from: 1 to: 734

124 GAGATTTTGAATTTTTCACCTGCGGTGCGGACACACCCATGGGCC 75
|||||:
439 GlyaspLeuTyrrgluProProAlaSerAlaAlaThrserGlnGlyr 455
74 CACGGCGACGACACTAGGCTGCGCGCCGACGA..... 40
|||||:
455 ThrAlaGlySerSerMet.SerSerGluProGlyAspAsnGlyAspTyr 471
40 40
472 ThrGluMetAlaPheGlyValAlaAlaThrProProGlnProIleValAl 488
39GGACGACCATCATCTGGGAGCC 18
: : : : :
488 aProProLysProgluGluAlaArgValAlaSerProThrSerGlyLeu 505
17 GCCCGACATCCCTG 4
: : : : :
505 ySarGlyLeuSerLeu 509

seq_name: sp_phage:064317

seq_documentation_block:
ID 064317 PRELIMINARY; PRT: 640 AA.

AC 064317;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE TERMINASE LARGE SUBUNIT.
GN GENE 2.
OS Bacteriophage N15.
OC Viruses.
RN [1]
RP SEQUENCE FROM N.A.
RA HENDRIX R.W., RAVIN V.K., CASJENS S.R., FORD M.E., RAVIN N.V.,
RA SMIRNOV I.K.;
RT Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF064539; AAC19038.1; -
SQ SEQUENCE 640 AA; 73094 MW; E1B34267 CRC32;

alignment_scores:
Quality: 63.00 Length: 99

Ratio: 1.340 Gaps: 4
Percent Similarity: 47.475 Percent Identity: 26.263

alignment_block:

US-09-240-675-1_COPY_1_229 x 064317 ..

Align seg 1/1 to: 064317 from: 1 to: 640

```

8 GATCGCGGCGGCTCCAGATGATGT..... 34
   ||||| ||||| |||||
101 GluLeuLeuTrpLeuProThrAspValAspAsnPhenMetLys 117
   ||||| ||||| ||||| |||||
35 .....CGTCCTCTGGCGGAGCAGCCAGTCTGCTGCGCGGCG 77
   ||||| ||||| ||||| |||||
117 HisValGluProThrIleArgAspValProSerLeuLeuSerLeuAla 133
   ||||| ||||| ||||| |||||
78 CCATG.....GCTGTCTCCGCA..... 95
   ||||| ||||| ||||| |||||
134 ProTrpTyrGlyLysLysHisArgAspAsnThrLeuSerMetLysArgPh 150
   ||||| ||||| ||||| |||||
96 .....GCCGCGAGTGAATAAATCTAAATCTC 123
   ||||| ||||| ||||| |||||
150 eThrsnGlyArgGlyPheTrpCysLeuGlyLysAlaIleLysAsnT 167
   ||||| ||||| ||||| |||||
124 CTCAAAAAGTAGAGTCGACATCATAGACACTTATCTCGAGGTGG 173
   ||||| ||||| ||||| |||||
167 YArgGluLysSerValAspValValGlyTyrAspGluLeuAlaIlePhe 183
   ||||| ||||| ||||| |||||
174 AACAGAGCGAGTACTCTCGGAATGACTTTTCTTCTGAT 218
   ||||| ||||| ||||| |||||
184 AspAlaAspIleGluLysGluLysSerProThrPheLeuGlyAsp 198

```

seq_name: sp_human:Q13507

seq_documentation_block:
ID Q13507 PRELIMINARY: PRT: 848 AA.

```

AC Q13507: 000593:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE TRANSIENT RECEPTOR POTENTIAL RELATED CHANNEL 3 PROTEIN.
GN TRPC3 OR HTRP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96234226.
RA ZHU X., JIANG M., PEYTON M., BOULAY G., HUNST R., STEFANI E.,
RA BIRNBAUMER L.;
RT "TRP, a novel mammalian gene family essential for agonist-activated
RT capacitative Ca2+ entry."
RL Cell 85:661-671(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97358541.
RA XU X.Z.S., LI H.S., GUGGINO W.B., MONTELL C.;
RT "Coassembly of TRP and TRPL produces a distinct store-operated
RT conductance."
RL Cell 89:1155-1164(1997).
DR EMBL: U47050; AAC51653.1; -
DR PFM: Y13758; CAA74083.1; -
DR PRINTS: PR01097; TRNSRCEPTRP.
SEQUENCE 848 AA: 97354 MW: 78kD29D CRC32:

```

alignment_scores:
Quality: 63.00 Length: 75
Ratio: 1.537 Gaps: 3
Percent Similarity: 54.667 Percent Identity: 33.333

alignment_block:

US-09-240-675-1_COPY_1_229 x Q13507 ..
Align seg 1/1 to: Q13507 from: 1 to: 848

```

30 ATGGTCGTCCTCGGCGGAGCAGCCAGTCTGCTGCGCGGCGGCC 79
   ||||| ||||| ||||| |||||
351 LeuValValLeuValValAlaLeuGlyLeuProPheLeuAlaIleGlyTyr 367
   ||||| ||||| ||||| |||||
80 ATGGGTCTTCTCCGAGCCGCGAGTGTGAATAAATCTAAATCTCTCAAA 129
   ||||| ||||| ||||| |||||
367 rTriPheLeuProCysSerArgLeuGlyLysIleLeuArgSerProPheM 384
   ||||| ||||| ||||| |||||
130 AAGTAGAGTC.....GACATCATAGATGACACTTATCTCTG 167
   ||||| ||||| ||||| |||||
384 eLysPheValAlaHisAlaLaserPheIleIlePheLeuGlyLeuLeu 400
   ||||| ||||| ||||| |||||
168 AGGTGAGACGAGGAGTACTGTCTGG.....AATGT 202
   ||||| ||||| ||||| |||||
401 ValPheAsnAlaSerAspArgPheGluGlyIleThrThrLeuProAsnIle 417
   ||||| ||||| ||||| |||||
203 GACTTTTCTATTCGATTATCAAAA 227
   ||||| ||||| ||||| |||||
417 eThrValThr...AspTyrProLys 424

```

seq_name: sp_rodent:Q60697

seq_documentation_block:
ID Q60697 PRELIMINARY: PRT: 1344 AA.

```

AC Q60697:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 07, Last annotation update)
DE P162 PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-LYMPHOID TUMOR;
RA FISHER R., FILLMORE H., REYNOLDS A.B.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U14172; AAA90910.1; -
SEQUENCE 1344 AA: 161949 MW: 86593FEF CRC32:

```

alignment_scores:
Quality: 63.00 Length: 103
Ratio: 1.432 Gaps: 7
Percent Similarity: 42.718 Percent Identity: 31.068

alignment_block:
US-09-240-675-1_COPY_1_229 x Q60697 ..

Align seg 1/1 to: Q60697 from: 1 to: 1344

```

11 CTGCGGCGGCTC.....CC 24
   ||||| ||||| ||||| |||||
936 LeuArgArgLeuGlyGlyAspAspGluLargGluSerLeuArgP 952
   ||||| ||||| ||||| |||||
25 AGATGATGTCCTCTCTCT.....GGGCGGAGCAGCCAGTCTGCTGTC 68
   ||||| ||||| ||||| |||||
952 oAspAspAspArgIleProArgArgGlyLeuAspAspArgGlyProA 969
   ||||| ||||| ||||| |||||
69 GCGGTGGCGCATGGGTGTCTCCGAGCCGAG..... 103
   ||||| ||||| ||||| |||||
965 rArgGlyProAspGluAspArgPheSerArgArgGlyThrAspAsp 985
   ||||| ||||| ||||| |||||
104 .....TGGAAAAAATCT.....AAATCTC 123
   ||||| ||||| ||||| |||||
986 ArgProSerTrpArgAsnAlaAspAspArgProArgArgIleG 1002
   ||||| ||||| ||||| |||||
124 CTCAAAAAGTAGAGT.....CGACATCATGATGACAACTTATCTCTG 167
   ||||| ||||| ||||| |||||

```

1002 yaspasparglysertrparghis.thraspaspargpropro 1018
 168 AGG.....TGGAACAGAGCGATGATC 190
 1019 ArArglyleuaspasparglysertrparghis.thraspaspargpropro 1035
 191 TGTCGGG 197
 1035 parggly 1037

seq_name: sp_invertebrate:Q94603

seq_documentation_block:
 ID Q94603 PRELIMINARY; PRT; 326 AA.
 AC Q94603;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-JAN-1999 (TREMBLrel. 09, Last annotation update)
 DE MTC.
 GN MTC.
 OS Leishmania major.
 OC Eukaryota; Eukaryota; Kinetoplastida; Trypanosomatidae; Leishmania.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FRIEDLIN;
 RA MYLER P.J., AUDLEMAN L., HIXSON G., KISER P., LEMLEY C., RICKEL E.,
 RA SISK E., SUNKIN S., SMARTZELL S., WESTLAKE T., MAGNESS C., BASTIEN P.,
 RA FU G., IVENS A., STUART K.,
 RT "Leishmania major Friedlin chromosome 1 has only two polycistronic
 RT units of protein coding genes."
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN [12]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FRIEDLIN;
 RA MYLER P.J.;
 RT "The nucleotide sequence of Leishmania major Friedlin chromosome 1."
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE001274; AAC24664.1; -
 SO SEQUENCE 326 AA; 36141 MW; A629DA98 CRC32;

alignment_scores:
 Quality: 62.50 Length: 66
 Ratio: 1.645 Gaps: 3
 Percent Similarity: 57.576 Percent Identity: 30.303

alignment_block:
 US-09-240-675-1_COPY_1_229 x Q94603 ..
 Align seg 1/1 to: Q94603 from: 1 to: 326

12 TGGGGGGGGCCAGATGATGCTGCTCCTG.....GG 46
 156 Cysgllyserleuathrvalmetrplethlyargleprothrgl 172
 47 CGGAGACCGCTAGTCTGCTC...GCCGTGGCCCATGGGTGTGCG 93
 172 ythrthsrthrleuathrvalprophelalaValS 189
 94 CAGCCGAGGTGGAATAATCTAAATCTCCTCAAAAGTAGAG..... 137
 189 erCysalaalatrvalasleuasermetarglyasnclutrpLeu 205
 138GTGACATCATAGATGACACTTATCTGAGG 170
 206 SerSerClylnclyllearvalaspasparglyvalthrarg 221

seq_name: sp_plant:O23212

seq_documentation_block:
 ID O23212 PRELIMINARY; PRT; 573 AA.
 AC O23212;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)

DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE SPLICING FACTOR-LIKE PROTEIN.
 GN CTA10.670.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC eudicotyledons; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
 OC Arabidopsis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA BEVAN M., TERRY N., VOS P., HEIJNEN L., MEMES H.W., SCHUELLER C.,
 RA CHALMERS N.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z99708; CAB16828.1; -
 DR HSSP; P19339; 2SL.
 DR PFAM; PF00076; trm; 2.
 SO SEQUENCE 573 AA; 63551 MW; 07954A00 CRC32;

alignment_scores:
 Quality: 62.50 Length: 75
 Ratio: 1.645 Gaps: 3
 Percent Similarity: 50.667 Percent Identity: 33.333

alignment_block:
 US-09-240-675-1_COPY_1_229 x O23212 ..
 Align seg 1/1 to: O23212 from: 1 to: 573

5 AGGATCTCGGCGGCTCCAGATGATGCTGCTCCTGGGCGGAC.. 52
 46 Arggluthserargserlyasparglulysgllyargasp 62
 53GACCTAGTCTGCTGCTGCTGCTGCTGCTGCTG 89
 62 sasprgluargaspserglulysargser..... 74
 90 TCCGACCGCGGCGGGAATAATCTCCTCAAAAGT..... 133
 75 ..Argaspargaspglulysserlysgluargserargsp 90
 134AGAGTCATCATGATGACACACTTATCTGAGCGGA 174
 91 Argaspargaspglulysargserargserargsp 107
 107 farggluargglulysargglu 115

seq_name: sp_mammal:O77699

seq_documentation_block:
 ID O77699 PRELIMINARY; PRT; 117 AA.
 AC O77699;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE TRP3 PROTEIN (FRAGMENT).
 GN TRP3.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA WISSENBACH U., PHILIP S., FLOCKERZ V.;
 RT "Cloning and analysis of TRP channels."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ006781; CA07246.1; -
 FT NON_TER 1 1
 FT NON_TER 117 117
 SO SEQUENCE 117 AA; 13295 MW; B9F9B808 CRC32;

alignment_scores:

Quality: 62.00 Length: 75
 Ratio: 1.512 Gaps: 3
 Percent Similarity: 54.667 Percent Identity: 33.333

alignment_block:

us-09-240-675-1_copy_1_229 x 077699 ..

Align seg 1/1 to: 077699 from: 1 to: 117

```

30 ATGTCGTCCTCTGGCGCGACGACCTAGTCGTGCGCGCGGCC 79
   :::::::::::::: :: ::::::::::::::
25 LeuValValLeuValAlaLeuGlyLeuProPheLeuAlaIleGly 41
   :::::::::::::: ::::::::::::::
80 ATGGGTGTTCGCCGACGCCGAGTGGAATAATCTAAATCTCTCAA 129
   :::::::::::::: ::::::::::::::
41 rTTPLeuAlaProCysSerArgLeuGlyLysValLeuArgSerPro 58
   :::::::::::::: ::::::::::::::
130 AAGTAGAGGTC.....GACATCATGATGACACATTATCTCTG 167
   :::::::::::::: ::::::::::::::
58 eLysPheValAlaHisAlaAlaSerPheIleIlePheLeuGlyLeu 74
   :::::::::::::: ::::::::::::::
168 AGGTGGAACAGAGCGATGATGTCGTGCGG.....AATGT 202
   :::::::::::::: ::::::::::::::
75 ValPheAlaAlaSerAspArgPheGlyIleThrThrLeuProAsn 91
   :::::::::::::: ::::::::::::::
203 GACCTTTTCATTCGATTATCAAAA 227
   :::::::::::::: ::::::::::::::
91 eThrVal...IleAspTyrProLys 98

```

seq_name: sp_human:095927

seq_documentation_block:

ID 095927 PRELIMINARY: PRT: 290 AA.
 AC 095927:
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE D1465N24.2.1 (PUTATIVE NOVEL PROTEIN) (ISOFORM 1).
 GN D1465N24.2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA WILSON S.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL031432; CAB37992.1; ..
 SQ SEQUENCE 290 AA; 33613 MM; B59E0C18 CRC32;

alignment_scores:

Quality: 62.00 Length: 62
 Ratio: 2.296 Gaps: 1
 Percent Similarity: 43.548 Percent Identity: 29.032

alignment_block:

us-09-240-675-1_copy_1_229 x 095927 ..

Align seg 1/1 to: 095927 from: 1 to: 290

```

32 GGTGTCCTCTGGCGCGACGACCTAGTCGTGCGCGGCCCAT 81
   :::::::::::::: ::::::::::::::
11 GlySerProGlnGluLysAspSerProSerThrSerArgSerGlycylse 27
   :::::::::::::: ::::::::::::::
82 GGGTGTTCGCCGACGCCG.....AATGT 100
   :::::::::::::: ::::::::::::::
27 rSerArgLeuSerArgSerArgSerArgSerPheSerArgSerSer 44
   :::::::::::::: ::::::::::::::
101 .....AGGTGAAAAAATCT 115
   ::::::::::::::

```

```

44 rGSerHisSerArgValSerSerArgPheSerSerArgSerArgSer 60
116 AAATCTCTCAAAAAGTAGAGTCGACATCATAGA 151
   :::::::::::::: ::::::::::::::
61 LysSerArgSerArgSerArgArgArgHisGlnArg 72

```


GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 1, 2000, 00:40:12 ; Search time 42.08 Seconds

(Without alignments)
114.265 Million cell updates/sec

Title: US-09-240-675-2_COPY_27_229

Perfect score: 1072
Sequence: 1 GKNLSPQKVEVDIDNFI.....WKIGYSPVHCITVENEL 203

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_35.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1072	100.0	436	1 R14487	Soluble Interferon
2	1072	100.0	436	1 R28495	Sequence of a soul
3	1072	100.0	436	1 R1773	IFN receptor extra
4	1072	100.0	557	1 R1958	Human alpha-Interf
5	1072	100.0	557	1 R1468	Complete Interfero
6	1072	100.0	557	1 R28496	Sequence of a soul
7	1072	100.0	557	1 R42635	Human Interferon r
8	1072	100.0	557	1 R73356	Human IFN receptor
9	1067	99.5	434	1 W21805	Spliced-deleted in
10	1067	99.5	496	1 W21806	Spliced-deleted in
11	1067	99.5	557	1 W21804	Transmembranial int
12	214	20.0	325	1 W52296	CRFB4 protein. New
13	199	18.6	332	1 R75782	IFN-gamma receptor
14	166.5	15.5	553	1 W79159	Zcytor7 cytokine r
15	144	13.4	337	1 R1035	Human IFN-gamma ac
16	142	13.2	311	1 R75783	IFN-gamma receptor
17	131.5	12.3	237	1 W97864	Human cytokine rec
18	131.5	12.3	574	1 W97861	Human cytokine rec
19	111	10.4	210	1 R14643	Gamma interferon r
20	111	10.4	227	1 R14642	Gamma interferon r
21	111	10.4	231	1 R14641	Gamma interferon r
22	111	10.4	473	1 R55749	Extracellular doma
23	111	10.4	489	1 R07469	Plasmaid PBABLU hu
24	111	10.4	942	1 R70113	Gamma-IFN-R-GBP 13
25	108	10.1	245	1 R62023	Soluble human inte
26	93.5	8.7	219	1 W17734	Human truncated ti
27	93.5	8.7	263	1 W17725	Human tissue facto
28	92	8.6	265	1 R80063	Human IFNAB-BPI en
29	90.5	8.4	219	1 W17749	Human truncated ti
30	90.5	8.4	219	1 W17750	Human truncated ti
31	90.5	8.4	263	1 W17742	Human tissue facto
32	90.5	8.4	263	1 W17743	Human tissue facto
33	90.5	8.4	553	1 W35856	Human CD45 for use
34	89.5	8.3	219	1 W17751	Human truncated ti

35	89.5	8.3	219	1 W17732	Human truncated ti
36	89.5	8.3	219	1 W17733	Human truncated ti
37	89.5	8.3	263	1 W17744	Human tissue facto
38	89.5	8.3	263	1 W17723	Human tissue facto
39	89.5	8.3	263	1 W17724	Human tissue facto
40	89.5	8.3	223	1 W26356	Rabbit LDL recepto
41	89	8.3	239	1 R80067	Human IFNAB-BPI
42	89	8.3	331	1 R80066	Human IFNAB-BPI. N
43	88.5	8.3	219	1 W69605	Human truncated ti
44	87.5	8.2	219	1 W17752	Human truncated ti
45	87.5	8.2	219	1 W17728	Human truncated ti

ALIGNMENTS

RESULT 1	
R14487	
ID R14487 standard: Protein; 436 AA.	
AC R14487	
DE 16-JAN-1992 (first entry)	
DE Soluble Interferon-alpha/Beta receptor.	
KW IFN; autoimmune disease; graft rejection; histocompatibility.	
OS Homo sapiens.	
PN FR2657881-A.	
PD 09-AUG-1991.	
PF 05-FEB-1990; 001298.	
PR 05-FEB-1990; FR-001298.	
PA (FBI-) LAB EURO BIOTECHNO.	
PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE;	
PI Tovey MG, Uze G;	
DR WPI; 91-319778/44.	
DR N-PSDB; Q14239.	
PT New water-soluble polypeptide(s) with affinity for IFN-alpha and	
PT beta - used to treat e.g. lupus erythematosus, Behcet's disease,	
PT aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.	
PS Claim 2; Page 45; 52pp; French.	
CC The transmembrane and cytoplasmic domains of the native IFN receptor	
CC have been deleted to obtain a soluble, circulating form of the	
CC receptor. Potentially immunogenic epitopes have thus been eliminated.	
CC Derivatives obtained by substitution or deletion of this sequence	
CC are also claimed as are hybrid molecules comprising the soluble	
CC receptor (or deriv.) and an immunoglobulin such as IgG1.	
CC See also Q14240.	
SO Sequence 436 AA;	

Query Match 100.0%; Score 1072; DB 1; Length 436;
Best Local Similarity 100.0%; Pred. No. 1.1e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1	GKNLSPQKVEVDIDNFIILRNRSDESVGNVTFSPDYORTGMDNNIKLSGCONITSTK 60
DB 27	GKNLSPQKVEVDIDNFIILRNRSDESVGNVTFSPDYORTGMDNNIKLSGCONITSTK 86
QY 61	CNFSLLKLVYEELIKRIRAEKENTSSWYEDSTFPERKAOIGPEVHLEDEKAIYIHI 120
DB 87	CNFSLLKLVYEELIKRIRAEKENTSSWYEDSTFPERKAOIGPEVHLEDEKAIYIHI 146
QY 121	SPGKDSYMAALDGLSPFYSLLIKNNSGVEERLENTYSRKIKYKLSPEYTYCLKVRAL 180
DB 147	SPGKDSYMAALDGLSPFYSLLIKNNSGVEERLENTYSRKIKYKLSPEYTYCLKVRAL 206
QY 181	LTSWKIGYSPVHCITVENEL 203
DB 207	LTSWKIGYSPVHCITVENEL 229

RESULT 2
R28495
ID R28495 standard: Protein; 436 AA.
AC R28495:
DT 31-MAR-1993 (first entry)

DE Sequence of a soluble form of the interferon (IFN) receptor
 DE with a high affinity for IFN-alpha and -beta.
 KM Interferon receptor; alpha-interferon; beta-interferon.
 OS Synthetic.
 PN MO9218626-A.
 PD 29-OCT-1992.
 PF 17-APR-1991; F00318.
 PF 17-APR-1991; WO-F00318.
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
 PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,
 PI Tovey M, Uze G.
 DR WPI: 92-38210/46.
 DR N-PSDB: Q30532.
 PT Water soluble polypeptide(s) strongly bind interferon(s) alpha
 PT and beta - useful as immunosuppressants, for treating auto-immune
 PT diseases and transplant rejection
 PS Claim 2: Fig 1: 58pp: English.
 CC DNA encoding the water-soluble polypeptide with a high affinity for
 CC IFN-alpha and -beta is isolated by PCR, using appropriate
 CC oligonucleotides as primers and cloned cDNA as template. For example,
 CC bacteriophage lambda ZAP, containing the entire coding sequence of
 CC the IFN-alpha and -beta receptor (Q30533), was incubated with oligos
 CC Q30534 and Q30535. R28496 represents the complete receptor. R28495
 CC lacks the transmembrane and cytoplasmic domains. Both forms bind
 CC IFN in the same way as antibodies so are immunosuppressants e.g. for
 CC treating autoimmune diseases and graft rejection. They lack the
 CC toxic side-effects of known immunosuppressants such as steroids.
 SO Sequence 436 AA.

Query Match 100.0%; Score 1072; DB 1; Length 436;
 Best Local Similarity 100.0%; Pred. No. 1.1e-101;
 Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GKNLSPKQVEVDIIDDNFILRNKRSDESGVNTFSFDYQKTGMWIKLSGCCNITSTK 60
 DB 27 GKNLSPKQVEVDIIDDNFILRNKRSDESGVNTFSFDYQKTGMWIKLSGCCNITSTK 86
 OY 61 CNFSSLKLVNVEEIKLRIRAKENTSSWYEDSFTPFRAKQIGPPEVHLEADKAIVYHI 120
 DB 87 CNFSSLKLVNVEEIKLRIRAKENTSSWYEDSFTPFRAKQIGPPEVHLEADKAIVYHI 146
 OY 121 SPGTSDSYMALDGLSFTYSLLIMKNSGVEERIEINYSRRKIYKLSPEPTYCLKVKAL 180
 DB 147 SPGTSDSYMALDGLSFTYSLLIMKNSGVEERIEINYSRRKIYKLSPEPTYCLKVKAL 206
 OY 181 LTSWKIGVSPVHCITVTENEL 203
 DB 207 LTSWKIGVSPVHCITVTENEL 229

RESULT 3
 R71723

ID R71723 standard; Protein: 436 AA.
 AC R71723;
 DT 16-OCT-1995 (first entry).
 KM IFN receptor extracellular domain.
 DE IFN receptor; interferon receptor; interferon-alpha;
 KM interferon-beta; monoclonal antibody; immunomodulator; AIDS.
 OS Homo sapiens.
 PN MO9507716-A.
 PD 23-MAR-1995.
 PF 16-SEP-1994; E03114.
 PF 17-SEP-1993; EP-402279.
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
 PI Benizri EJ, Tovey MG;
 DR WPI: 95-131187/17.
 DR N-PSDB: Q86457.
 PT Compos. of monoclonal antibodies against interferon receptor -
 PT useful as immunomodulator, eg. for treating AIDS
 PS Disclosure: Fig.2A-2B: 105pp: English.
 CC A recombinant soluble form of the human interferon class I receptor
 CC protein extracellular domain, given in R71723, was expressed in

CC either E. coli or COS cell hosts. The protein was used to raise
 CC immunomodulatory monoclonal antibodies.
 SO Sequence 436 AA.

Query Match 100.0%; Score 1072; DB 1; Length 436;
 Best Local Similarity 100.0%; Pred. No. 1.1e-101;
 Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GKNLSPKQVEVDIIDDNFILRNKRSDESGVNTFSFDYQKTGMWIKLSGCCNITSTK 60
 DB 27 GKNLSPKQVEVDIIDDNFILRNKRSDESGVNTFSFDYQKTGMWIKLSGCCNITSTK 86
 OY 61 CNFSSLKLVNVEEIKLRIRAKENTSSWYEDSFTPFRAKQIGPPEVHLEADKAIVYHI 120
 DB 87 CNFSSLKLVNVEEIKLRIRAKENTSSWYEDSFTPFRAKQIGPPEVHLEADKAIVYHI 146
 OY 121 SPGTSDSYMALDGLSFTYSLLIMKNSGVEERIEINYSRRKIYKLSPEPTYCLKVKAL 180
 DB 147 SPGTSDSYMALDGLSFTYSLLIMKNSGVEERIEINYSRRKIYKLSPEPTYCLKVKAL 206
 OY 181 LTSWKIGVSPVHCITVTENEL 203
 DB 207 LTSWKIGVSPVHCITVTENEL 229

RESULT 4

ID R11958 standard; Protein: 557 AA.
 AC R11958;
 DT 18-JUL-1991 (first entry)
 DE Human alpha-interferon receptor protein.
 KM Human alpha IFN; IFN agonists; antiviral; anti tumour agent;
 KW drug targeting.
 OS Homo sapiens.
 FT Key location/Qualifiers
 FT peptide 1..27 /label= signal peptide
 PN MO9105862-A.
 PD 02-MAY-1991.
 PF 19-OCT-1980; F00758.
 PF 20-OCT-1989; FR-013770.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 PI Mogensen KE, Uze G, Lutfalla G, Gresser I;
 DR WPI: 91-148740/20.
 DR N-PSDB: 011701.
 PT New human alpha-interferon receptor protein - useful for testing
 PT interferon agonists and in treatment or diagnosis
 PS Disclosure: fig 4; 30pp: French.
 CC This recombinant human alpha interferon (IFN) receptor protein is
 CC useful for the testing of IFN agonists and for treatment and diag-
 CC nosis of viral diseases and tumours. Antibodies raised against
 CC this protein can be used for blocking the receptor when required,
 CC eg where overexpression of alpha-IFN is harmful. The Abs are
 CC also useful for eg drug targeting. Variants of the protein,
 CC having residue 164 (Thr) replaced by Arg and an Asp inserted
 CC between residues 479 and 480, are also useful.
 SO Sequence 557 AA.

Query Match 100.0%; Score 1072; DB 1; Length 557;
 Best Local Similarity 100.0%; Pred. No. 1.5e-101;
 Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GKNLSPKQVEVDIIDDNFILRNKRSDESGVNTFSFDYQKTGMWIKLSGCCNITSTK 60
 DB 27 GKNLSPKQVEVDIIDDNFILRNKRSDESGVNTFSFDYQKTGMWIKLSGCCNITSTK 86
 OY 61 CNFSSLKLVNVEEIKLRIRAKENTSSWYEDSFTPFRAKQIGPPEVHLEADKAIVYHI 120
 DB 87 CNFSSLKLVNVEEIKLRIRAKENTSSWYEDSFTPFRAKQIGPPEVHLEADKAIVYHI 146
 OY 121 SPGTSDSYMALDGLSFTYSLLIMKNSGVEERIEINYSRRKIYKLSPEPTYCLKVKAL 180

Db 147 SPGTRDSVMALDGLSFTSYSLIMKNSGVEERINISRHKIKYKLSPEPTYCLVKAKAL 206
OY 181 LTRMKIGVSPVHCIKITVENEL 203
Db 207 LTRMKIGVSPVHCIKITVENEL 229

RESULT 5

R14488 5
ID R14488 standard; Protein: 557 AA.
AC R14488;
DT 16-JAN-1992 (first entry)
DE Complete interferon-alpha/beta receptor.
KW IFN; autoimmune disease; graft rejection; histocompatibility.
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 437..457
FT /label= transmembrane
FT 458..557
FT /label= cytoplasmic
PN FR2657881-A.
PD 09-AUG-1991.
PF 05-FEB-1990; 001298.
PR 05-FEB-1990; FR-001298.
PA (EUBI-) LAB EURO BIOTECHNO.
PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE;
PI Tovey MG, Uze G;
PI WPI: 91-31978/44.
DR N-PSDB: Q14240.
PT New water-soluble polypeptide(s) with affinity for IFN-alpha and
PT beta - used to treat e.g. lupus erythematosus, Behcet's disease,
PT aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.
PS Disclousure: Page 47: 52pp: French.
CC The invention covers derivatives of the interferon-alpha and/or beta
CC receptor obtained by deleting the transmembrane and cytoplasmic domains
CC of the native receptor or by substitution. Potentially immunogenic
CC epitopes are eliminated and the deriv. can be secreted from
CC transformed cells. Soluble deriv.s block the activity of IFN alpha/beta
CC and can be used to treat autoimmune diseases or to inhibit graft
CC rejection. See also Q14239.
SQ Sequence 557 AA;

Query Match 100.0%; Score 1072; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 1.5e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GKNLKSPOKVEVDIIDNFIIRNRSDESVGNVTFSPDYOKTGMNWKILSGCQNTSTK 60
Db 27 GKNLKSPOKVEVDIIDNFIIRNRSDESVGNVTFSPDYOKTGMNWKILSGCQNTSTK 86
OY 61 CNFSSKLNVYEIKLRIRAEKENTSSWEVDSFTPPKAOIGPPEVHLEADKAIYIHI 120
Db 87 CNFSSKLNVYEIKLRIRAEKENTSSWEVDSFTPPKAOIGPPEVHLEADKAIYIHI 146
OY 121 SPGTRDSVMALDGLSFTSYSLIMKNSGVEERINISRHKIKYKLSPEPTYCLVKAKAL 180
Db 147 SPGTRDSVMALDGLSFTSYSLIMKNSGVEERINISRHKIKYKLSPEPTYCLVKAKAL 206
OY 181 LTRMKIGVSPVHCIKITVENEL 203
Db 207 LTRMKIGVSPVHCIKITVENEL 229

RESULT 6
ID R28496
AC R28496 standard; Protein: 557 AA.
DT 31-MAR-1993 (first entry)
DE Sequence of a soluble form of the interferon (IFN) receptor
DE with a high affinity for IFN-alpha and -beta.
KW Interferon receptor; alpha-interferon; beta-interferon.

OS Synthetic.
PN WO9218626-A.
PD 29-OCT-1992.
PF 17-APR-1991; F00318.
PR 17-APR-1991; WO-F00318.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,
PI Tovey M, Uze G;
PI WPI: 92-38210/46.
DR N-PSDB: Q30533.
PT Water soluble polypeptide(s) strongly bind interferon(s) alpha
PT and beta - useful as immunosuppressants, for treating autoimmune
PT diseases and transplant rejection
PS Claim 3; Fig 2; 58pp: English.
CC DNA encoding the water-soluble polypeptide with a high affinity for
CC IFN-alpha and -beta is isolated by PCR, using appropriate
CC oligonucleotides as primers and cloned cDNA as template.
CC bacteriophage lambda ZAP, containing the entire coding sequence of
CC the IFN-alpha and -beta receptor (Q30533), was incubated with oligos
CC Q30534 and Q30535. R28496 represents the complete receptor. R28495
CC lacks the transmembrane and cytoplasmic domains. Both forms bind
CC IFN in the same way as antibodies so are immunosuppressants e.g. for
CC treating autoimmune diseases and graft rejection. They lack the
CC toxic side-effects of known immunosuppressants such as steroids.
SQ Sequence 557 AA;

Query Match 100.0%; Score 1072; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 1.5e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GKNLKSPOKVEVDIIDNFIIRNRSDESVGNVTFSPDYOKTGMNWKILSGCQNTSTK 60
Db 27 GKNLKSPOKVEVDIIDNFIIRNRSDESVGNVTFSPDYOKTGMNWKILSGCQNTSTK 86
OY 61 CNFSSKLNVYEIKLRIRAEKENTSSWEVDSFTPPKAOIGPPEVHLEADKAIYIHI 120
Db 87 CNFSSKLNVYEIKLRIRAEKENTSSWEVDSFTPPKAOIGPPEVHLEADKAIYIHI 146
OY 121 SPGTRDSVMALDGLSFTSYSLIMKNSGVEERINISRHKIKYKLSPEPTYCLVKAKAL 180
Db 147 SPGTRDSVMALDGLSFTSYSLIMKNSGVEERINISRHKIKYKLSPEPTYCLVKAKAL 206
OY 181 LTRMKIGVSPVHCIKITVENEL 203
Db 207 LTRMKIGVSPVHCIKITVENEL 229

RESULT 7
ID R42635
AC R42635 standard; Protein: 557 AA.
DT 20-APR-1994 (first entry)
DE Human interferon receptor.
KW IFN-R; extracellular domain; monoclonal antibody; viral infection;
KW cell proliferation; allograft rejection; systemic lupus erythematosus;
KW psoriasis; multiple sclerosis; Behcet's Disease; aplastic anaemia;
KW immunodeficiency; measles virus; interferon-alpha-beta.
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 1..436
FT /label= extracellular_domain
FT /note= "soluble, immunogenic form of IFN-R"
PN EP-563487-A.
PD 06-OCT-1993.
PF 31-MAR-1992; 400902.
PR 31-MAR-1992; EP-400902.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
PI Benoit P, Maguire D, Meyer F, Plavec I, Tovey MG;
PI WPI: 93-312951/40.
DR P-PSDB: R42635.
PT Monoclonal antibody to human interferon type-I receptor - having
PT neutralising activity against human type I interferon, used for

PT therapy and diagnosis
PS Disclosure: Fig.3: 21pp: English.
CC Monoclonal antibodies produced against soluble forms of the human
CC interferon alpha-beta receptor based on the full-length human IFN-R
CC sequence are claimed. The antibodies are useful for treatment and
CC prophylaxis of disorders involving cell proliferation and/or viral
CC infection.
SO Sequence 557 AA;

Query Match 100.0%; Score 1072; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 1.5e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKNLSPQKVEVDIIDDNFILRMNSDSVGNVTFSPDYQKTGMNMWIKLSCGQNTSTK 60
DB 27 GKNLSPQKVEVDIIDDNFILRMNSDSVGNVTFSPDYQKTGMNMWIKLSCGQNTSTK 86
QY 61 CNFSSKLNVYEELIRIRAEKENTSMYEVDSFTPRKAOIGPPEVHLEADKAIYIHI 120
DB 87 CNFSSKLNVYEELIRIRAEKENTSMYEVDSFTPRKAOIGPPEVHLEADKAIYIHI 146
QY 121 SPGTRDSVMALDGLSTFTYSLIMKNSGVEERINISRHKIYKLSPTTYCLKVAAL 180
DB 147 SPGTRDSVMALDGLSTFTYSLIMKNSGVEERINISRHKIYKLSPTTYCLKVAAL 206
QY 181 LTSWKIGVSPVHCITVENEL 203
DB 207 LTSWKIGVSPVHCITVENEL 229

RESULT 8

R75356
ID R75356 standard: Protein; 557 AA.
AC R75356;
DT 16-OCT-1995 (first entry)
DE Human IFN receptor.
KW IFN receptor; interferon receptor; interferon-alpha;
KW interferon-beta; monoclonal antibody; immunomodulator; AIDS.
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 1..436
FT /label= Extracellular_domain
FT W09507716-A.
PD 23-MAR-1995.
PR 16-SEP-1994; E03114.
PR 17-SEP-1993; EP-402279.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
PI Benlzri EJ, Tovey MG;
DR N-PSDB; 086458.
PT Compn. of monoclonal antibodies against interferon receptor -
PT useful as immuno-modulator, eg. for treating AIDS
PS Disclosure: Fig.3A-2B; 105pp; English.
CC The amino acid sequence of human interferon class I receptor is
CC given in R75356. A recombinant soluble form of the extracellular
CC domain of this receptor (R71723) has been used to raise
CC immunomodulatory monoclonal antibodies.
SO Sequence 557 AA;

Query Match 100.0%; Score 1072; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 1.5e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKNLSPQKVEVDIIDDNFILRMNSDSVGNVTFSPDYQKTGMNMWIKLSCGQNTSTK 60
DB 27 GKNLSPQKVEVDIIDDNFILRMNSDSVGNVTFSPDYQKTGMNMWIKLSCGQNTSTK 86
QY 61 CNFSSKLNVYEELIRIRAEKENTSMYEVDSFTPRKAOIGPPEVHLEADKAIYIHI 120
DB 87 CNFSSKLNVYEELIRIRAEKENTSMYEVDSFTPRKAOIGPPEVHLEADKAIYIHI 146

QY 121 SPGTRDSVMALDGLSTFTYSLIMKNSGVEERINISRHKIYKLSPTTYCLKVAAL 180
DB 147 SPGTRDSVMALDGLSTFTYSLIMKNSGVEERINISRHKIYKLSPTTYCLKVAAL 206
QY 181 LTSWKIGVSPVHCITVENEL 203
DB 207 LTSWKIGVSPVHCITVENEL 229

RESULT 9

W21805
ID W21805 standard: Protein; 434 AA.
AC W21805;
DT 23-SEP-1997 (first entry)
DE Spliced-deleted interferon alpha-receptor form 1.
KW Interferon alpha-receptor; IFNAR.
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 1..427
FT /label= Extracellular_domain
FT /note= "comprises amino acids 1-427 of the
FT transmembrane IFNAR"
FT 428..434
FT /label= S-domain
FT AU9475977-A.
PD 11-MAY-1995.
PR 20-OCT-1994; 075977.
PR 24-OCT-1993; IL-107378.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (ABRA/) ABRAMOVICH C.
PI Abramovich C, Ratovitski E, Revel M;
DR WPI: 95-200634/27.
PT New mammalian soluble interferon alpha-receptor forms - used for
PT inhibiting, modulating or modifying the activities of interferon(s)
PS Example 2; Fig 7; 46pp; English.
CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 1
CC (W21805) is characterised by a new domain (S) which follows an
CC end-deleted extracellular domain when compared to transmembrane
CC IFNAR (W21804). There is no transmembrane domain. The amino acid
CC sequence is predicted from a cDNA clone (see also T73520) obtd.
CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR
CC splice-deleted forms 1 and 2 (see also W21806) probably regulate
CC the response of human cells to IFNs, either by acting as IFN
CC antagonists or by regulating the activity of the multiple IFN
CC subtypes. They can be expressed in host cells and used to inhibit,
CC modulate or modify the activities of IFNs alpha and beta in cells,
CC tissues or organisms, or for diagnostic purposes.
SO Sequence 434 AA;

Query Match 99.5%; Score 1067; DB 1; Length 434;
Best Local Similarity 99.5%; Pred. No. 3.5e-101;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GKNLSPQKVEVDIIDDNFILRMNSDSVGNVTFSPDYQKTGMNMWIKLSCGQNTSTK 60
DB 27 GKNLSPQKVEVDIIDDNFILRMNSDSVGNVTFSPDYQKTGMNMWIKLSCGQNTSTK 86
QY 61 CNFSSKLNVYEELIRIRAEKENTSMYEVDSFTPRKAOIGPPEVHLEADKAIYIHI 120
DB 87 CNFSSKLNVYEELIRIRAEKENTSMYEVDSFTPRKAOIGPPEVHLEADKAIYIHI 146
QY 121 SPGTRDSVMALDGLSTFTYSLIMKNSGVEERINISRHKIYKLSPTTYCLKVAAL 180
DB 147 SPGTRDSVMALDGLSTFTYSLIMKNSGVEERINISRHKIYKLSPTTYCLKVAAL 206
QY 181 LTSWKIGVSPVHCITVENEL 203
DB 207 LTSWKIGVSPVHCITVENEL 229

RESULT 10

W21806

ID W21806 standard; Protein: 496 AA.
AC W21806:
DT 23-SEP-1997 (first entry)
DE Spliced-deleted interferon alpha-receptor form 2.
KW Interferon alpha-receptor; IFNAR.
OS Homo sapiens.
FH Key
FT domain
FT 1.419
FT /label= Extracellular_domain
FT /note= "Comprises amino acid residues 1-413 and
FT 422-427 of transmembrane IFNAR"
FT 420..496
FT domain
FT /label= Intracellular_domain
FT /note= "Comprises amino acids 481-557 of
FT transmembrane IFNAR"
PN AU9475977-A.
PD 11-MAY-1995.
PF 20-OCT-1994; 075977.
PR 24-OCT-1993; IL-107378.
PA (YEDA) YEDA RES & DEV CO LTD.
PI (ABRA/) ABRAMOVICH C.
PI Abramovich C, Ratovitski E, Revel M;
DR WPI: 95-200634/27.
PT New mammalian soluble interferon alpha-receptor forms - used for
PT inhibiting, modulating or modifying the activities of interferon(s)
PS Example 3; Fig 7; 46pp; English.
CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 2
CC (W21806) is characterised by a double deletion when compared to
CC transmembrane IFNAR (W21804). The extracellular domain is
CC shortened by 6 amino acid residues and is followed by a truncated
CC intracellular domain. There is no transmembrane region. The amino
CC acid sequence is predicted from a cDNA clone (see also T73521) obtd.
CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR
CC splice-deleted forms 1 (see also W21805) and 2 may regulate the
CC response of human cells to IFNs, either by acting as IFN
CC antagonists or by regulating IFN activities. They can be expressed
CC in host cells and used to inhibit, modulate or modify the
CC activities of IFNs alpha and beta in cells, tissues and organisms,
CC or for diagnostic purposes.
SQ Sequence 496 AA;

Query Match 99.5%; Score 1067; DB 1; Length 496;
Best Local Similarity 99.5%; Pred. No. 4.3e-101;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GKNLKSPOKYEVDIIDNFI LRNRSDES VGNVTFSDYQKTGMWNKILSGCONITSTK 60
DB 27 GKNLKSPOKYEVDIIDNFI LRNRSDES VGNVTFSDYQKTGMWNKILSGCONITSTK 86
QY 61 CNFSSKLNVYEIEIKLRIRAEKENTSSWEVDSFTPPRKAQIGPPEVHLEADKAIVIH 120
DB 87 CNFSSKLNVYEIEIKLRIRAEKENTSSWEVDSFTPPRKAQIGPPEVHLEADKAIVIH 146
QY 121 SPQTKDSVMALDGLSTFTSLIMKNSSGVEERIENTYSRHKIYKSPETTYCLKVAAL 180
DB 147 SPQTKDSVMALDGLSTFTSLIMKNSSGVEERIENTYSRHKIYKSPETTYCLKVAAL 206
QY 181 LTSWKIGVSPVHCITKTVENEL 203
DB 207 LTSWKIGVSPVHCITKTVENEL 229

RESULT 11
ID W21804 standard; Protein: 557 AA.
AC W21804:
DT 23-SEP-1997 (first entry)
DE Transmembrane interferon alpha-receptor.
KW Interferon alpha-receptor; IFNAR.
OS Homo sapiens.
FH Key
FT domain
FT 1.436

FT domain
FT 437.
FT /label= Extracellular_domain
FT /label= Transmembrane_domain
FT 458.
FT domain
FT /label= Intracellular_domain
PN AU9475977-A.
PD 11-MAY-1995.
PF 20-OCT-1994; 075977.
PR 24-OCT-1993; IL-107378.
PA (YEDA) YEDA RES & DEV CO LTD.
PI (ABRA/) ABRAMOVICH C.
PI Abramovich C, Ratovitski E, Revel M;
DR WPI: 95-200634/27.
PT New mammalian soluble interferon alpha-receptor forms - used for
PT inhibiting, modulating or modifying the activities of interferon(s)
PS Disclosure; Fig 7; 46pp; English.
CC Human transmembrane interferon alpha receptor (IFNAR) (W21804)
CC includes a 21-amino acid transmembrane region. Novel, splice-
CC deleted IFNAR forms 1 (W21805) and 2 (W21806) have been detected
CC that lack this transmembrane domain. These, soluble non-membrane
CC bound polypeptides can be expressed in host cells and used to
CC inhibit, modulate or modify the activities of interferons alpha
CC and beta in cells, tissues and organisms, or for diagnostic
CC purposes.
SQ Sequence 557 AA;

Query Match 99.5%; Score 1067; DB 1; Length 557;
Best Local Similarity 99.5%; Pred. No. 5e-101;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GKNLKSPOKYEVDIIDNFI LRNRSDES VGNVTFSDYQKTGMWNKILSGCONITSTK 60
DB 27 GKNLKSPOKYEVDIIDNFI LRNRSDES VGNVTFSDYQKTGMWNKILSGCONITSTK 86
QY 61 CNFSSKLNVYEIEIKLRIRAEKENTSSWEVDSFTPPRKAQIGPPEVHLEADKAIVIH 120
DB 87 CNFSSKLNVYEIEIKLRIRAEKENTSSWEVDSFTPPRKAQIGPPEVHLEADKAIVIH 146
QY 121 SPQTKDSVMALDGLSTFTSLIMKNSSGVEERIENTYSRHKIYKSPETTYCLKVAAL 180
DB 147 SPQTKDSVMALDGLSTFTSLIMKNSSGVEERIENTYSRHKIYKSPETTYCLKVAAL 206
QY 181 LTSWKIGVSPVHCITKTVENEL 203
DB 207 LTSWKIGVSPVHCITKTVENEL 229

RESULT 12
ID W52296 standard; Protein: 325 AA.
AC W52296:
DT 23-JUN-1998 (first entry)
DE CRP4 protein.
KW CRP4; Interleukin-10; IL-10; IL-10 receptor; allograft rejection;
KW vaccine; photosensitivity; inflammation; autoimmune disease;
KW septic shock; immune response; organ rejection; gene therapy.
OS Homo sapiens.
PN MO9802542-A1.
PD 22-JAN-1998.
PF 17-JUL-1997; U12455.
PR 17-JUL-1996; US-683743.
PA (UYNE-) UNIV NEW JERSEY.
PI Kotenko SV, Pestka S;
PI WPI: 98-110590/10.
DR N-PSDB: V19874.
PT New recombinant DNA - comprises sequences encoding interleukin-10
PT and CRP4 linked to operator, useful, e.g. preventing allograft
PT rejection
PS Claim 2; Page -: 79pp; English.
CC This sequence is the human CRP4 sequence, DNA encoding it is used in the
CC recombinant DNA (1) of the invention. (1) comprises a sequence (S1)
CC encoding the interleukin-10 (IL-10) receptor (IL10R) and a sequence (S2)

CC encodind CRF4, both operably linked to expression control sequences.
CC Cells containing (I) may be used to identify agonists/antagonist of
CC IL-10. Agonists are potentially useful, e.g. for preventing allograft
CC rejection, as vaccine adjuvants, for treatment of photosensitivity,
CC inflammation, autoimmune disease and septic shock, while antagonists are
CC potentially useful for increasing immune responses against tumours,
CC viruses, bacteria and parasites (especially intracellular pathogens) and
CC for preventing organ rejection. A vector containing (I) is used to
CC restore, e.g. by gene therapy, IL-10 sensitivity to a cell that expresses
CC a dysfunctional IL10R and is able to bind IL-10 but not to transduce a
CC signal. Antisense CRF4 sequences (especially ribozymes), can inhibit
CC IL-10 activity in cells. Antibodies specific for CRF4 are used to
CC measure and localise CRF4, for diagnosis of defective IL-10 activity.
CC Fragments of (I) are used as primers or probes to assay CRF4-specific
CC RNA. Agonists/antagonists may be administered parenterally, orally or
CC rectally especially by intravenous injection or directly into a tumour or
CC allograft. 325 AA:
90 Sequence

Query Match	20.0%	Score 214	DB 1	Length 325
Best Local Similarity	30.5%	Pred. No. 4.1e-14		
Matches	60	Conservative	39	Mismatches 86
				Indels 12
				Gaps 7

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OY 7 POKEVVDIIIDNFI LRNRSDSEVCNVTYFSPDYOKTGDMNIXKLSGCONITSTGCNSSL 66
Db 24 PENVMNNSVNRKRNITQWSESPAFKGNLTFTAOY---LSYRI FODKCNNTLTICDSS- 79
OY 67 KLNYEEIKLRIRAE-KENTSSWEVDSTFPRKAOIGPPEVHEA-EDKAIYIHISPGT 124
Db 79 -LSKGDHTLIRAEFAEBHSDWNI -TFCYVDDTIIPQMOYEVLA DSIHMFLLPKI 133
OY 125 KDSV-MALADGL -SFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPEPTYCLKAYAL 181
Db 137 ENEYETFMKNVNYMNTVNOGYMKNGKDEKQIFPQOYEVFLRNLEPWTTCVGVREGLP 196
OY 182 TSMKIGVSPVHCITTT 198
Db 197 DRNKAGWSEVPCEQTT 213

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Accession	Protein	Length	Source	Species	Organism	Strain	Reference
R75782	13						
AC	R75782 standard: Protein: 332 AA.						
DT	R75782:						
DE	13-NOV-1995 (first entry)						
KM	IFN-gamma receptor beta-subunit.						
KV	Interferon-gamma receptor beta subunit; muIFN;						
OS	interferon-gamma-antagonist.						
FM	Mus sp.						
FT	Key						
FT	peptide						
FT	Location/Qualifiers						
FT	1..18						
FT	/label= Sig-peptide						
FT	19..242						
FT	/label= Extracellular_domain						
FT	243..266						
FT	/label= Transmembrane_anchoring_domain						
FT	267..332						
FT	/label= Cytoplasmic_domain						
PN	W09516036-A.						
PD	15-JUN-1995.						
PF	07-DEC-1994: U14277.						
PR	09-DEC-1993: US-164596.						
PA	(AGUE/) AGUER M.						
PA	(BOEH/) BOEHNI R.						
PA	(HEMM/) HEMMI S.						
DR	Aquet M, Boehni R, Hemmi S.						
DR	WPI: 95-224321/29.						
DR	N-PSDB: Q90808.						
PT	Novel Interferon gamma receptor polypeptide - for						
PT	treatment of inflammatory bowel disease and liver damage						
CC	Claim 3; Fig. 2A; 86pp: English.						
CC	The IFN-gamma receptor beta-subunit encoded by a cDNA clone derived						

CC from mouse B-cells is given in R15782. Recombinant beta-subunit,
CC pref. with the transmembrane anchoring domain deleted or
CC inactivated and with the cytoplasmic domain deleted, may be
CC used to treat pathological conditions associated with endogenous
CC IFN-gamma production.
SQ Sequence 332 AA;

Query Match	18.6%;	Score 199;	DB 1;	Length 332;
Best Local Similarity	30.1%;	Pred. NO. 1.4e-12;		
Matches 65;	Conservative 38;	Mismatches 81;	Indels 32;	Gaps 12

[illegible]

RESULT	14	
ID	W79159	
AC	W79159	standard; Protein: 553 AA.
DT	20-NOV-1998	(first entry)
DE	Zcyto7 cytokine receptor polypeptide.	
KW	Zcyto7; cytokine receptor; ligand-binding polypeptide; kidney; pancreas;	
KW	type 2 cytokine receptor family; CRF2; prostate tissue; nervous tissue;	
KW	agonist; cell proliferation; cell differentiation; renal disease; human;	
KW	neural disease; pancreatic disease.	
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	Domain	30..250
FT		/note="extracellular (ligand-binding) domain;
FT		sequence claimed in claim 1"
FT	Domain	275..553
FT		/note="intracellular domain"
FN	W09837193-A1.	
PD	27-AUG-1998.	
PF	18-FEB-1998; U03029.	
PR	02-OCT-1997; US-943087.	
PR	20-FEB-1997; US-803305.	
PA	(ZYMO) ZYMOGENETICS INC.	
PI	Adams RL, Farrah TM, Jelineberg AC, Kho CJ, Lok S,	
P1	Whitmore TE	
P1	WPI: 98-480798/41.	
DR	N-PSDE: V57515.	
PT	Novel human Zcyto7 DNA encodes a type 2 cytokine receptor - useful	
PT	for treating renal, neural, pancreatic and prostatic diseases	
PS	Claim 1: Pages 55-59; 72pp; English.	
CC	This represents the Zcyto7 cytokine receptor. Zcyto7 is a ligand-	
CC	binding receptor polypeptide and is a novel member of the type 2 cytokine	
CC	receptor family (CRF2). An expression vector containing the Zcyto	
CC	polynucleotide, operably linked to transcription promoter, a sequence	
CC	encoding a transmembrane and intracellular domain, or both, and a	
CC	transcriptional terminator can be used to transform host cells for the	
CC	recombinant production of the polypeptide. The sequences can be used to	
CC	study the Zcyto7 gene and to isolate ligands binding to it. Zcyto7 is	
CC	preferentially expressed in the kidney, pancreas, prostate or nervous	
CC	tissue. Agonists of Zcyto7 can be used to stimulate proliferation and	
CC	differentiation of cell in these organs. The antagonists and agonists can	
CC	also be used in the treatment of renal, neural, pancreatic and prostate	
CC	diseases.	
SO	Sequence	553 AA;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 1, 2000, 04:17:53 ; Search time 23.82 Seconds

(without alignments)
123,039 Million cell updates/sec

Title: US-09-240-675-2_COPY_27_229

Perfect score: 1072

Sequence: 1 GKNLSPQKVEVDIIDNFI.....WKIGYSPYCHIKTIVNEL 203

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 145308 seqs, 14437401 residues

Total number of hits satisfying chosen parameters: 145308

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 08

Listing first 45 summaries

Database : Issued Patents,AA,*

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3: /cgn2_6/ptodata/1/1aa/6.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PC/US.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1072	100.0	434	1	US-08-328-256-11
2	1072	100.0	436	2	US-08-307-588-2
3	1072	100.0	496	1	US-08-328-256-12
4	1072	100.0	557	1	US-08-328-256-10
5	1072	100.0	557	1	US-08-411-454-2
6	1072	100.0	557	2	US-08-466-974-2
7	1072	100.0	557	2	US-08-471-453-2
8	1072	100.0	557	2	US-08-307-588-4
9	490.5	45.8	202	4	PCT-US94-14277-3
10	214	20.0	325	2	US-08-683-743-4
11	199	18.6	332	4	PCT-US94-14277-2
12	192	17.9	223	4	PCT-US94-14277-6
13	172.5	16.1	221	2	US-08-943-087-56
14	167.5	15.6	221	2	US-08-943-087-54
15	166.5	15.5	221	2	US-08-943-087-50
16	166.5	15.5	553	2	US-08-943-087-2
17	166.5	15.5	553	2	US-08-943-087-14
18	166.5	15.5	553	2	US-08-943-087-16
19	166.5	15.5	553	2	US-08-943-087-18
20	166.5	15.5	553	2	US-08-943-087-20
21	166.5	15.5	553	2	US-08-943-087-22
22	166.5	15.5	553	2	US-08-943-087-24
23	166.5	15.5	553	2	US-08-943-087-26
24	166.5	15.5	553	2	US-08-943-087-28
25	166.5	15.5	553	2	US-08-943-087-30
26	166.5	15.5	553	2	US-08-943-087-32
27	166.5	15.5	553	2	US-08-943-087-34
28	166.5	15.5	553	2	US-08-943-087-36
29	166.5	15.5	553	2	US-08-943-087-38

30	166.5	15.5	553	2	US-08-943-087-40	Sequence 40, Appl
31	166.5	15.5	553	2	US-08-943-087-42	Sequence 42, Appl
32	166.5	15.5	553	2	US-08-943-087-44	Sequence 44, Appl
33	166.5	15.5	553	2	US-08-943-087-46	Sequence 46, Appl
34	166.5	15.5	553	2	US-08-943-087-48	Sequence 48, Appl
35	165.5	15.4	221	2	US-08-943-087-52	Sequence 52, Appl
36	163.5	15.3	221	2	US-08-943-087-60	Sequence 60, Appl
37	160.5	15.0	221	2	US-08-943-087-58	Sequence 58, Appl
38	145	13.5	200	4	PCT-US94-14277-4	Sequence 4, Appl
39	142	13.2	337	2	US-08-906-713-2	Sequence 8, Appl
40	131.5	12.3	574	2	US-08-906-713-2	Sequence 2, Appl
41	111	10.4	489	4	PCT-US93-11110-1	Sequence 1, Appl
42	111	10.4	489	5	5221789-1	Patent No. 5221789
43	92	8.6	265	2	US-08-385-191A-14	Sequence 14, Appl
44	89.5	8.3	2213	1	US-08-727-034-3	Sequence 3, Appl
45	89	8.3	239	2	US-08-385-191A-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-328-256-11
Sequence 11, Application US/08328256
Patent No. 5643749
GENERAL INFORMATION:
APPLICANT: REVEL, Michel
APPLICANT: ABRAMOVICH, Carolina
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,256
FILING DATE: 24-OCT-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: IT 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: REVEL-13
REFERENCE/DOCKET NUMBER: 25,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ. ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-328-256-11

Query Match 100.0%; Score 1072; DB 1; Length 434;

Best Local Similarity 100.0%; Pred. No. 4.9e-112;

Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKNLSPQKVEVDIIDNFIILRNRSDESYGNVTFSDYQKIGMDNWKISGCONITSTK 60

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Db 27 GNLKSPQKVEVDIIDNFIILRMNRSDSVGNVTFSDYQKTMGMWIKLSGCONITSTK 86
QY 61 CNFSSKLNYEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLEADKAIVIH 120
Db 87 CNFSSKLNYEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLEADKAIVIH 146
QY 121 SPGRKDSVMALDGLSFTYSLILWKNSSGVEERENIYSRHKIKYKLSPEPTYCLKVAAL 180
Db 147 SPGRKDSVMALDGLSFTYSLILWKNSSGVEERENIYSRHKIKYKLSPEPTYCLKVAAL 206
QY 181 LTSWKIGYSPVHCIKITVENEL 203
Db 207 LTSWKIGYSPVHCIKITVENEL 229

RESULT 2
US-08-307-588-2
; Sequence 2, Application US/08307588
; Patent No. 5919453
; GENERAL INFORMATION:
; APPLICANT: BENOIT, Patrick
; APPLICANT: MEYER, Francois
; APPLICANT: MAGUIRE, Deborah
; APPLICANT: PLAVEC, Ivan
; APPLICANT: TOVEY, Michael G.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/307,588
; FILING DATE: 05-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00770
; FILING DATE: 30-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92400902.0
; FILING DATE: 31-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 17283/117/GUPL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5339
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 436 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-307-588-2

Query Match 100.0%; Score 1072; DB 2; Length 436;
Best Local Similarity 100.0%; Pred. No. 5e-112;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNLKSPQKVEVDIIDNFIILRMNRSDSVGNVTFSDYQKTMGMWIKLSGCONITSTK 60
Db 27 GNLKSPQKVEVDIIDNFIILRMNRSDSVGNVTFSDYQKTMGMWIKLSGCONITSTK 86

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QY 61 CNFSSKLNYEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLEADKAIVIH 120
Db 87 CNFSSKLNYEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLEADKAIVIH 146
QY 121 SPGRKDSVMALDGLSFTYSLILWKNSSGVEERENIYSRHKIKYKLSPEPTYCLKVAAL 180
Db 147 SPGRKDSVMALDGLSFTYSLILWKNSSGVEERENIYSRHKIKYKLSPEPTYCLKVAAL 206
QY 181 LTSWKIGYSPVHCIKITVENEL 203
Db 207 LTSWKIGYSPVHCIKITVENEL 229

RESULT 3
US-08-328-256-12
; Sequence 12, Application US/08328256
; Patent No. 5643749
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: ABRAMOVICH, Carolina
; APPLICANT: RATOVITSKI, Edward
; TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,256
; FILING DATE: 24-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 107378
; FILING DATE: 24-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: REVEL-13
; REFERENCE/DOCKET NUMBER: 25,618
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 496 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-328-256-12

Query Match 100.0%; Score 1072; DB 1; Length 496;
Best Local Similarity 100.0%; Pred. No. 6e-112;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNLKSPQKVEVDIIDNFIILRMNRSDSVGNVTFSDYQKTMGMWIKLSGCONITSTK 60
Db 27 GNLKSPQKVEVDIIDNFIILRMNRSDSVGNVTFSDYQKTMGMWIKLSGCONITSTK 86
QY 61 CNFSSKLNYEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLEADKAIVIH 120
Db 87 CNFSSKLNYEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLEADKAIVIH 146

OY 121 SPGTRDSVMMALDGLSTFYSLILMKNSGVEERIENTISRRKIYKLSPEYTYCLKVAAL 180
|
DB 147 SPGTRDSVMMALDGLSTFYSLILMKNSGVEERIENTISRRKIYKLSPEYTYCLKVAAL 206
OY 181 LTSWKIGVSPVHCICKTTVENEL 203
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DB 207 LTSWKIGVSPVHCICKTTVENEL 229

RESULT 4

US-08-328-256-10
; Sequence 10, Application US/08328256
; Patent No. 5643749
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: ABRAMOVICH, Carolina
; APPLICANT: RANOVITSKI, Edward
; TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
; PREPARATION AND USE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,256
; FILING DATE: 24-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 107378
; FILING DATE: 24-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: REVEL-13
; REFERENCE/DOCKET NUMBER: 25,618
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-328-256-10

Query Match 100.0%; Score 1072; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 7.2e-112;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|
DB 27 GKNLSPQKVEVDIIDNFIILMNRSDSVGNVTFSPDYOKTGMDNMWIKLSGCONITSTK 86
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|
DB 87 CNFSSLKLVYEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPEVHLEAEKAIYIHI 146
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|
DB 147 SPGTRDSVMMALDGLSTFYSLILMKNSGVEERIENTISRRKIYKLSPEYTYCLKVAAL 206
OY 181 LTSWKIGVSPVHCICKTTVENEL 203

DB 207 LTSWKIGVSPVHCICKTTVENEL 229
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RESULT 5

US-08-471-454-2
; Sequence 2, Application US/08471454
; Patent No. 5731169
; GENERAL INFORMATION:
; APPLICANT: MOESEN, Knud E.
; APPLICANT: UZE, Gilles
; APPLICANT: LUTFALLA, Georges
; APPLICANT: GRESSER, Ion
; TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
; THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
; PREPARATION OF THE CORRESPONDING PROTEIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHAYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,454
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/900,642
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: FR 89/13770
; FILING DATE: 20-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 960-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-471-454-2

Query Match 100.0%; Score 1072; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 7.2e-112;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GKNLSPQKVEVDIIDNFIILMNRSDSVGNVTFSPDYOKTGMDNMWIKLSGCONITSTK 60
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DB 27 GKNLSPQKVEVDIIDNFIILMNRSDSVGNVTFSPDYOKTGMDNMWIKLSGCONITSTK 86
OY 61 CNFSSLKLVYEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPEVHLEAEKAIYIHI 120
|
DB 87 CNFSSLKLVYEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPEVHLEAEKAIYIHI 146
OY 121 SPGTRDSVMMALDGLSTFYSLILMKNSGVEERIENTISRRKIYKLSPEYTYCLKVAAL 180
|
DB 147 SPGTRDSVMMALDGLSTFYSLILMKNSGVEERIENTISRRKIYKLSPEYTYCLKVAAL 206
OY 181 LTSWKIGVSPVHCICKTTVENEL 203

Db 207 LTRKIGVSPVHCITVENEL 229

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RESULT 6
US-08-466-974-2
; Sequence 2, Application US/08466974
; Patent No. 5861258
; GENERAL INFORMATION:
; APPLICANT: MOGENSEN, Knud E.
; APPLICANT: UZE, Gilles
; APPLICANT: LUTFALLA, Georges
; APPLICANT: GRESSER, Ion
; TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
; TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
; TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,974
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/900,642
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: FR 89/13770
; FILING DATE: 20-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 960-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-466-974-2
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Query Match 100.0%; Score 1072; DB 2; Length 557;
Best Local Similarity 100.0%; Pred. No. 7.2e-112;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GKNLSPQKVEVDIIDNFIILRNRSDESVGNVTFSDYQKTGMNWKILSGCONITSTK 60
DB 27 GKNLSPQKVEVDIIDNFIILRNRSDESVGNVTFSDYQKTGMNWKILSGCONITSTK 86
QY 61 CNFSSKLNVVEEIKLIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLEADKAIYIHI 120
DB 87 CNFSSKLNVVEEIKLIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLEADKAIYIHI 146
QY 121 SPGRKDSVMAALDGLSTFTSLILKRNSSGVEERIENTIYSRHKIYKLSPTTYCLKVAAL 180
DB 147 SPGRKDSVMAALDGLSTFTSLILKRNSSGVEERIENTIYSRHKIYKLSPTTYCLKVAAL 206
QY 181 LTRKIGVSPVHCITVENEL 203
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Db 207 LTRKIGVSPVHCITVENEL 229

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|||||
RESULT 7
US-08-471-453-2
; Sequence 2, Application US/08471453
; Patent No. 586153
; GENERAL INFORMATION:
; APPLICANT: MOGENSEN, Knud E.
; APPLICANT: UZE, Gilles
; APPLICANT: LUTFALLA, Georges
; APPLICANT: GRESSER, Ion
; TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
; TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
; TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,453
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/900,642
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: FR 89/13770
; FILING DATE: 20-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 960-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-471-453-2
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Query Match 100.0%; Score 1072; DB 2; Length 557;
Best Local Similarity 100.0%; Pred. No. 7.2e-112;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GKNLSPQKVEVDIIDNFIILRNRSDESVGNVTFSDYQKTGMNWKILSGCONITSTK 60
DB 27 GKNLSPQKVEVDIIDNFIILRNRSDESVGNVTFSDYQKTGMNWKILSGCONITSTK 86
QY 61 CNFSSKLNVVEEIKLIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLEADKAIYIHI 120
DB 87 CNFSSKLNVVEEIKLIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLEADKAIYIHI 146
QY 121 SPGRKDSVMAALDGLSTFTSLILKRNSSGVEERIENTIYSRHKIYKLSPTTYCLKVAAL 180
DB 147 SPGRKDSVMAALDGLSTFTSLILKRNSSGVEERIENTIYSRHKIYKLSPTTYCLKVAAL 206
QY 181 LTRKIGVSPVHCITVENEL 203
```

Db 207 LITSMKIGVSPVHCITKTVENEL 229

RESULT 8

US-08-307-588-4
Sequence 4, Application US/08307588
Patent No. 5919453
GENERAL INFORMATION:
APPLICANT: BENOIT, Patrick
APPLICANT: MEYER, Francois
APPLICANT: MAGUIRE, Deborah
APPLICANT: PLAYEC, Ivan
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
TITLE OF INVENTION: INTERFERON
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00770
FILING DATE: 30-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92400902.0
FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Bernhard P.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 17283/117/GUPL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-307-588-4

Query Match

Best Local Similarity 100.0%; Score 1072; DB 2; Length 557;
Pred. No. 7.2e-112; Mismatches 0; Indels 0; Gaps 0;

Db 1 GKNLSPKQVEVDIIDDFILRMNRSDESGVGNVTFSPFYOKTGMNDWIKLSGCONITSTK 60
Db 27 GKNLSPKQVEVDIIDDFILRMNRSDESGVGNVTFSPFYOKTGMNDWIKLSGCONITSTK 86
Db 61 CNFSSLKLVYEEIKLRIRAEKENTSSWYEVDSFTPFKRAOIGPEVHLEADKAIVYIH 120
Db 87 CNFSSLKLVYEEIKLRIRAEKENTSSWYEVDSFTPFKRAOIGPEVHLEADKAIVYIH 146
Db 121 SPGRKDSYMAALDGLSTFTYSLIMKNSSGVEERENIYSRHKIKYKLSPEYTYCKVKAAL 180
Db 147 SPGRKDSYMAALDGLSTFTYSLIMKNSSGVEERENIYSRHKIKYKLSPEYTYCKVKAAL 206
Db 181 LITSMKIGVSPVHCITKTVENEL 203
Db 207 LITSMKIGVSPVHCITKTVENEL 229

RESULT 9

PCT-US94-14277-3
Sequence 3, Application PC/TUS9414277
GENERAL INFORMATION:
APPLICANT: Aguet, Michel
APPLICANT: Bonni, Ruth
APPLICANT: Hemmi, Silvio
TITLE OF INVENTION: Receptor subunit Polypeptides
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14277
FILING DATE: 07-DEC-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/164596
FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 866PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 202 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US94-14277-3

Query Match

Best Local Similarity 45.8%; Score 490.5; DB 4; Length 202;
Pred. No. 2.4e-47; Mismatches 69; Indels 1; Gaps 1;

Db 2 KNLSPKQVEVDIIDDFILRMNRSDESGVGNVTFSPFYOKTGMNDWIKLSGCONITSTK 61
Db 1 ENLKPENIDYIIDDVYTLKMSHGESMGSVTSAEYRTRDKRWLKKXECQITTTTC 60
Db 62 NFSSLKLVYEEIKLRIRAEKENTSSWYEVDSFTPFKRAOIGPEVHLEADKAIVYIH 120
Db 61 EFSILDINXYIKQFRRVRAEGNSTSSWNEVDPIFYTAHMSPEVRLREDKAIVYIH 120
Db 121 SPGRKDSYMAALDGLSTFTYSLIMKNSSGVEERENIYSRHKIKYKLSPEYTYCKVKAAL 180
Db 121 SPGRKDSYMAALDGLSTFTYSLIMKNSSGVEERENIYSRHKIKYKLSPEYTYCKVKAAL 202
Db 181 LITSMKIGVSPVHCITKTVENEL 202
Db 181 PSUKKHSNYSSTXOCISTTVANK 202

RESULT 10

US-08-683-743-4
Sequence 4, Application US/08683743
Patent No. 5843697
GENERAL INFORMATION:
APPLICANT: Pestka, Sidney

APPLICANT: Kotenko, Serguei
TITLE OF INVENTION: CYTOKINE RECEPTOR SIGNAL TRANSDUCTION
TITLE OF INVENTION: CHAIN
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,743
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601-1-050
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
TOPOLOGY: linear
HYPOTHETICAL: NO
FRAGMENT TYPE:
US-08-683-743-4

Query Match 20.0%; Score 214; DB 2; Length 325;
Best Local Similarity 30.5%; Pred. No. 4.9e-16;
Matches 60; Conservative 39; Mismatches 86; Indels 12; Gaps 7;
Oy 7 POKVEVDIIDNFIILNRNRSDESGVNTFSPDYOKTGMNMTKLSGCONISTKCNFSSL 66
Db 24 PENVMNSVNFENKNILOMESPAFAKGNLTFTAOY---LSYRILODKCMNTLTTECDSS- 79
Oy 67 KLVYEEIKLRIRAE-KENTSSWYEVDSFTPPRAQIGPPEVHLBA-EDKAIIVHISPGT 124
Db 79 -LSKIGDHLIRAFRAFEHSDWNI-FTCPYVDOTIIGPPGQYEVVLADSLHMRFLAPKI 136
Oy 125 KDSV-MMALDGL--SFTYSLIWKNSGVEERIEINISRHKIYKLSPEPTYCLKYKALL 181
Db 137 ENEYETMTMKKNVNSMTYVNWQKNGTDEKFOITPOYDFEVLRLNPEWTTCVQYRGELP 196
Oy 182 TSMKIGVSPVHCITKT 198
Db 197 DRNKGWSEPVCEQTT 213

RESULT 11
PCT-US94-14277-2
Sequence 2, Application PC/TUS9414277
GENERAL INFORMATION:
APPLICANT: Aguet, Michel
APPLICANT: Bohml, Ruth
APPLICANT: Hemmi, Silvio
TITLE OF INVENTION: Receptor Subunit Polypeptides
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd

CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patln (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14277
FILING DATE: 07-DEC-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/164596
FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 866PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/223-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US94-14277-2

Query Match 18.6%; Score 199; DB 4; Length 332;
Best Local Similarity 30.1%; Pred. No. 2.4e-14;
Matches 65; Conservative 38; Mismatches 81; Indels 32; Gaps 12;
Oy 4 LKSPQVEVDIIDNFIILNRNRSDESGVNTFSPDYOKTGMNMTKLSGCONISTKCNFSSL 54
Db 29 LAELNPRHLHXNDQILTWEPSSNDPRPVYQVYKSF-----IDGSMHRLLEPNC 82
Oy 55 NITSTKCNFSS--LKINYE-EIKLRIRAEKEN-TSSWYEVDSFTPPRAQIGPPE-VH 108
Db 83 DITETKCDLNGGGRKLFPHPTVFLVRAKRGMLTSKWGLLEPFOYEWNTVGPKNIS 142
Oy 109 LEADKAIIVHISGTDVSMALDGLSFTYSLIWKNSGVEERIEINISRHKIY--KL 166
Db 143 VTPKGSILVHFSPED---VFHGATFOYLVIHWKSESTQEOQVGPKNISIVLGNL 197
Oy 167 SPETTYCLKYKAL-LTSMKI---GVYSPVHCITKT 198
Db 198 KPYRYVCLQTEAQLLNKKIRPAGLLSNVSCHETT 233

RESULT 12
PCT-US94-14277-6
Sequence 6, Application PC/TUS9414277
GENERAL INFORMATION:
APPLICANT: Aguet, Michel
APPLICANT: Bohml, Ruth
APPLICANT: Hemmi, Silvio
TITLE OF INVENTION: Receptor Subunit Polypeptides
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/803,305
 FILING DATE: 20-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Lunn, Paul G
 REGISTRATION NUMBER: 32,743
 REFERENCE/DOCKET NUMBER: 96-24C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-442-6627
 TELEFAX: 206-442-6678
 TELEX:
 INFORMATION FOR SEQ ID NO: 54:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 221 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-08-943-087-54

Query Match	15.6%	Score	167.5	DB 2	Length	221			
Best Local Similarity	26.1%	Pred	No. 4.5e-11						
Matches	49	Conservative	34	Mismatches	88	Indels	17	Gaps	5

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0Y      4 LASHQKAEVLDIDINE LHMNRSDSEVG -NTSEFEDQKQKMDMWIKLSGQNTTTRKCN 62
      8 LPRPANITFELSNKKNVLQMTPEGLQGVKTYTYOQFVFLYQKQKMLKSECRINIRTYCD 67
0Y      63 FSSLKLVNYEIKLIRI -EKENTSSWEVDSEFPFRKAQIGPREVHLEADKAIYHIS 121
      68 LSAETSDYEHQYVAKKIMGTCKSKWESGREFPLETOIGPREVALTTDEKISVLT 127
0Y      122 PGTG-----DSYMMALDGLSFYTSLLLMKXSSGVEERIKENIYSRHKRYK --LSPET 170
      128 APEKMRKRPEDLPVYSMOOLYSLNLYKRVNSVLTKSKNRTRMSQCVTB---HTLVLTWLEPNT 183
0Y      171 TYCLKVKRA 178
      184 LYCVAVES 191
Db

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RESULT 15
 US-08-943-087-50
 Sequence 50, Application US/08943087
 Patent No. 5945511
 GENERAL INFORMATION:
 APPLICANT: Lok, Si
 APPLICANT: Koo, Choon J.
 APPLICANT: Jelmberg, Anna C.
 APPLICANT: Adams, Rodyn L.
 APPLICANT: Whitmore, Theodore E.
 APPLICANT: Farrah, Theresa M.
 TITLE OF INVENTION: CYTOKINE RECEPTOR
 NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:
 ADDRESS: ZymoGenetics, Inc.
 STREET: 1201 Eastlake Avenue East
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98102
 COMPUTER READABLE FORM:
 MEDIUM TYPE: diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/943,087
 FILING DATE:
 CLASSIFICATION: 536
 PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/803,305
 FILING DATE: 20-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Lunn, Paul G
 REGISTRATION NUMBER: 32,743
 REFERENCE/DOCKET NUMBER: 96-24C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-442-6627
 TELEFAX: 206-442-6678
 TELEX:
 INFORMATION FOR SEQ. ID NO.: 50:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 221 amino acids
 type: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-08-943-087-50

Query Match	15.5%;	Score 166.5;	DB 2;	Length 221;
Best Local Similarity	26.1%;	Pred. No. 5.8e-11;		
Matches 49;	Conservative 34;	Mismatches 88;	Indels 17;	Gaps 5

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QY      4 LKSOQKEVLIIDNFIILNNRSDSEVG-NYTESFEDQKGMGNMILSCQNTSPKCN 62
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      8 LPRKANTIFLSTNNKNVLOMTPEGLQGVATYTVQVFTTGGKKMLKXSECRNINRYCD 67

QY      63 FSSKLNLVYEBIKLIRA-EKENTSSWEYDSTFPKKAQIGPPEVHLEADKAIVHIS 121
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      68 LSAETSDVEHQYAKVAKIMOTCKSWAESGRFYPLETOIGPREVALTTDEKISVLT 127

QY      122 PGR-----DSVMMALDGLSFTTSLILMKRSSGVEERIEITYSRHAIYK--LSPE 170
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      128 APEKWRKRPEDLPVSMOOIYSNLKYNAVSLNTKSNRPMQCVTN---HPLVLTWLEPNT 183

QY      171 TYGLKYKA 178
      1 : : : :
Db      184 LYCVHVES 191

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Search completed: June 1, 2000, 04:17:54
Job time: 15448 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 1, 2000, 04:35:09 ; Search time 64.83 seconds
(without alignments)
183.585 Million cell updates/sec

Title: US-09-240-675-2_COPY_27_229
Perfect score: 1072
Sequence: 1 GKNLKSPOKVEVDIIDDNFI.....WKIGVYSPVHCITVENEL 203

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR_63: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	1072	100.0	557	2	A32694	interferon alpha/b
2	708	66.0	560	2	S27387	interferon alpha r
3	525.5	49.0	590	2	A45283	interferon alpha/b
4	219	20.4	273	2	G04418	cytokine receptor
5	216	20.1	349	2	JC6311	interferon recepto
6	214	20.0	325	2	A47003	cytokine receptor
7	199	18.6	332	2	A49947	interferon gamma r
8	144	13.4	337	2	I38500	interferon gamma r
9	111	10.4	489	2	A31555	interferon gamma r
10	97.5	9.1	6831	2	T27934	hypothetical prote
11	97.5	9.1	6839	2	S57242	twitichin - Caenorh
12	97.5	9.1	7160	2	T27935	hypothetical prote
13	95.5	8.9	925	2	T29585	hypothetical prote
14	92.5	8.6	292	1	KFE03	tissue factor prec
15	92	8.6	477	2	A34368	interferon gamma r
16	90.5	8.4	1304	1	A46546	leukocyte common a
17	90	8.4	315	1	S14222	chalcone reductase
18	89.5	8.3	2033	2	T09123	hyalid receptor So
19	89.5	8.3	2215	2	T00348	Lr11 protein - mou
20	89	8.3	331	2	A54295	interferon alpha/b
21	89	8.3	331	2	S59501	interferon recepto
22	89	8.3	515	2	S59502	interferon recepto
23	89	8.3	1152	2	S20106	hypothetical prote
24	88	8.2	515	2	I39073	interferon alpha-b
25	87.5	8.2	575	2	A49667	interleukin-10 rec
26	87.5	8.2	6805	2	JC20901	titlin - rabbit (fr
27	87	8.1	639	2	SI3391	dnak - type molecula
28	87	8.1	26926	1	I38344	titlin, cardiac mus
29	86.5	8.1	429	2	S58773	26S proteasome reg
30	85.5	8.0	295	1	KFH03	tissue factor prec

31	85.5	8.0	578	2	I56215	interleukin-10 rec
32	84.5	7.9	623	1	VGBE68	glycoprotein E - h
33	84.5	7.9	1220	2	S64916	probable membrane
34	83.5	7.8	306	2	A25698	probable protein x
35	82.5	7.7	406	2	B64432	capsular polysacch
36	82.5	7.7	1068	2	S01519	hypothetical prote
37	82	7.6	415	2	S12357	hypothetical prote
38	82	7.6	817	2	A48721	titlin, muscle - ch
39	81.5	7.6	292	1	KFRB3	tissue factor prec
40	81	7.6	1009	2	C64483	hypothetical prote
41	81	7.6	1120	2	S67208	hypothetical prote
42	81	7.6	1375	2	T13822	trazazled gene prot
43	81	7.6	1526	2	T13823	trazazled gene prot
44	80	7.5	780	1	S39110	valosin-containing
45	80	7.5	878	1	A40091	interleukin-3 rece

ALIGNMENTS

RESULT 1

A32694 Interferon alpha/beta receptor precursor - human

C:Species: Homo sapiens (man)

C:Date: 22-Jun-1990 #sequence, revision 22-Jun-1990 #text, change 22-Oct-1999

C:Accession: A32694; S17112

R:Uze, G.; Luftalla, G.; Gresser, I.

Cell 60, 225-234, 1990

A:Title: Genetic transfer of a functional human interferon alpha receptor into mou

A:Reference number: A32694; MUID:90124632

A:Accession: A32694

A:Molecule type: mRNA

A:Residues: 1-557 <UZE>

A:Cross-references: GB:003171; NID:g184645; PIDN:AAA52730.1; PID:g306914

R:Luftalla, G.

submitted to the EMBL Data Library, July 1991

A:Description: The structure of the human interferon alpha/beta receptor gene.

A:Reference number: S17112

A:Accession: S17112

A:Molecule type: DNA

A:Residues: 1-16, 'A', 18-329, 'V', 343-557 <LUM>

A:Cross-references: EMBL:X60459; NID:932671

C:Genetics:

A:Gene: GDB:IFNAR1; IFNAR; IFRC

A:Cross-references: GDB:120078; OMIM:107450

A:Map position: 21q22.1-21q22.1

Query Match 100.0%; Score 1072; DB 2; Length 557;

Best Local Similarity 100.0%; Pred. No. 3e-87;

Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GKNLKSPOKVEVDIIDDNFIIRMNRSDESGVNTFSPYQTKGMDNWKLSGCONITSTK	60
DB	27	GKNLKSPOKVEVDIIDDNFIIRMNRSDESGVNTFSPYQTKGMDNWKLSGCONITSTK	86
QY	61	CNFSLLKNVYEIKLRIRAKENTSSYEVDSFPFRKAOIGPPEVHLEADKAIVIH	120
DB	87	CNFSLLKNVYEIKLRIRAKENTSSYEVDSFPFRKAOIGPPEVHLEADKAIVIH	146
QY	121	SPGTDSTWMAALDGLSFTYLLINKSSGVEERINITSRRKIYKLSPEYTYCKLVKAA	180
DB	147	SPGTDSTWMAALDGLSFTYLLINKSSGVEERINITSRRKIYKLSPEYTYCKLVKAA	206
QY	181	LTSWKIGVYSPVHCITVENEL 203	
DB	207	LTSWKIGVYSPVHCITVENEL 229	

RESULT 2
257387
Interferon alpha receptor type 1 precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Dates: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
A:Accession: S27387; S33770
R:Mouchel-Vieilh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G.
FEBS Lett. 313, 255-259, 1992
A:Title: Specific antiviral activities of the human alpha interferons are determined at
A:Reference number: S27387; MUID:93076508
A:Accession: S27387
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-560 <MOU>
A:Cross-references: EMBL:X68443; NID:g431; PIDN:CAA48484.1; PID:g432
A:Experimental source: MDBK cells
R:Lim, J.K.; Langer, J.A.
Biochim. Biophys. Acta 1173, 314-319, 1993
A:Title: Cloning and characterization of a bovine alpha interferon receptor.
A:Reference number: S33770; MUID:93305725
A:Accession: S33770
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-421, 'V', 423-560 <Lim>
A:Cross-references: EMBL:L06620; NID:g163187; PIDN:AAA02571.1; PID:g163188
A:Experimental source: Lung
C:Keywords: antiviral; cytokine receptor; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-560/Product: interferon alpha receptor type 1 #status predicted <MAT>

```

Query March      66.08; Score 708; DB 2; Length 560;
Best Local Similarity 67.2%; Pred. No. 5.le-55;
Matches 137; Conservative 28; Mismatches 35; Indels 4; Gaps 4;

OY   3 NLSPOKVEVDIIDDNFLNRMSDESVGNFTFSFYOKTGMNNIKLSCGONITSTCN 62
    ||| : |::||| ||| : |::||| ||| : |::||| ||| : |::||| ||| : |::|||
Db    NLK-PENVEIHIIIDNFPILKNSSSESYKVNTFSAQDYIIGTDNMKKILSGCHISTCKN 85
OY   63 FSSLKL-NVYEIEIKRFAEK-EHTSSWYEVDSFFPFKAQIQPEPVHLEADKATIVHI 120
    ||::: | ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db    86 FSVELLEVNFKEIRIAEAGNNSTIWEEVFEPFLFEAQGPDPVLHEADKAIITISI 145
OY   121 S-PGTGDVMAMDLDSTYSLLINKNSSGVGERIENTISRRKIYKLSPETTYCLKVKAA 179
    ||| |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db    146 SPPTGKDSDIMAMADRSSRIYVIWNKNSSLERETIETYPEDKIYLSPETITYCLKVAE 205
OY   180 LLTSMKIGVSYPVHCIRTVENEL 203
    I : : | |||::| I : : 
Db    206 LRLOSRCGYCSPYCINTTERHKV 229

RESULT       3
A45283
Interferon alpha/Beta receptor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1995
C:Accession: A45283; I48423; I48424; I48425; I48426; I48427; I48428; I48429
R:Dze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E.
P:Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992
A>Title: Behavior of a cloned murine interferon alpha/Beta receptor expressed in homosp...
A:Reference number: A45283; MUID:92262522
A:Accession: A45283
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-590 <GB>#
A:Cross-references: GB:M89641; NID:g194111; PIDN:AAA37890.1; PTD:g194112
A>Note: Sequence extracted from NCBI backbone (NCBIN:102354, NCBITP:102357)
R:Lutfalla, G.: Dze, G.
Gene 148, 343-346, 1994
A>Title: Structure of the murine Interferon alpha/Beta receptor encoding gene: hghn-freec...
A:Reference number: I48423; MUID:95047447
```

A:Accession: I48423
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 118-125 <RES>
A:Cross-references: EMBL:U06237; NID:g497103; PIDN:AAA65003.1; PID:g755810
A:Accession: I48424
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 127-224 <RE2>
A:Cross-references: EMBL:U06238; NID:g497104; PIDN:AAC01749.1; PID:g755811
A:Accession: I48425
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 243-264 <RE3>
A:Cross-references: EMBL:U06239; NID:g497106; PIDN:AAA65004.1; PID:g510261
A:Accession: I48426
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 265-375 <RE4>
A:Cross-references: EMBL:U06240; NID:g497108; PIDN:AAA65005.1; PID:g510262
A:Accession: I48427
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 397-424 <RE5>
A:Cross-references: EMBL:U06241; NID:g497110; PIDN:AAA65006.1; PID:g755812
A:Accession: I48428
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 426-445 <RE6>
A:Cross-references: EMBL:U06242; NID:g497112; PIDN:AAA65007.1; PID:g755813
A:Accession: I48429
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 473-590 <RE7>
A:Cross-references: EMBL:U06244; NID:g497114; PIDN:AAA65008.1; PID:g510265
C:Genetics:
A:Gene: IFNAR
A:Introns: 177/3; 331/1
C:Keywords: cytokine receptor; transmembrane protein

```

Query Match Length      49.0%; Score 525.5; DB 2; length 590;
Best Local Similarity   51.0%; Pred. No.7,8e-39;
Matches    104; Conservative    36; Mismatches    69; Indels     1; Gaps     1;

OY      1 GKNLSPQKVEYDITDDNFILMKNRSDSGVNTTSPDYQTGMDNWKILSCQNITSTK 60
       1 :| | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
DB      26 GNMLPPENIDIVYIIDDNLTLMKSSHGSGMSGVTSAEVRTDEAKMKLVPCQHITTYIK 85
       1 :| | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
OY      61 CFFSLKLNVEYEIKRTIARAEEKN-TSSWYEVDSFTPFKAQIGCPPEVLLEADRAIVIH 119
       1 :| | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
DB      86 CEFSLLDNINVIYIKTFRRVARECGNSTSSMENVEDPPIPTTAHMSPPFVALMEDKAILVH 145
       1 :| | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
OY      120 ISPGRKDSVMALDGLSTYSLLTIKNSSGVERLENITYSRKIYKLSETTYCLKVKAA 179
       1 :| | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
DB      146 ISPPQCDGNMALEKPSFSYTRIRWOKSSDXKRKTINSTYYEKIPPELLPYTYCLEVKAI 205
       1 :| | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
OY      180 LITSWKIGVSPFHCIKTIVENEL 203
       1 :| | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
DB      206 HPSLKHNSYSTVQCISTTVANKM 229
       1 :| | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

RESULT      4
G01418
cytokine receptor family II, member 4 - human
C.Species: Homo sapiens (man)
C.Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
C.Accession: G01418
R.Lutfalla, G.
submitted to the EMBL Data Library, April 1994
A.Reference number: G06935
A.Accession: G01418
A.Status: preliminary; translated from GB/EMBL/DDBU
```

A:Molecule type: DNA
A:Residues: 1-273 <UNT>
A:Cross-references: EMBL:U08988; NID:g571235; PID:g571236
C:Genetics:
A:Gene: GDB:CFRFB4; GRF2-4
A:Cross-references: GDB:113168; OMIM:123889
A:Map position: 21q22.1-21q22.2
A:Introns: 17/1, 58/2, 111/1, 166/3, 216/1

Query Match	20.48;	Score 219;	DB 2;	Length 273;	.
Best Local Similarity	30.58;	Pred. No. 3.9e-12;			
Matches 60;	Conservative 41;	Mismatches 84;	Indels 12;	Gaps 7;	

```

OY      7  POKVEEIIIDNFIILNRRSDESSGANTFESDYOKTOMDMWIKISGCONITTSKRNSSL 66
D      14  PENTRBMNSVNRKNILOHESPAFAGNLTFTQY----LSYRIPODKCMNLTLECDPSS- 79
OY      67  KLANVEIEIKLIRAE-KENTSSWYEVDSFTFERKAQIGPEVHLLEADKAVIYH-ISPGT 124
D      79  -LSKYGDHITLVRAEFADDEHSDMWNI--TFCEVDDTITIGPGMQGEVLDLSHRFLPAKI 136
OY      125  KDSV-MMALDGL--SFYISLLIMKNSSGVEERINITSRKIKYLSFETTYCLAKYRAAL 181
D      137  ENERYETIMKKNVNVSNMYSWYVNOVMKNGDEKDFQIPPOYDFEYLRNLBLEPMTIYCVQVGRFLP 196
OY      182  TSMKIGVYSPVHCIKTT 198
D      197  DRNKAGEWSEPYCEOTT 213

```

```

RESULT      5
JC6311
Interferon receptor-class II cytokine receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999
C:Accession: JC6311
R:Gibbs, V.C.: Pennica, D.
Gene 186, 97-101, 1997
A:Title: CRF2-8: Isolation of cDNA clones encoding the human and mouse proteins
A:Reference number: JC6311
A:Accession: JC6311
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-349 <GIB>
A:Cross-references: GB:U53696

```

Query Match	20.1%	Score 216;	DB 2;	Length 349;
Best Local Similarity	28.6%	Pred. No. 1e-11;		
Matches	58;	Conservative	43;	Mismatches 76;
				Indels 26;
				Gaps 8

```
OY      7 POKVEJDIIDNFIILNRMSDESQVNTFFSDYO--KTGMDNMATKLGCONITSTKNFS   64  
OY      | : : : : : ||| : : : : : | : : : : : | : : : : : |  
Db     24 PEKVAMNSVNPRKNIIQMWEVPAPRKTNLFTAQYESYSRFODH-----CRRTASTGDDFS   77  
  
OY      65 SLKLNVYEIKLRIRAE-KENTSSMYEVDSTFPFRAKOIGPEPVHLBAEDKAIVHTS--    122  
Db     78 -HLSKYGDYNVRVAFLADEHESEWVAN-TCSPVEDTITIGPEMOETSLERESAP    134  
  
OY      122 -----PGKRDSVMALDDL-SFYISLLIMNSSVERIENITSRKRIYKLESETTYCL    174  
        | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |  
Db     135 QIENEPEP-----WTLKNIYDSMAYRWQWMNGNEKPQVVSPYDSEVLRLNFLPETYYCI    189  
OY      175 KVKALLTFMKRGVSPVHCIACT    197  
Db     190 OVOGFLLDONRKGEMSEPICERT    212
```

RESULT 6
A47003
cytokine receptor family class II protein CRP2-4 precursor - human
C1:Species: Homo sapiens (mn)

C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 10-Sep-1997
C:Accession: A47003
R:Luttfalla, G.; Gardiner, K.; Uze, G.
Genomics 16, 366-373, 1993
A:Title: A new member of the cytokine receptor gene family maps on chromosome 21 at
A:Reference number: A47003; MIM:93300510

	Query Match	20.0%; Score 214; DB 2;	Length 325;
	Best Local Similarity	30.5%; Pred. No. 1,4e-11;	
	Matches	60; Conservative	39; Mismatches 86; Indels 12; Gaps
Oy	7 POKYEVDIIDNFIEMRNKDESVGAVTFEFQDKGMQMWIKLSSCONITSTKCFSSL	66	
	::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::		
Db	24 PENRKMVSVEKNKILOESPFAKGNITTAQT----LSRIPODKCMNTTILECDFSS-	79	
Oy	67 KLVNYEELIRIAAE-KENTSSWEVDSTFPRKAQIGPEPVHLEA-EDKAIVIHISPGT	124	
	::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::		
Db	79 -LSYTGCHTLRVRAFEFDSDHWANI-TCEPVDVTIIIGPGMGEVLALSHLRFLAPKI	136	
Oy	125 KDSEVMMALDGL-SFYSLIWMNSGSVERIEENIYSRHRIKYLSPEPTTYCLCAVAALL	181	
	::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::		
Db	137 ENEEETMTMKRVVISMWYINNOYKKNGNDKDFQILTPDYDEVLLNLLEPMTTYCQVAGFLP	196	
Oy	182 TSMKIGVSPVHCICKTT	198	
	: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::		
Db	197 DRNRAGEWSPEVCQTT	213	

```

RESULT      7
A49947
Interferon gamma receptor beta subunit - mouse
N:Alternate names: IFN-gamma R beta chain; IFN-gamma R species-specific cofactor;
C:Species: Mus musculus (house mouse)
C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A49947
R:Hemmi, S.; Bohni, R.; Stark, G.; Di Marco, F.; Aguet, M.
Cell 76, 803-810, 1994
A:Title: A novel member of the interferon receptor family complements functionality
A:Reference number: A49947; MUID:94170381
A:Accession: A49947
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-332 <GB>
A:Cross-references: NID:9545841; PIDN:AB30165.1; PID:9545842
A:Experimental source: early B-cell line Y16
A:Note: sequence extracted from NCBI backbone (NCBIN:145654, NCBIIP:145656)
C:Keywords: cytokine receptor

```

Query Match	Score	DB 2;	Length
18.68;	199;	DB 2;	332;

	Matches	65;	Conservative	38;	Mismatches	81;	Indels	32;	Gaps
QY	4	LKSPQKVEVDIIDNDFLRNKRDE	-----	VGNTFFSDFYDKTGM	D-NWIKL	-SGGQ	54		
Db	29	LAAPLNPRLHLYNEOLLTEPSPSSNDPPVYQVEYS	-----	IDGWHALLPNC	T	82			
QY	55	NITSRKCFSS--LKLNYE-EIKLRIRAKEN-TSSMYEVSFTFRKAQIGPE	-VH	108					
Db	83	DITTECOLTGGGLKLFEPHFYELVNRKRGNLSKMYGLERFQHYENVTYGPKNIS	142						
QY	109	LEAEKAIIVHSIGTKDSYMMALDGLSFYSLILNKNSSGVERIEINYSRRIY	-FL	166					
Db	143	VTPGKGLVTHFSPFD-----VFHGATFQYLVHYMKSETOEOGVCEGFKNSIYLGNL	197						


```

Db 41 PTNVLKSYNLPVYCWETQNM---OTPIFTVOVKYISGSW---TDSCNTISDHCC---- 92
QY 66 LKLNVEEIK-----LRIRAE-KENTSSWYEVDSTPFRRQIGPP--EVHLEAEDKA 115
Db 92 ---NIGQIMYPDVSAWAKVAKVGOKESDYARSKFELMCKGKVGPPGLEIRRKKEQL 148
QY 116 IVIHISP-----GTRDSVMAALDG---LSFTYSLIMKNSSGVEERIENTISRHKIYKLS 167
Db 149 SYLVFHPPEVVVNGESOGIMEG-DGSCYTFDYTYVEHNRSG-----EILHTKHTEVEREE 202
QY 168 PETTYC-LKYKALITS 183
Db 203 CNETLCELNISVSTLDS 219

```

Search completed: June 1, 2000, 04:35:14
 Job time: 14294 sec

KW Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism;
 RX Phosphorylation.
 FT SIGNL 1 27 POTENTIAL.
 FT CHAIN 28 557 INTERFERON-ALPHA/BETA RECEPTOR ALPHA
 FT DOMAIN 28 436 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 437 457 POTENTIAL.
 FT DOMAIN 458 557 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 199 220 BY SIMILARITY.
 FT MOD.RES 466 466 PHOSPHORYLATION (BY TYR2) (PROBABLE).
 FT MOD.RES 481 481 PHOSPHORYLATION (BY TYR2) (PROBABLE).
 FT MOD.RES 50 50 POTENTIAL.
 FT CARBOHYD 58 58 POTENTIAL.
 FT CARBOHYD 81 81 POTENTIAL.
 FT CARBOHYD 86 86 POTENTIAL.
 FT CARBOHYD 110 110 POTENTIAL.
 FT CARBOHYD 172 172 POTENTIAL.
 FT CARBOHYD 254 254 POTENTIAL.
 FT CARBOHYD 313 313 POTENTIAL.
 FT CARBOHYD 314 314 POTENTIAL.
 FT CARBOHYD 376 376 POTENTIAL.
 FT CARBOHYD 416 416 POTENTIAL.
 FT CARBOHYD 433 433 POTENTIAL.
 FT VARIANT 168 168 L -> V.
 FT CONFLICT 17 17 /Frid-VAR.002717.
 FT SEQUENCE 557 AA: 63525 MW: 0F6744C8A1ADB673 CRC64;

Query Match 100.0%; Score 1072; DB 1; Length 557;
 Best Local Similarity 100.0%; Pred. No. 1,1e-88;
 Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GKNKSPKQKVEVDIIDDNFILRNRSDESGVNTFSFDYKGTGDMNRIKSGCONITSTK 60
 DB 27 GKNKSPKQKVEVDIIDDNFILRNRSDESGVNTFSFDYKGTGDMNRIKSGCONITSTK 86
 OY 61 CNFSSLNLYVEEIKLRRAKENTSSWYEDSFTPRKAOIGPEVHLEAEDEKAIVYIH 120
 DB 87 CNFSSLNLYVEEIKLRRAKENTSSWYEDSFTPRKAOIGPEVHLEAEDEKAIVYIH 146
 OY 121 SPGTRDSVMALDGLSFTYSLIMKNSGVEERIENTISRRKIYKLSPEYTYCLVKYAA 180
 DB 147 SPGTRDSVMALDGLSFTYSLIMKNSGVEERIENTISRRKIYKLSPEYTYCLVKYAA 206
 OY 181 LTSWKIGVSPVHCITTYENEL 203
 DB 207 LTSWKIGVSPVHCITTYENEL 229

RESULT 2
 INRL_BOVIN STANDARD; PRT; 560 AA.
 AC 004790;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
 GN IFNARI OR IFNAR.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
 OC Bovine; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LONG;
 RX MEDLINE; 93076908.
 RA Mouchel-Vielh E., Lutfalla G., Mogensen K.E., Uze G.;
 RT "Specific antiviral activities of the human alpha interferons are
 determined at the level of receptor (IFNAR) structure.";
 RL FEBS Lett. 313:255-259(1992).
 RN [2]

RP SEQUENCE FROM N.A.
 RA MEDLINE; 93305725.
 RA Lim J.-K., Langer J.A.;
 RT "Cloning and characterization of a bovine alpha interferon receptor.";
 RL Blochim. Biophys. Acta 1173:314-319(1993).
 CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
 CC I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
 CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
 CC SUBUNITS THEMSELVES.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTRAINS 2 FIBROBLAST TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC or send an email to license@isb-sib.ch).

DR EMBL; X68443; CAA48484.1; -
 DR EMBL; L06320; AAA02571.1; -
 DR PIR; S33770; S33770.
 DR PIR; S27387; S27387.
 DR PFAM; PF00041; fn3; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNL 1 24 BY SIMILARITY.
 FT CHAIN 25 560 INTERFERON-ALPHA/BETA RECEPTOR ALPHA

FT DOMAIN 25 437 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 438 458 POTENTIAL.
 FT DOMAIN 459 560 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 199 220 BY SIMILARITY.
 FT MOD.RES 466 466 BY SIMILARITY.
 FT MOD.RES 481 481 POTENTIAL.
 FT MOD.RES 50 50 POTENTIAL.
 FT CARBOHYD 58 58 POTENTIAL.
 FT CARBOHYD 81 81 POTENTIAL.
 FT CARBOHYD 86 86 POTENTIAL.
 FT CARBOHYD 110 110 POTENTIAL.
 FT CARBOHYD 172 172 POTENTIAL.
 FT CARBOHYD 254 254 POTENTIAL.
 FT CARBOHYD 313 313 POTENTIAL.
 FT CARBOHYD 314 314 POTENTIAL.
 FT CARBOHYD 376 376 POTENTIAL.
 FT CARBOHYD 434 434 POTENTIAL.
 FT CONFLICT 422 422 F -> V (IN REF. 2).
 FT SEQUENCE 560 AA: 63818 MW: 66D76B72861E1D11 CRC64;

Query Match 66.0%; Score 708; DB 1; Length 560;
 Best Local Similarity 67.2%; Pred. No. 4,6e-56;
 Matches 137; Conservative 28; Mismatches 35; Indels 4; Gaps 4;

OY 3 NKSPOKVEVDIIDDNFILRNRSDESGVNTFSFDYKGTGDMNRIKSGCONITSTKCN 62
 DB 27 NLK-PENVEIHIIDDNFILRNRSDESGVNTFSADYQILGIDNMKKLSGCQITSTKCN 85
 OY 63 FSSILKL-NVYEETIKLRRAK-ENTSSWYEDSFTPRKAOIGPEVHLEAEDEKAIVYIH 120
 DB 86 FSSVLEENFEKELIRAEKGNSTWYEFVFLQIOIPRVHLEAEDEKAIIISI 145
 OY 121 S-PGTRDSVMALDGLSFTYSLIMKNSGVEERIENTISRRKIYKLSPEYTYCLVKYAA 179
 DB 146 SPGTRDSVMALDGLSFTYSLIMKNSGVEERIENTISRRKIYKLSPEYTYCLVKYAA 205
 OY 180 LTSWKIGVSPVHCITTYENEL 203
 DB 206 LRLQSRVGCSPVHCITTYENEL 229

RESULT 3
 INRL_SHEEP STANDARD; PRT; 560 AA.
 ID INRL_SHEEP
 AC Q28389; Q95206;

DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC)
DE (INTERFERON ALPHA/BETA RECEPTOR-1).
GN IFNARI OR IFNAR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Caprinae; Ovis.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-ENDOMETRIUM.
RX MEDLINE; 97135690.
RA Kaluz S., Fisher P.A., Kaluzova M., Sheldrick E.L., Flint A.P.F.;
RT "Structure of an ovine interferon receptor and its expression in
RT endometrium."
RT J. Mol. Endocrinol. 17:207-215(1996).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE-ENDOMETRIUM.
RX MEDLINE; 98006426.
RA Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.;
RT "Molecular cloning of ovine and bovine type I interferon receptor
RT subunits from uterus and endometrial expression of messenger
RT ribonucleic acid for ovine receptors during the estrous cycle and
RT pregnancy."
RT Endocrinology 138:4757-4767(1997).
CC -I- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
CC I PMS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
CC SUBUNITS THEMSELVES.
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -I- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT
CC CONCEPT AT DAY 15 OF PREGNANCY.
CC -I- SIMILARITY: CONTAINS 2 FIBROBLAST TYPE III-LIKE DOMAINS.
CC -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.

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DR EMBL; X95939; AAA65183.1; -.
DR EMBL; U65978; AAB84231.1; -.
DR PRAM; PF00041; fn3; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 560
FT FT
FT DOMAIN 25 437
FT TRANSHEM 438 458
FT DOMAIN 459 560
FT DISULFID 76 84
FT DISULFID 199 220
FT CARBOHYD 47 47
FT CARBOHYD 55 55
FT CARBOHYD 85 85
FT CARBOHYD 108 108
FT CARBOHYD 109 109
FT CARBOHYD 172 172
FT CARBOHYD 222 222
FT CARBOHYD 285 285
FT CARBOHYD 313 313
FT CARBOHYD 359 359
FT CARBOHYD 377 377
FT CARBOHYD 434 434
FT CARBOHYD 434 434
FT CONFLICT 352 352
FT CONFLICT 522 522
FT SEQUENCE 560 AA; 63918 MW; E7198A1905D4805C CRC64;
A -> D (IN REF. 2).
S -> G (IN REF. 2).

[illegible]

FT CARBOHYD 214 214 POTENTIAL.
 FT CARBOHYD 314 314 POTENTIAL.
 FT CARBOHYD 370 370 POTENTIAL.
 FT CARBOHYD 409 409 POTENTIAL.
 FT CARBOHYD 413 413 POTENTIAL.
 SQ SEQUENCE 590 AA: 65776 MW: 76C6DF370185D3A CRC64:

Query Match 49.0%; Score 525.5; DB 1; Length 590;
 Best Local Similarity 51.0%; Pred. No. 1, le-39;
 Matches 104; Conservative 36; Mismatches 63; Indels 1; Gaps 1;

OY 1 GKNLSPQKVEVDIIDNFIILRNKSDSEVGNVTFSDYQKTDGMDNMIKSGCONITSTK 60
 DB 26 GEMLKPPENDIYIIIDNTLTKTSGHSGSVTFSAEYTKDEAKMLKVPCEQHTTTTK 85
 OY 61 CRRSLKLVYEIKLRIRAEKEN-TSSWEVDSFTPRKAQIGPPEVHLAEADKAIIVH 119
 DB 86 CEFSLDTNVIYITQPRVRAEGNSTSWNEVDPIFPYTAHMSPEVRLAEADKAIIVH 145
 OY 120 ISPGTDSVMALDGLSFTYSLLIMKNSGVEERIEIYSRHKIYKLSPEYTCYKAA 179
 DB 146 ISPPGDDGNMALEKSPFTTIRIMOKSSSDKTIINSTIYVEKIPPELTTCYCLEVKAI 205
 OY 180 LLSMKIGVSPVHCIRKTYENEL 203
 DB 206 HPSLKKHSNYSYOCISTYVANKM 229

RESULT 5

CRF4_HUMAN STANDARD; PRT; 325 AA.

AC 008334;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE CYTOKINE RECEPTOR CLASS-II CRF2-4 PRECURSOR.
 GN CRF4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=FETAL BRAIN;
 RX MEDLINE: 93300510.
 RA Luftalla G., Gardiner K., Uze G.;

RT "A new member of the cytokine receptor gene family maps on chromosome 21 at less than 35 kb from IFNAR."
 RL Genomics 16:366-373(1993).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE: 96054036.
 RA Luftalla G., McInnis M.G., Antonarakis S.E., Uze G.;

RT "Structure of the human CRF4 gene: comparison with its IFNAR neighbor."
 RL J. Mol. Evol. 41:338-344(1995).
 CC - FUNCTION: IS PROBABLY INVOLVED IN THE INTERFERON SYSTEM.
 CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC - SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC - SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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CC
 CC
 DR EMBL: Z17227; CAA78933.1;
 DR EMBL: U08988; AAA86872.1;
 DR PIR: A47003; A47003.
 DR HSP: P13726; IDAN.

DR MM: 123889; -
 KM Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 325
 FT DOMAIN 20 220
 FT TRANSMEM 221 249
 FT DOMAIN 250 325
 FT DISULFID 66 74
 FT CARBOHYD 188 209
 FT CARBOHYD 49 49
 FT CARBOHYD 68 68
 FT CARBOHYD 102 102
 FT CARBOHYD 161 161
 FT CARBOHYD 124 124
 FT CONFLICT 269 273
 FT CONFLICT 274 325
 SQ SEQUENCE 325 AA: 37011 MW: 66706C79F8514B23 CRC64;

Query Match 20.0%; Score 214; DB 1; Length 325;
 Best Local Similarity 30.5%; Pred. No. 4, 2e-12;
 Matches 60; Conservative 39; Mismatches 86; Indels 12; Gaps 7;

OY 7 POKVEYDIIDNFIILRNKSDSEVGNVTFSDYQKTDGMDNMIKSGCONITSTKCNFSSL 66
 DB 24 PENVRNNSVNFKNILQWESPAFAGNLTFTAOY---LSYRFQDKCMNTLTCEDFS- 79
 OY 67 KLVYEEIKLRIRAE-KENTSSWEVDSFTPRKAQIGPPEVHLAE-EDKAIIVHISPGT 124
 DB 79 -LSKYGDLTKLRARAFADSHDWNVI-TFCPYDDTIITPPGKQVAVLDSLHMRRLAKI 136
 OY 125 KDSV-MMALDGL-SFTYSLLIMKNSGVEERIEIYSRHKIYKLSPEYTCYKAAAL 181
 DB 137 ENEYETWTKKNYNSMTVQYWKNGTDEKFOITPOYDFEVLRLNEPWTYCVQVRCGLP 196
 OY 182 TSMKIGVSPVHCIRKTY 198
 DB 197 DRNKGWSEPVCEQT 213

RESULT 6

INGS_HUMAN STANDARD; PRT; 337 AA.

AC P38484;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (INTERFERON-GAMMA RECEPTOR ACCESSORY FACTOR-1) (AF-1) (INTERFERON-GAMMA TRANSUCER-1).
 GN IFNGR2 OR IFNGT1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG FIBROBLAST;
 RX MEDLINE: 94170380.
 RA Soh J., Donnelly R.J., Kotenko S., Mariano T.M., Cook J.R., Wang N., Emanuel S.L., Schwartz B., Miki T., Pestka S.;

RT "Identification and sequence of an accessory factor required for activation of the human interferon gamma receptor."
 RL Cell 76:793-802(1994).
 CC - FUNCTION: PART OF THE RECEPTOR FOR INTERFERON GAMMA. REQUIRED FOR SIGNAL TRANSDUCTION. THIS ACCESSORY FACTOR IS AN INTEGRAL PART OF THE IFN-GAMMA SIGNAL TRANSDUCTION PATHWAY AND IS LIKELY TO INTERACT WITH GAF, JAK1, AND/OR JAK2.

CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC - SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC - SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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DR EMBL: 005875; AAA16955.1; -
DR EMBL: 005877; AAA16956.1; -
DR MIM: 147369; -
DR PFM: PF00041; fn3; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 337 INTERFERON-GAMMA RECEPTOR BETA CHAIN.
FT DOMAIN 28 247 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 248 268 POTENTIAL.
FT DOMAIN 269 337 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 56 85 POTENTIAL.
FT CARBOHYD 85 85 POTENTIAL.
FT CARBOHYD 110 110 POTENTIAL.
FT CARBOHYD 137 137 POTENTIAL.
FT CARBOHYD 219 219 POTENTIAL.
FT CARBOHYD 231 231 POTENTIAL.
FT VARIANT 64 64 R -> Q.
FT SEQUENCE 337 AA; 37834 MW; 18C61B10AD90E509 CRC64; /FTID-VAR.002718.

Query Match 13.4%; Score 144; DB 1; Length 337;
Best Local Similarity 24.7%; Pred. NO. 8.1e-06;
Matches 56; Conservative 39; Mismatches 86; Indels 46; Gaps 12;

OY 4 LKSPKQEVVDIIDDNFILRW-----NRSDSEGVNTSFYDQKGMWIKLS----- 52
DB 30 LPAPHKPKRLNNAEQVLSMEVALNSNRPVYRQVRYTQSK-----WFTADIMSTGV 84
OY 52 GQONTSTKCNSS-----LKLNVYEIKLRIRAKENT-SSMYEVDSTPRKQI 102
DB 85 NCTQITAECDFTASPSKGFPMDEVN-----TLRLAEAGLHSAWVTPFHQHNVTV 140
OY 103 GPPEVHLE---AEKAIYVHISPGTKDSYVMAIDGLSFTYSLIMKNSGVEERENIYS 159
DB 141 GPPE-NIEVTPGEGSLINFSSPFIADISTAF---FCYYVHYME--KGIQGVYGPFR 193
OY 160 RKRIY-KLSPETTYCLAKYKALLTS---WKIGVSPHCKITVE 200
DB 194 SSSISLDNLKPSRYVCLQVADQLWKNKSNIFRVGHLSNISCYETMAD 240

RESULT 7
INGR_HUMAN STANDARD: PRT; 489 AA.
AC P15260;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1989 (Rel. 38, Last annotation update)
DE INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDM119).
GN IFNGR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89003065.
RA Aguet M., Dembic Z., Merlin G.;
RT "Molecular cloning and expression of the human interferon-gamma
RT receptor";
RL Cell 55:273-280(1988).
RN [2]
RP DISULFIDE BONDS, PARTIAL SEQUENCE, AND MUTAGENESIS.
RX MEDLINE: 93183911.
RA Stuber D., Friedlein A., Fountoulakis M., Lahm H.-W., Garotta G.;
RT "Alignment of disulfide bonds of the extracellular domain of the
RT interferon gamma receptor and investigation of their role in
RT biological activity";

RL Biochemistry 32:2423-2430(1993).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 26-248.
RX MEDLINE: 95342235.
RA Walter M.R., Windsor W.T., Nagabhushan T.L., Lundell D.J., Lunn C.A.,
RA Zauodny P.J., Narula S.K.;
RT "Crystal structure of a complex between interferon-gamma and its
RT soluble high-affinity receptor";
RL Nature 376:230-235(1995).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 28-122 COMPLEX WITH ANTIBODY.
RX MEDLINE: 98035727.
RA Sogabe S., Stuart F., Henke C., Bridges A., Williams G., Birch A.,
RA Winkler F.K., Robinson J.A.;
RT "Neutralizing epitopes on the extracellular interferon gamma receptor
RT (IFNGAMR), alpha-chain characterized by homology scanning mutagenesis
RT and X-ray crystal structure of the A6 fab-IFNGAMR1-108 complex";
RL J. Mol. Biol. 273:882-897(1997).
CC -1- FUNCTION: RECEPTOR FOR INTERFERON GAMMA. TWO RECEPTORS BIND ONE
CC INTERFERON-GAMMA DIMER.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- PM: PHOSPHORYLATED AT SER/THR RESIDUES.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 FIBROBLAST TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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DR EMBL: J03143; AAA52731.1; -
DR PIR: A31555; A31555.
DR PDB: 1JRH; 25-MAR-98.
DR MIM: 107470; -
DR MIM: 209950; -
KW Receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation;
KW Immunoglobulin domain; 3D-structure.
FT SIGNAL 1 17
FT CHAIN 18 489 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.
FT DOMAIN 18 245 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 246 266 POTENTIAL.
FT DOMAIN 267 489 CYTOPLASMIC (POTENTIAL).
FT DISULFID 77 85
FT DISULFID 122 167
FT DISULFID 195 200
FT DISULFID 214 235
FT CARBOHYD 34 34 POTENTIAL.
FT CARBOHYD 79 79 POTENTIAL.
FT CARBOHYD 86 86 POTENTIAL.
FT CARBOHYD 179 179 POTENTIAL.
FT CARBOHYD 240 240 POTENTIAL.
FT SEQUENCE 489 AA; 54404 MW; DCF9574D8F47400 CRC64;

Query Match 10.4%; Score 111; DB 1; Length 489;
Best Local Similarity 22.2%; Pred. NO. 0.012;
Matches 45; Conservative 41; Mismatches 83; Indels 34; Gaps 7;

OY 3 LKSPKQEVVDIIDDNFILRNRSDESGNV-TESFDYQKGMWIKLSGQNTSTK 61
DB 28 SVPTPTNTYISYNNNPVYWEY-QINPQVDFVEYKNGVKNSEWIDACINISHYC 85
OY 62 NFSSKLNVYEIKRITA---EKENTSSKVEVDSFTPRKQIOPPEVHLEAEKAVI 118
DB 86 NISDHWGDPNSLWVRAVGRQKE-SAYAKSEFAVCRQKIGPPPLDIRKEKQMTI 143
OY 119 HT-----SPGTX-----DSYVMAIDGLSFTYSLIMKNSGVEERINI 157

Db 144 DIFHPVFNVDGEVDYDETCYIRVNVYVAMNGSEIOYKILTKR-----EDDCDEI 198
 Oy 158 YSRHKYKLSPEPTYCKVKAAL 180
 Db 199 QCOLAIPVSSLNSGYCVSAGCVL 221

RESULT 8
 PMP2_CAEEL STANDARD: PRT: 925 AA.

AC PMP2_CAEEL 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE PERIODIC TRYPTOPHAN PROTEIN 2 HOMOLOG.
 OS F55F8.3
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
 OC Rhabditina; Rhabditioidea; Rhabditidae; Pelodierinae; Caenorhabditis.
 RN (1)

RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2:
 RA Gattung S., Scheet P., Kemp K.
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).
 CC -1- SIMILARITY: BELONGS TO THE PMP2 FAMILY OF WD-REPEAT PROTEINS.

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CC
 DR EMBL: U00447; AAB37807.1; -
 DR WORMPEP; F55F8.3; CE11192.
 DR PRINTS: PR00320; GPROTEINBRP.
 DR PROSITE: PS00678; WD_REPEATS; 1.
 DR PPM: PF00400; WD40; 4.
 KW Hypothetical protein; Repeat; WD repeat.
 FT REPEAT 188 218 WD1.
 FT REPEAT 358 388 WD2.
 FT REPEAT 400 430 WD3.
 FT REPEAT 486 514 WD4.
 FT REPEAT 524 554 WD5.
 FT REPEAT 599 627 WD6.
 SQ SEQUENCE 925 AA; 103899 MW; 439F35881B398CD1 CRC64;

Query Match 8.9%; Score 95.5; DB 1; Length 925;
 Best Local Similarity 25.7%; Pred. No. 0.64; Mismatches 21; Gaps 4;
 Matches 38; Conservative 19; Indels 70;

Oy 44 MDNWKISGCONIT--STKCNFSSKLNYEEI--KLRIRAKENTSSWYVDSFTPRK 99
 Db 1 MDNFKLSNCGIYVYRDGYAFSKDGYSVISPIGNKLSIFDLRNNTSKTLDIDCNVNIKR 60
 Oy 100 AQIGPREVHLEADKAIVIH-----SPGTKSVYMAALDGLSFTY---SL 142
 Db 61 LLSISPGYVHLLASDERGVHVFHLLSEFKITFRSNKRPISGLSPATRAVAICRENDIQ 120
 Oy 143 IMKNSGVEERIENTYSRHKYKLSPEP 170
 Db 121 IHFGKSIENKYNPFLSRTYKLSDDS 148

RESULT 9
 TF_BOVIN STANDARD: PRT: 292 AA.
 ID TF_BOVIN
 AC P30931;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III).
 GN F3

OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
 OC Bovinae; Bos.
 RN (1)

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE-ADRENAL GLAND;
 RX MEDLINE: 92109720.

RA Takeyenko Y., Muta T., Miyata T., Iwanaga S.;
 RL "CDNA and amino acid sequences of bovine tissue factor";
 RL Biochem. Biophys. Res. Commun. 181:1145-1150(1991).

CC -1- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
 CC CIRCULATING FACTOR VII OR VIIA. THE [TF-VIIA] COMPLEX ACTIVATES
 CC FACTORS IX OR X BY SPECIFIC LIMITED PROTEOLYSIS. TF PLAYS A ROLE IN
 CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
 CC PROPAGATION OF THE COAGULATION PROTEINASE CASCADE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

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CC
 DR EMBL: S74147; AAB20755.1; -
 DR PIR: JQ1319; KFB03.
 DR HSSP: P24055; 1A21.
 DR PRINTS: PR00346; TISSUEFACTOR.
 DR PROSITE: PS00621; TISSUE_FACTOR; 1.
 DR PPM: PF01108; Tissue_fac; 1.
 KW Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;
 KW Palmitate.
 FT SIGNAL 1 35
 FT CHAIN 36 292
 FT DOMAIN 36 248
 FT TRANSMEM 249 271
 FT DOMAIN 272 292
 FT SITE 46 48
 FT CARBOHYD 43 43
 FT CARBOHYD 153 153
 FT CARBOHYD 181 181
 FT DISULFID 81 89
 FT DISULFID 215 238
 FT LIPID 274 274
 SQ SEQUENCE 292 AA; 32475 MW; 5E471D928FBCE163 CRC64;

Query Match 8.6%; Score 92.5; DB 1; Length 292;
 Best Local Similarity 22.7%; Pred. No. 0.28; Mismatches 70; Indels 31; Gaps 9;
 Matches 40; Conservative 35;

Oy 44 MDNWKISGCONIT--STKCNFSSKLNYEEI--KLRIRAKENTSSWYVDSFTPRK 96
 Db 74 LGNW--KNCFTYTNTECVTDEIYKNNVRETYLARIASLPATSSSTVPPPTNSPEFTP 131
 Oy 97 FRRAGQGP-----EVHLEADKAIVIHISPGTDSYVMAALD---GLSFTYSLII 143
 Db 132 YLETNIGOPTIOSFEQGVGKLVNTYQDARTVLR-----ANSAFSLRDVFGKDLNVTLY 186
 Oy 144 WK NSGVEERIENTYSRHKYKLSPEPTYCKVKAALTSKRIKIGYVPHDKIKTT 198
 Db 187 WKASSTGKKRATN--TNGFLIDVDXGNYCFHYQAVIL--SRVVKSSPSPICKT 239

RESULT 10
 INGR_MOUSE STANDARD: PRT: 477 AA.
 ID INGR_MOUSE
 AC P15261;

RX MEDLINE: 89017162.
 RA Chabouneau H., Tonks N.K., Walsh K.A., Fischer E.R.;
 RT "The leukocyte common antigen (CD45): a putative receptor-linked
 RL protein tyrosine phosphatase".
 RN Proc. Natl. Acad. Sci. U.S.A. 85:7182-7186(1988).
 RP [3]
 RP MUTAGENESIS.
 RA Streuli M., Krueger N.X., Thai T., Tang M., Saito H.;
 RT "Distinct functional roles of the two intracellular phosphatase like
 RT domains of the receptor-linked protein tyrosine phosphatases LCA and
 RT LAR".
 CC EMBL: J. 9:2399-2407(1990).
 CC -1- RECEPTOR. REQUIRED FOR T-CELLS ACTIVATION THROUGH THE ANTIGEN
 CC RECEPTOR. THE FIRST PTASE DOMAIN HAS ENZYMACTIC ACTIVITY. WHILE
 CC THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE
 CC THE FIRST ONE.
 CC -1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O -
 CC PROTEIN TYROSINE + ORTHOPHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: THERE ARE 8 DIFFERENT VARIANTS OF L-CA,
 CC WHICH ARISE BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- DATABASE: NAME-PROW; NOTE-CD guide CD45 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd45.htm".
 CC -----
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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: Y00638; CAA68669.1; -.
 DR HSSP: P18052; LYFO.
 DR MIM: 151460; -.
 DR PRINTS: PR00700; PRTYPHPTASE.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE: PS00056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE: PS00055; TYR_PHOSPHATASE_PTP; 2.
 DR PFAM: PF00041; fn3; 2.
 DR PFAM: PF00102; Y-phosphatase; 2.
 DR Glycoprotein: Transmembrane; phosphorylation; B-cell; T-cell; Repeat;
 KM Alternative splicing; Hydrolase; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 1304
 FT DOMAIN 24 575
 FT TRANSMEM 576 597
 FT DOMAIN 598 1304
 FT DOMAIN 387 479
 FT DOMAIN 480 571
 FT DOMAIN 670 919
 FT DOMAIN 961 1235
 FT ACT_SITE 851 851
 FT ACT_SITE 1167 1167
 FT MUTAGEN 851 851
 FT CARBOHYD 78 78
 FT CARBOHYD 90 90
 FT CARBOHYD 95 95
 FT CARBOHYD 184 184
 FT CARBOHYD 190 190
 FT CARBOHYD 197 197
 FT CARBOHYD 232 232
 FT CARBOHYD 260 260
 FT CARBOHYD 270 270
 FT CARBOHYD 276 276
 FT CARBOHYD 335 335
 FT CARBOHYD 378 378
 FT CARBOHYD 419 419
 FT CARBOHYD 468 468
 FT CARBOHYD 488 488

FT CARBOHYD 529 529 POTENTIAL.
 SQ SEQUENCE 1304 AA; 147253 MW; 1F357BC5632618B2 CRC64;
 Query Match 8.4%; Score 90.5; DB 1; Length 1304;
 Best Local Similarity 20.9%; Pred. No. 2.8;
 Matches 36; Conservative 23; Mismatches 60; Indels 53; Gaps 6;
 OY 27 DESVNTVFSPDYOKTGDMNKLKSGCONITSTCNFSLKLNVEEIKRIRAEKENTS 86
 DB 221 DEKYNITVDLYLNK-----EKKFTALNNENEC-----GNNTC 263
 OY 87 SWEVDSFTPRKAGIGPEVHLEAEKAIYHISPGT----- 125
 DB 264 TNEVHNHLECKNNAVSISHSNSTPDKRTLLDPVGEKFOHDCQVEKADFTICLKW 323
 OY 125 KDSVNMALDGLSTYSL---LWKNSGVEERENIYSRRKIYKSPETTY 172
 DB 324 KNIETFTDTONITVFQCGNMIFDNK--EIKLENLEPERE-YKQSEILY 371
 RESULT 12
 ID 6DCS_SOYBN STANDARD; PRT; 315 AA.
 AC P26690;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-AUG-1992 (Rel. 23, Last annotation update)
 DE NAD(P)H DEPENDENT 6'-DEOXYCHALCONE SYNTHASE (EC 1.-.-).
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
 OC Glycine.
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN-CV. HAROSY 63;
 RA MEDLINE: 91177016.
 RA Welle R., Schroeder G., Schiltz E., Grisebach H., Schroeder J.;
 RT "Induced plant responses to pathogen attack. Analysis and
 RT heterologous expression of the key enzyme in the biosynthesis of
 RT phytoalexins in soybean (Glycine max L. Merr. cv. Harosoy 63).";
 RL Eur. J. Biochem. 196:423-430(1991).
 CC -1- FUNCTION: CO-ACTS WITH CHALCONE SYNTHASE IN FORMATION OF
 CC 4,2',4'-TRIHYDROXYCHALCONE, INVOLVED IN THE BIOSYNTHESIS OF
 CC GLYCEROLIN TYPE PHYTOALEXINS.
 CC -1- PATHWAY: THIS IS THE KEY ENZYME IN THE BIOSYNTHESIS OF
 CC PHYTOALEXINS IN SOYBEAN.
 CC -1- SUBUNIT: MONOMER.
 CC -1- INDUCTION: BY PATHOGEN ATTACK.
 CC -1- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X55730; CAA39261.1; -.
 DR PIR: S14222; S14222.
 DR HSSP: P14550; 2ALR.
 DR PRINTS: PR00069; ALDKETREDTASE.
 DR PROSITE: PS00062; ALDOKETO_REDUCTASE_2; 1.
 DR PROSITE: PS00063; ALDOKETO_REDUCTASE_3; 1.
 DR PROSITE: PS00798; ALDOKETO_REDUCTASE_1; 1.
 DR PFAM: PF00248; Aldo_Ket_Red; 1.
 DR Flavonoid biosynthesis; Oxidoreductase; NADP.
 SQ SEQUENCE 315 AA; 35490 MW; C3A6BE07EF330F47 CRC64;
 Query Match 8.4%; Score 90; DB 1; Length 315;

RX	DISCUSSION OF VARIOUS FORMS, AND PARTIAL SEQUENCE.
RP	MEDLINE: 95279874.
RT	Novick D., Cohen B., Tal N., Rubinstein M.:
RL	*Soluble and membrane-anchored forms of the human IFN-alpha/beta receptor.*;
CC	J. Leukoc. Biol. 57:712-718(1995).
CC	-I- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. THE LONG AND SOLUBLE FORMS ARE DIRECTLY INVOLVED IN SIGNAL TRANSDUCTION DUE TO THEIR INTERACTION WITH THE TYR KINASE, JAK1. THE LONG FORM ALSO INTERACTS WITH THE TRANSCRIPTIONAL FACTORS, STAT1 AND STAT2. BOTH FORMS ARE POTENT INHIBITORS OF TYPE I IFN ACTIVITY.
CC	-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC	-I- ALTERNATIVE PRODUCTS: THREE ISOFORMS; A LONG FORM/IFNAR2-2 (SHOWN HERE), A SHORT FORM/IFNAR2-1 AND A SOLUBLE FORM/IFNAR2-3/P40; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC	-I- PFM: UPON BINDING, IFNAR2 IS PHOSPHORYLATED ON TYROSINE RESIDUES.
CC	-I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC	-----
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DR	EMBL; L42243; AAB46417.1; JOINED.
DR	EMBL; L42238; AAB46417.1; JOINED.
DR	EMBL; L42239; AAB46417.1; JOINED.
DR	EMBL; L42340; AAB46417.1; JOINED.
DR	EMBL; L42323; AAB46417.1; JOINED.
DR	EMBL; L42241; AAB46417.1; JOINED.
DR	EMBL; L42242; AAB46417.1; JOINED.
DR	EMBL; L42243; AAB46418.1; JOINED.
DR	EMBL; L42239; AAB46418.1; JOINED.
DR	EMBL; L42340; AAB46418.1; JOINED.
DR	EMBL; L42323; AAB46418.1; JOINED.
DR	EMBL; L42241; AAB46418.1; JOINED.
DR	EMBL; L42243; AAB46419.1; JOINED.
DR	EMBL; L42238; AAB46419.1; JOINED.
DR	EMBL; L42239; AAB46419.1; JOINED.
DR	EMBL; L42340; AAB46419.1; JOINED.
DR	EMBL; L42323; AAB46419.1; JOINED.
DR	EMBL; L42241; AAB46419.1; JOINED.
DR	EMBL; L42242; AAB46419.1; JOINED.
DR	EMBL; L41944; AAB46415.1; JOINED.
DR	EMBL; L41943; AAB46414.1; JOINED.
DR	EMBL; L41942; AAB46413.1; JOINED.
DR	EMBL; X77732; CAAS4785.1; JOINED.
DR	EMBL; U29584; AAC50202.1; JOINED.
DR	EMBL; X89772; CAA61914.1; JOINED.
KW	MIM: 602376; .
KW	Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing; Phosphorylation.
KM	SIGNAL
FT	CHAIN 1 26
FT	CHAIN 27 515
FT	INTERFERON-ALPHA/BETA RECEPTOR BETA CHAIN.
FT	DOMAIN 27 243
FT	TRANSMEM 244 264
FT	DOMAIN 265 515
FT	DISULFID 85 93
FT	DISULFID 207 227
FT	CARBOHYD 58 58
FT	CARBOHYD 87 87
FT	CARBOHYD 116 116
FT	CARBOHYD 188 188
FT	CARBOHYD 192 192
FT	VARSPLIC 238 239
FT	VARSPLIC 240 331
FT	VARSPLIC 281 331
FT	SA -> FS (IN ISOFORM 2-3). MISSING (IN ISOFORM 2-3). NRHNFLAMPFPNLPLEADMDMEVYINKKKYWDNYNDE SSDDTLAAGR -> RGLKLGNAVAIHRSNRAQCSPE LKSSCLSPSSWDYRASLCPSD (IN ISOFORM 2-

FT	VARSPIC	332	515	1)	MISSING (IN ISOFORM 2-1).
FT	CONFLICT	10	10	F -> V (IN REF. 2 AND 4).	
FT	CONFLICT	151	151	M -> V (IN REF. 3).	
SO	SEQUENCE	515 AA:	57758 MM:	4D7730D93AA739F4	CRC64:
Query Match	Best Local Similarity	8.3%	Score 89;	DB 1;	Length 515;
Matches	46;	Conservative %	26;	Mismatches	83;
				Indels	48;
				Gaps	10;
OY	18	FF--ILRNNSDESGANTSFSDYQKGMDMWIK-LSGCOVITSTCKNFSFKINYEI	74		
DB	47	NERSLISMLKNHSIVPTHYLLTILNMSKPEDLVVKNKCAITTSFCDLIDEMRSTHEAY	106		
OY	75	KLRIAEKENT-----SSWYED-SPTPEPKAIGPEVHLAEADKAIVIHIS-PGTR	125		
DB	107	VYVLEGFSGNTLTSCSNFMFLAIDMSE-----PPEEIVGFTNHIVVWPKPSIV	158		
OY	126	DSVMALDGLSFTYSLTIWKNSSGVEEITENIYSNRK-----IYKLSPTT	171		
DB	159	E-----ELQFDLSLVI-----EEOSEGIYVKNKPEIKGNMNGNETYIIDKLPNTN	205		
OY	172	YCLKVKALLTSWKIGVSPVHC	194		
DB	206	YCVSVYLEHSDEQAV-IKSPKLC	227		
RESULT	15				
ID	110R	MUSE	STANDARD:	PRT:	575 AA.
AC	061727				
DT	15-JUL-1998	(Rel. 36, Created)			
DT	15-JUL-1998	(Rel. 36, Last sequence update)			
DT	15-DEC-1998	(Rel. 37, Last annotation update)			
GN	INTERLEUKIN-10 RECEPTOR PRECURSOR (IL-10R).				
OS	IL10RA OR IL10R.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
OC	Eukaryota; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-C57BL/6 X AJ F1; TISSUE-HEMATOPOIETIC;				
RX	MEDLINE: 94068585.				
RA	HO A.S.-Y., Liu Y., Khan T.A., Hsu D.-H., Bazan J.F., Moore K.W.;				
RI	"A receptor for interleukin 10 is related to interferon receptors."				
RL	Proc. Natl. Acad. Sci. U.S.A. 90:11267-11271(1993).				
CC	-1- FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.				
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.				
CC	-1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.				
CC					
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CC	use by non-profit institutions as long as its content is in no way				
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC					
DR	EMBL: L12120; AAA16156.1; -.				
KM	MGD: MGI:96538; IL10RA.				
FT	Receptor; Transmembrane; Glycoprotein; signal.				
FT	SIGNAL	1	16	POTENTIAL.	
FT	CHAIN	17	575	INTERLEUKIN-10 RECEPTOR.	
FT	DOMAIN	17	241	INTRACELLULAR (POTENTIAL).	
FT	TRANSMEM	242	262	POTENTIAL.	
FT	DOMAIN	263	575	CYTOPLASMIC (POTENTIAL).	
FT	DISULFID	204	225	POTENTIAL.	
FT	CARBOHYD	50	50	POTENTIAL.	
FT	CARBOHYD	66	66	POTENTIAL.	
FT	CARBOHYD	113	113	POTENTIAL.	
FT	CARBOHYD	182	182	POTENTIAL.	
FT	CARBOHYD	238	238	POTENTIAL.	

SO SEQUENCE 575 AA; 64248 MM; 820B9CD576F686B7 CRC64;

Query Match 8.2%; Score 87.5; DB 1; Length 575;
Best Local Similarity 20.0%; Pred. No. 1.8;
Matches 47; Conservative 38; Mismatches 89; Indels 61; Gaps 10;

```
OY 1 GKNLKSPOKEVDIIDDNFILRW---NRSDSVGNVTFSPDYOKTGMDNWKLSGCONT 56
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 23 GTELPSPSPYVWFENRFFQHIHWKPIPNQSESTYEVAL---KQYGNSTWMDIHCRKA 78
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 57 TSTKCNFSSKLNYEE---IKLRIRA-EKENTSSWEVDS-FTPFKRAQIGPEVHLEA 111
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 79 QALSCDLTFTLTLHRSYGRARAVDNSQYSNWTTERFT----- 123
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 112 EDKAIYIHISPGTKDSV-MMALDGLSEFYSLIMKNSGVEERIEIYSRHKIYKLS--- 168
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 123 VDEVIL-----TVDSVTLKAMDGIYGTIHPRTIIPAGDEYEQVFKDLRVYKISIRK 176
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 168 -----PET-----TYCLKYKALLTSMKIGVYSPVHCITVE 200
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 177 FSELKNATKRYKOEFTLTPVIGVRKFCVKVLPRLSRINKAEWSEEQCLLITTE 231
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

Search completed: June 1, 2000, 04:38:52
Job time: 14315 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 1, 2000, 04:38:06 ; Search time 69.16 Seconds

(Without Alignments)
203.511 Million cell updates/sec

Title: us-09-240-675-2_COPY_27_229

Perfect score: 1072

Sequence: 1 GKNLKSPOKVEVDIIDNFI.....WKIGVSPVHCITVTENEL 203

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPREMBL.12:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_plant:*
10: sp_rodent:*
11: sp_virus:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	415.5	38.8	569	13	O9YHWO
2	215	20.1	349	11	Q61180
3	199	18.6	332	11	Q63953
4	179	16.7	341	13	O9YGC8
5	107	10.0	484	4	O14936
6	97.5	9.1	6048	5	O23020
7	97.5	9.1	6831	5	O23550
8	97.5	9.1	7160	5	O23551
9	90.5	8.4	1143	4	O16614
10	89.5	8.3	2033	11	O54711
11	89.5	8.3	2213	6	O95209
12	89.5	8.3	2215	11	O95209
13	89	8.3	239	4	O15467
14	87.5	8.2	504	4	O93624
15	87.5	8.2	6875	6	O28733
16	87	8.1	26926	4	O10466
17	86.5	8.1	429	3	O06103
18	86	8.0	508	13	O9YH9
19	84.5	7.9	1220	3	O12465
20	84.5	7.9	2214	4	O92673

21	82.5	7.7	406	1	O58459
22	82	7.6	817	13	Q07784
23	82	7.6	1093	11	O70535
24	81	7.6	1009	1	O58863
25	81	7.6	1120	3	O08773
26	81	7.6	1375	5	O94537
27	81	7.6	1526	5	O94538
28	81	7.6	2340	11	O60705
29	80.5	7.5	962	4	O94977
30	80	7.5	513	11	O35664
31	79.5	7.4	431	10	O23861
32	79.5	7.4	1074	2	O9X257
33	79	7.4	247	11	O35663
34	79	7.4	248	11	O35983
35	79	7.4	430	11	O23854
36	79	7.4	513	11	O35238
37	79	7.4	531	11	O62319
38	79	7.4	828	5	O9XND9
39	78.5	7.3	395	5	O01531
40	78.5	7.3	497	12	P89031
41	78.5	7.3	1825	5	O61210
42	78	7.3	331	11	O55205
43	78	7.3	373	11	O55203
44	78	7.3	746	12	O90754
45	77.5	7.2	342	5	P91305

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	569 AA.
O9YHWO	O9YHWO			
ID	O9YHWO			
AC	O9YHWO			
DT	01-MAY-1999 (TREMBL)	10, Created		
DT	01-MAY-1999 (TREMBL)	10, Last sequence update		
DT	01-MAY-1999 (TREMBL)	10, Last annotation update		
DE	INTERFERON ALPHA/BETA RECEPTOR 1.			
GN	IFNAR1.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;			
CC	Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.			
RM	[1]			
RP	SEQUENCE FROM N.A.			
RA	TISSUE-LAYER:			
RC	REBOU J., GARDNER K., MONNERON D., UZE G., LUTPALLA G.;			
RT	"Comparative genomic analysis of the Interferon/Interleukin-10			
RT	receptor gene cluster."			
RL	Genome Res. 0:0-0(1999).			
DR	EMBL; AF082664; AAD13669.1; -.			
KW	Receptor.			
SO	SEQUENCE	569 AA;	64055 MW;	F99BC099 CRC32;

Query Match	38.8%;	Score 415.5;	DB 13;	Length 569;
Best Local Similarity	45.1%;	Pred. No. 1e-29;		
Matches	92;	Conservative	36;	Mismatches 65;
				Indels 11;
				Gaps 6;
OY	3	NLKSPOKVEVDIIDNFIILRNRSDESGVTFFSPDQ-----KTGMDNWKLSGCONIT	57	
DB	31	NLKSPODQYAVAVNTFLMNNYTGDT-NYTFSAQYOCFDDLTSEPEMKELSGCONVS	89	
OY	58	STKNFSLKLVVEEIKLRIRAE-KENTSSWEVDSTFPRKAQIGPPEVHLAEADKAI	116	
DB	90	HTEDFSALIRAYVADTHIRIRAEKRSKWSIFEMIPYEINQIGPELALDSINGAI	149	
OY	117	VHISPGKDSV--MMAIDGLSFTYSLILKNSGVEERINITSRKIKYILSPETTYCL	174	
DB	150	KINISPEANQVRKM-LISVFYKYNVIMNNSNV-EKVASLIPIDINDLAETTYCL	207	
OY	175	KVKAAALTSWKIGVSPVHCITKT	198	
DB	208	KVQATVPLEDKGGLFSPHCITKT	231	


```
OY 122 -PRTKSDVWMLDGL--STYSLIMKNSGVEERINISRRK---IYKLSPEPTYCK 175
DB 137 PAADREHDKWSLKQYGVSGMYIRILYK--RGSNKKVIHDTKNSSELLSQLPEWTYICIO 194
OY 176 VKAALLTSM-KIGVSPFHCIKTT 198
DB 195 VQ-CVIEPMWKTGERSELCQRT 217

RESULT 5
ID 014936 PRELIMINARY: PRT: 484 AA.
AC 014936:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89003065.
RA AGUET M., DEMBIC Z., MERLIN G.;
RT "Molecular cloning and expression of the human interferon-gamma
RT receptor."
RT Cell 55:273-280(1988).
RN [2]
RP PARTIAL SEQUENCE FROM N.A.
RX MEDLINE: 97246734.
RA MERLIN G., VAN DER LEDE B.-J.M., MCKUNE K., KNEZEVIC N.,
RA BANNARATH W., KOMOUIN N., VIEGAS-PROUIGNOT E., KIEFER H., AGUET M.,
RA DEMBIC Z.;
RT "The gene for the ligand binding chain of the human interferon gamma
RT receptor."
RT Immunogenetics 45:413-421(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX DEMBIC Z.;
RT Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U19247; AAC52064.1; -.
DR EMBL: U19241; AAC52064.1; JOINED.
DR EMBL: U19242; AAC52064.1; JOINED.
DR EMBL: U19243; AAC52064.1; JOINED.
DR EMBL: U19244; AAC52064.1; JOINED.
DR EMBL: U19245; AAC52064.1; JOINED.
DR EMBL: U19246; AAC52064.1; JOINED.
SQ SEQUENCE 484 AA; 53818 MW; EBC99D1F CRC32;

Query Match 10.0%; Score 107; DB 4; Length 484;
Best Local Similarity 22.5%; Pred. No. 0.066;
Matches 40; Conservative 39; Mismatches 61; Indels 38; Gaps 7;

OY 3 NLKSPQVEVDIIDDNFIILNRNSDESQVNV-TFSPDYQTKGMDNWKLSGCCONITSTKC 61
DB 28 SVPTPTVTVIESYNNMNIYVMEY--QIMPOVPFTVEVKRYGVKNSEMDACINISHHYC 85
OY 62 NFSLSKLNYEEIKLRIRLRA---EKENTSSWYEVDSFTPPKKAQIGPEVHLAEDKAIYI 118
DB 86 NISDHVGDPSNLSLWRYKAKAYGQKE--SAVAKSEEPFVCGDKIGPKLDIRKEEKQIMT 143
OY 119 HISPGTKDSVWMLDGLSFTYSLIMKNSGVEERINISRRKIYKLSPEPTYCKLV 176
DB 144 DI-----FHPVSFV-----NGDEQEV-----YDEFTTCYIRV 171

RESULT 6
ID 023020 PRELIMINARY: PRT: 6048 AA.
AC 023020: 027232;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
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DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE TWITCHIN.
GN UNC-22 OR ZK617.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
OC Rhabditina; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-BRISTOL N2;
RX MEDLINE: 90044042.
RA BENJAN G.M., KIEF J.E., NECKELMANN N., MOERYAN D.G., WATERSON R.H.;
RT "Sequence of an unusually large protein implicated in regulation of
RT myosin activity in C. elegans."
RT Nature 342:45-50(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-BRISTOL N2;
RX MEDLINE: 93387664.
RA BENJAN G.M., L'HERNAULT S.N., MORRIS M.E.;
RT "Additional sequence complexity in the muscle gene, unc-22, and its
RT encoded protein, twitchin, of Caenorhabditis elegans."
RT Genetics 134:1097-1104(1993).
RN [3]
RP SEQUENCE FROM N.A.
RA HARRIS B.;
RT Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: X15423; CAA33463.1; -.
DR EMBL: 273899; CAA98081.1; ALT. INIT.
DR EMBL: 273897; CAA98081.1; JOINED.
DR HSP: 063450; IAO6. 31.
DR PFAM: PF00041; I03. 31.
DR PFAM: PF00047; I9. 13.
DR PFAM: PF00069; PKinase; 1.
DR PRINTS: PR00014; FNTYPEITI.
KW Myosin; Kinase.
SQ SEQUENCE 6048 AA; 668449 MW; 1977C602 CRC32;

Query Match 9.1%; Score 97.5; DB 5; Length 6048;
Best Local Similarity 22.8%; Pred. No. 12;
Matches 44; Conservative 22; Mismatches 74; Indels 53; Gaps 10;

OY 4 LKSPQK---VEV-DIIDDNFIILNRNSDESQVNVTFSPDYQK--TGMDNWKLSGCCONI 56
DB 1073 LRPSPKPNPLSDVDFEDNLMSWKPDDGGEPELEYEVEKLTATGRWVP---CAKV 1129
OY 57 TETKCFSSSLKINYEIEIKLRIRLRA-EKENTSSWYEVDSFTPPKKAQIGPEVHLAEDKA 115
DB 1130 KOTKAHIDGLKKG--QTYOFKVAVKNKESASDALSTDKTKAKNPYDEPGKT----- 1180
OY 116 IYHISPGTKDSVWMLDGLSFTYSLILW---KNSGVEERINISRRKIYKLSPEPTY 172
DB 1180 -----GTPDVYDDADADVS-----LEWEPPKSDG-----APIQY 1210

OY 173 CLKVKAALLTSMK 185
DB 1211 VIEKKGKGRDQW 1223

RESULT 7
ID 023550 PRELIMINARY: PRT: 6831 AA.
AC 023550:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE UNC-22 PROTEIN.
GN GN
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
OC Rhabditina; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
```

RA WHITE S.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: 273897; CAA98064.1; -
 DR HSSP: 273899; CAA98064.1; JOINED.
 DR HSSP: P02751; 1FNA.
 DR PFAM: PF00041; fn3; 31.
 DR PFAM: PF00047; 1g; 17.
 DR PFAM: PF00069; PKinase; 1.
 DR PRINTS: PRO0014; FNTYPEIII.
 SO SEQUENCE 6831 AA; 752579 MW; 0A66C38 CRC32;

Query Match 9.1%; Score 97.5; DB 5; Length 6831;
 Best Local Similarity 22.8%; Pred. No. 14;
 Matches 44; Conservative 22; Mismatches 74; Indels 53; Gaps 10;

QY 4 LKSPQK---VEY-DIIDNFIILRNNSDESIGNVTFSPDYOK--TGMDNWKISGCCNT 56
 DB 1856 LDRPSKPNPLEVSDVEEDNLNLSKRPDDGGEPIEYVEKLDITAGRWVP---CAKV 1912
 QY 57 TSTKCNFSSLKLVYEIEIKLRIRA-EKENTSSWYEVDSEFTPRKAQIGPEVHLEADKA 115
 DB 1913 KDKRAHIDGLKKG--QTYQFVKAVKKEGASDALSTDKTKAKNPYDEPKT----- 1963
 QY 116 IVIHISPGTKDSYMAALDGLSTFTYSLITW--KNSGVEERIENTYSRHKIYKLSPEPTY 172
 DB 1963 -----GTPDYVDMADRVIS-----LEMEPPKSDGG-----APITQY 1993
 QY 173 CLKVKAALTSWK 185
 DB 1994 VIEKKGKRGDMQ 2006

RESULT 8
 ID Q23551 PRELIMINARY; PRT: 7160 AA.
 AC Q23551;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
 DE ZK617.1B PROTEIN.
 GN ZK617.1B.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
 OC Rhabditina; Rhabditioidea; Rhabditidae; Pelodermidae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA HARRIS B.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BEKKS M.,
 RA BONFIELD J., BORTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
 RA CAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIKKEN L., ROOPER A., SAUNDERS D., SHORRKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOULDMAN P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.";
 RT Nature 368:32-38(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA WHITE S.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: 273899; CAA98082.1; -
 DR EMBL: 273897; CAA98082.1; JOINED.
 DR EMBL: 273897; CAA98065.1; -
 DR EMBL: 273899; CAA98065.1; JOINED.

DR HSSP: P02751; 1FNA.
 DR PFAM: PF00041; fn3; 31.
 DR PFAM: PF00047; 1g; 17.
 DR PFAM: PF00069; PKinase; 1.
 DR PRINTS: PRO0014; FNTYPEIII.
 SO SEQUENCE 7160 AA; 789211 MW; EDD567FE CRC32;

Query Match 9.1%; Score 97.5; DB 5; Length 7160;
 Best Local Similarity 22.8%; Pred. No. 15;
 Matches 44; Conservative 22; Mismatches 74; Indels 53; Gaps 10;

QY 4 LKSPQK---VEY-DIIDNFIILRNNSDESIGNVTFSPDYOK--TGMDNWKISGCCNT 56
 DB 2185 LDRPSKPNPLEVSDVEEDNLNLSKRPDDGGEPIEYVEKLDITAGRWVP---CAKV 2241
 QY 57 TSTKCNFSSLKLVYEIEIKLRIRA-EKENTSSWYEVDSEFTPRKAQIGPEVHLEADKA 115
 DB 2242 KDKRAHIDGLKKG--QTYQFVKAVKKEGASDALSTDKTKAKNPYDEPKT----- 2292
 QY 116 IVIHISPGTKDSYMAALDGLSTFTYSLITW--KNSGVEERIENTYSRHKIYKLSPEPTY 172
 DB 2292 -----GTPDYVDMADRVIS-----LEMEPPKSDGG-----APITQY 2322
 QY 173 CLKVKAALTSWK 185
 DB 2323 VIEKKGKRGDMQ 2335

RESULT 9
 ID Q16614 PRELIMINARY; PRT: 1143 AA.
 AC Q16614;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
 DE T200 LEUKOCYTE COMMON ANTIGEN (CD45, LC-A) PRECURSOR (EC 3.1.3.48)
 DE (CD45, LC-A).
 GN PTPRC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 87275816.
 RA RALPH S.J., THOMAS M.L., MORTON C.C., TROMBRIDGE I.S.;
 RT "Structural variants of human T200 glycoprotein (Leukocyte-common
 antigen).";
 RT EMBO J. 6:1251-1257(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RX MEDLINE: 89009812.
 RA HALL L.R., STREUDT M., SCHLOSSMAN S.F., SAITO H.;
 RT "Complete exon-intron organization of the human leukocyte common
 antigen (CD45) gene.";
 RT J. Immunol. 141:2781-2787(1988).
 DR EMBL: M23462; AAD15273.1; JOINED.
 DR EMBL: M23461; AAD15273.1; JOINED.
 DR EMBL: M23462; AAD15273.1; JOINED.
 DR EMBL: M23466; AAD15273.1; JOINED.
 DR EMBL: M23467; AAD15273.1; JOINED.
 DR EMBL: M23468; AAD15273.1; JOINED.
 DR EMBL: M23469; AAD15273.1; JOINED.
 DR EMBL: M23470; AAD15273.1; JOINED.
 DR EMBL: M23471; AAD15273.1; JOINED.
 DR EMBL: M23472; AAD15273.1; JOINED.
 DR EMBL: M23473; AAD15273.1; JOINED.
 DR EMBL: M23474; AAD15273.1; JOINED.
 DR EMBL: M23475; AAD15273.1; JOINED.
 DR EMBL: M23476; AAD15273.1; JOINED.
 DR EMBL: M23477; AAD15273.1; JOINED.
 DR EMBL: M23478; AAD15273.1; JOINED.

DR EMBL: M23479; AAD15273.1; JOINED.
DR EMBL: M23480; AAD15273.1; JOINED.
DR EMBL: M23481; AAD15273.1; JOINED.
DR EMBL: M23482; AAD15273.1; JOINED.
DR EMBL: M23483; AAD15273.1; JOINED.
DR EMBL: M23484; AAD15273.1; JOINED.
DR EMBL: M23485; AAD15273.1; JOINED.
DR EMBL: M23486; AAD15273.1; JOINED.
DR EMBL: M23487; AAD15273.1; JOINED.
DR EMBL: M23488; AAD15273.1; JOINED.
DR EMBL: M23489; AAD15273.1; JOINED.
DR EMBL: M23490; AAD15273.1; JOINED.
DR EMBL: M23491; AAD15273.1; JOINED.
DR EMBL: Y00062; CAA68269.1; -.
DR HSSP: P18052; 1YFO.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR PFAM: PF00041; fn3; 2.
DR PFAM: PF00102; Y_Phosphatase; 2.
DR PRINTS: PRO0700; PRTPHPTASE.
DR SIGNAL: Alternative splicing; Hydrolase.
FT CHAIN 1 23 POTENTIAL.
FT SIGNAL 24 1143
SQ SEQUENCE 1143 AA; 130897 MW; 97A3A561 CRC32;

Query Match 8.4%; Score 90.5; DB 4; Length 1143;
Best Local Similarity 20.9%; Pred. No. 6.1;
Matches 36; Conservative 23; Mismatches 60; Indels 53; Gaps 6;

OY 27 DESVGVNTPSFYQKGMNMIKSCGONITKCNFSSLKLVNVEIKLRARENHS 86
DB 66 DKRYAIVTDYLYNK-----ETKLFYAKLVNNEVC-----GNNTC 102
OY 87 SWYEDSFPRKAOIGPEVHLAEADKAIVIHISPT----- 125
DB 103 TNEVHNLTCKNNAISISIHNSCTADKLLIDVPGVEKFOHLDCTOYEKADTTICLW 162
OY 125 KQVMWALDGLSFTYSL---LIWKNSSGVEERIEIENYSRHKIKYKLSPEPTY 172
DB 163 KNIETFTCDQNTITRYFQCGNMIFDK---EIKLENLEPEHE-YKCDSEILY 210

RESULT 10
O54711 PRELIMINARY; PRT; 2033 AA.
AC O54711;
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE SORILIN-RELATED RECEPTOR, LDLR CLASS A REPEATS-CONTAINING PRECURSOR
DE (GP250) (FRAGMENT).
GN SORL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA HERANS-BONGMEYER I., HAMPE W., SCHINKE B., METHNER A., NYKJAER A.,
MECH. Dev. 0:0-0(1997).
RL EMBL: AF01818; AAC16739.1; -.
DR HSSP: P01130; 1AJJ.
DR MGD: MGI:1202296; Sorl1.
DR PROSITE: PS01309; LDLRA_1; 10.
DR PFAM: PF00041; fn3; 4.
DR PFAM: PF00057; ldl_recept_a; 11.
DR PFAM: PF00058; ldl_recept_b; 5.
KW Glycoprotein.
FT NON_TER 1 1
SQ SEQUENCE 2033 AA; 227305 MW; DC8108CD CRC32;

Query Match 8.3%; Score 89.5; DB 11; Length 2033;
Best Local Similarity 19.2%; Pred. No. 16;
Matches 33; Conservative 33; Mismatches 77; Indels 29; Gaps 7;
OY 18 NFILMNRSDSEV-----GNV-TFSFDYQKGMNMIKSCGONITSTKCNFS 64
DB 1474 NQQLNREDEGVIIIGHNAPVHTGILREYIVESRSGSKMAQRAASSTEEK----- 1530
OY 65 SKLVNVEEIKLRIRAEKENTSSWYEDSFPRKAOIGPEVHLAEADKAIV----- 118
DB 1530 NLLNALVTVRY-AAVTSRGIGNMDSKSIITIKGVIAQAPNIIHSDYDENSLSFTLMD 1588
OY 118 --THSPGKDSVMWALDGLSFTYSLLIWKNSGVEERIEIENYSRHKIKYKLS 167
DB 1589 GDIKVY-GYVNLFWSPFAHQEKKTLSEFRGSALSHKVSNL-TAHTSYEIS 1638

RESULT 11
O95209 PRELIMINARY; PRT; 2213 AA.
ID O95209;
AC O95209;
DT 01-FEB-1997 (Tremblrel. 02, Created)
DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE Lr11.
OS Eucytolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE-LIVER;
RX MEDLINE: 96394640.
RA YAMAZAKI H., BUJO H., KUSUNOKI J., SEIMIYA K., KANAKI T., MORISAKI N.,
RA SCHNEIDER W.J., SAITO Y.;
RT "Elements of neural adhesion molecules and a yeast vacuolar protein
RT sorting receptor are present in a novel mammalian low density
RT lipoprotein receptor family member";
RL J. Biol. Chem. 271:24761-24768(1996).
DR EMBL: D86350; BAA13075.1; -.
DR HSSP: P01130; 1AJJ.
DR PROSITE: PS01209; LDLRA_1; 10.
DR PFAM: PF00057; ldl_recept_a; 11.
DR PFAM: PF00058; ldl_recept_b; 4.
DR PRINTS: PR00261; LDLRECEPTOR.
DR PRINTS: PR00014; FNTYPEI11.
KW Glycoprotein.
SQ SEQUENCE 2213 AA; 247764 MW; B35F3995 CRC32;

Query Match 8.3%; Score 89.5; DB 6; Length 2213;
Best Local Similarity 17.1%; Pred. No. 17;
Matches 32; Conservative 36; Mismatches 76; Indels 43; Gaps 7;

OY 6 SFQKVEVDIIDN---FILKMRSDSEVGNV-TFSFDYQKGMNMIKSCGONITSTK 61
DB 1652 APQNLQLSLHGECEVIGHMSPPRTHTGLIREYIVESRSGSKVWTERAASNETEK- 1711
OY 62 NFSSKLNVYEIKLRIRAEKENTSSWYEDSFPRKAOIGPEVHLAEADKAIVIHIS 121
DB 1711 ---NLVNTLVTVRY-AAVTSRGIGNMDSKSIITIKGVIAQAPNIIHSDYDENSLSFTLMD 1760
OY 122 PGTKDSVMWALDGLSFTYSL-----LIWKNSSGVEER-----IENYSRHKIKYKLS 165
DB 1760 -----NSLSFTLVQDNIIKGVYVNLFWAFDTHKQEKTKMNFQSGSVSHKYN 1808
OY 166 LSPETTY 172
DB 1809 LTAOTAY 1815

RESULT 12
O88307


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ID 088307 PRELIMINARY: PRT: 2215 AA.
AC 088307;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE LRI1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA KANAI T., BUJO H., HIRAYAMA S., TANAKA K., YAMAZAKI H., SEIMIYA K.,
RA MORISAKI N., SCHNEIDER W.J., SAITO Y.;
RT "Developmental regulation of LRI1 expression in murine brain.";
RL DNA Cell Biol. 0:0-0(1998);
DR EMBL: AB015790; BAA31219.1; -.
DR HSSP: P01130; IAUJ.
DR PROSITE: P501209; LDRLA_1; 10.
DR PFAM: PF00057; Idl_recept_a; 11.
DR PFAM: PF00058; Idl_recept_b; 5.
DR PFAM: PF00041; fn3; 4.
DR PRINTS: PR00261; LDLRECEPTOR.
DR PRINTS: PR00014; FNTPEPIT.
KM Glycoprotein.
SQ SEQUENCE 2215 AA: 247021 MW: DFEBCF8 CRC32:

Query Match 8.3%; Score 89.5; DB 11; Length 2215;
Best Local Similarity 19.2%; Pred. No. 17;
Matches 33; Conservative 33; Mismatches 77; Indels 29; Gaps 7;

OY 18 NFIIRNRSDSY-----GNV-TEFSDYOKTGMDNNTKLSGCONITSTKCNFS 64
DB 1656 NLOSLNREEGYILGMARPVHTGILREYIYERSGSKMAASQPAASNSTEIK----- 1712
OY 65 SLALNYEELIRIRAKENTSSWEYDSTPFRKAQIGPPEVLEADKAIV----- 118
DB 1712 NLNLALYTRV-AAVTSRGIQNMDSKSTITIKGVIAQAPNHIDYDENSLSFTLTM 1770
OY 118 --IHISGTDSVMALDGLSTYSLIMKNSGVEERINYSRKITYLS 167
DB 1771 GDIKVN-GYVYNLFMSFPAKOEKTLSPFGSALSHKVNLS-TAHTSYEIS 1820

RESULT 13
O15467 PRELIMINARY: PRT: 239 AA.
AC 015467;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE SOLUBLE IFN ALPHA/BETA RECEPTOR PRECURSOR.
GN IFNABR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RA MEDLINE: 95279874.
RA NOVICK D., COHEN B., TAL N., RUBINSTEIN M.;
RT "Soluble and membrane-anchored forms of the human IFN-alpha/Beta
RT receptor.";
RL J. Leukoc. Biol. 57:712-718(1995).
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
KW EMBL: X89814; CAA61940.1; -.
DR Receptor; Signal.
FT SIGNAL 1 26 SOLUBLE IFN ALPHA/BETA RECEPTOR BETA
FT CHAIN 27 239 CHAIN
SQ SEQUENCE 239 AA: 27336 MW: 9DA1F03E CRC32:
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Query Match 8.3%; Score 89; DB 4; Length 239;
Best Local Similarity 22.7%; Pred. No. 1.1;
Matches 46; Conservative 26; Mismatches 83; Indels 48; Gaps 10;

OY 18 NF--ILNRNRSDSYGNVTEFSDYOKTGMDNNTK-LSGCONITSTKCNFSIKLVYEIR 74
DB 47 NRSILSWLKNHSHVPTTYITLLTIMSKPEDLKVKKNCANTRFCDLTDWRSTHEAY 106
OY 75 KLIRAKENT-----SSWEVD-STPFRKAQIGPPEVLEADKAIVIHIS-PGKT 125
DB 107 VTVLEEGSCNTLLFSCSHNFMLAIDMSFE-----PPEEIVFTNINMNVAFPSIV 158
OY 126 DSMVMAALDGLSTYSLIMKNSGVEERINYSRK-----TYKISPEPT 171
DB 159 E-----EELQDLSIV-----EEOSEGIVKAKHKEPIKGMGNGFTIYIDKLIPNTN 205
OY 172 YCLKVKAAALLTSWKIGYSPVHC 194
DB 206 YCVSVYLEHSDQAV-IKSPKLC 227

RESULT 14
O99624 PRELIMINARY: PRT: 504 AA.
AC 099624;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE TRANSPORTER PROTEIN.
GN G17.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA LATIF F., LERMAN M., MINNA J., DUH F.M., KOONIN E., BADER S.;
RL Submitted (FEB-1996) to the EMBL/Genbank/DBJ databases.
DR EMBL: U49082; AAB47236.1; -.
DR PFAM: PF01490; Ab_trans; 1.
SQ SEQUENCE 504 AA: 55772 MW: C41A273E CRC32:

Query Match 8.2%; Score 87.5; DB 4; Length 504;
Best Local Similarity 25.5%; Pred. No. 4;
Matches 41; Conservative 35; Mismatches 64; Indels 21; Gaps 7;

OY 55 NITSTKCNFSIKLVYEELIRAKEN--TSSWEYDSTP-----RKAQIGPPEV 107
DB 245 NFNNTTGNSSHVEI-VKEKVLQVEPEASAFCTPSYFTLNSQTAVTIPIMAFVCHPEV 303
OY 108 -----HLEDEDAIYIHISPGTKDSVMALDGLSTYSLIMKNSGVEERINYSRK 162
DB 304 LPITYELKDPSRKKWQHS-NLSIAVMYIMFLALFGYLTFY-N--GVESELHLYTS--- 358
OY 163 IYKLSPEPTYCLKVKAAALLTSWKIGYSPVHCIKTIVENEL 203
DB 358 --KVDPFDVLLCVRAVAVITAVTLVPIVFPVRAIQOML 396

RESULT 15
O28733 PRELIMINARY: PRT: 6875 AA.
AC 028733;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE TITIN (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE FROM N.A.
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RC STRAIN-CE12;
RA LABEIT S.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-6805 FROM N.A.
RC STRAIN-CE12;
RX MEDLINE: 92258380.
RA LABEIT S., GAUTEL M., LAKEY A., TRINICK J.;
RT "Towards a molecular understanding of titin."
RL EMBO J. 11:1711-1716(1992).
RN [3]
RP SEQUENCE OF 4305-5320 FROM N.A.
RC TISSUE-PSOAS MUSCLE;
RX MEDLINE: 90238553.
RA LABEIT S., BARLOW D.P., GAUTEL M., GIBSON T., HOLT J., HSIEH C.L.,
RA FRANCKE U., LEONARD K., WARDALE J., WHITING A., TRINICK J.;
RT "A regular pattern of two types of 100-residue motif in the sequence
of titin."
RL Nature 345:273-276(1990).
DR EMBL: X64696; CAA45937.1; -
DR EMBL: X17329; CAA35207.1; -
DR HSSP: P56276; 1TLX.
DR PRAM: PF00041; fn3: 50.
DR PRAM: PF00047; 19: 3.
KW Myosin; Muscle protein.
FT NON_TER 1
FT NON_TER 6875
SO SEQUENCE 6875 AA; 759127 MW; ESD3B61F CRC32;

Query Match 8.2%; Score 87.5; DB 6; Length 6875;
Best Local Similarity 21.0%; Pred. No. 1.1e+02;
Matches 48; Conservative 24; Mismatches 70; Indels 87; Gaps 9;

OY 2 KNLKSPQKVEVDIDDNFILMNRSDSVGNVTFSDYQKTGMNWKLSGC--QNTST 59
DB 233 RNLKIP-----DVSSDRCTIMWDPEDD-----GGCEIQNYILE 266
OY 60 KCNFSSLKLVY-----EIKLRIRAEKE-----NTSSWEVDSFTPF 97
DB 267 KCEKRWVMSYTSATVLTPTGTVRLIEGNEYIFRVRAENKIGTGPPEESKPIAKTKYD 326
OY 98 RKAQIGPPEVHLEAEDRAIVT-----HISPGTKDSVMALDGLSFTYSL 142
DB 327 RPRGRPDPEVTYKSKKEETVWMSPEYDGKSKITGYLEKKEKHSVRN----- 375
OY 143 IWRNSSGVEERENIENYSRHKIKYKLSPEPTYCLAKYKALITSMKIGYSP 191
DB 375 VPVNRKSAIPER-----RLKYQNLIPGHEYOFRVKA---ENEIGVGEP 413

Search completed: June 1, 2000, 04:38:14
Job time: 14306 sec

201 A 201
|
67 s 67

seq_name: A_Geneseq_36:R14487

seq_documentation_block:

ID R14487 standard; Protein: 436 AA.
AC R14487;
DT 16-JAN-1992 (first entry)
DE Soluble Interferon-alpha/Beta receptor.
KW IFN; autoimmune disease; graft rejection; histocompatibility.
OS Homo sapiens.
PN FR2657881-A.
PD 09-AUG-1991.
PF 05-FEB-1990; 001298.
PR 05-FEB-1990; FR-001298.
PA (EUBI-) LAB EURO BIOTECHNO.
PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE;
PI Tovey MG, Uze G;
DR WPI: 91-319778/44.
DR N-PSDB: Q14239.
PT New water-soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus, Behcet's disease, aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.
PS Claim 2: Page 45; 52pp: French.
CC The transmembrane and cytoplasmic domains of the native IFN receptor have been deleted to obtain a soluble, circulating form of the receptor. Potentially immunogenic epitopes have thus been eliminated.
CC Derivatives obtained by immunogenic substitution or deletion of this sequence are also claimed as are hybrid molecules comprising the soluble CC receptor (or deriv.) and an immunoglobulin such as IgG1.
CC See also Q14240.
SQ Sequence 436 AA;

alignment_scores:

Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x R14487 ..

Align seg 1/1 to: R14487 from: 1 to: 436

1 ATGATGCTGCTCTCTGGGCGGAGACCTAGTCTGTCGCCGTGGG 50
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
51 CCCATGGGTGTGTCGCCGAGCGAGTGAATAAATCTAAATCTCCCTC 100
|||||
17 yProtrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
51 AAAAGTAGAGGTGACATCATGATGACAACTTATCTGAGGTGGAAC 150
|||||
101 AAAAGTAGAGGTGACATCATGATGACAACTTATCTGAGGTGGAAC 150
|||||
34 InlYsValGluValAspIleIleAspAspAsnPhelIleLeuArgTrpAsn 50
151 AGGACGATGATGCTGTCGGGAATGTGACTTTTCATTCATTCATCAAA 200
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTrpGlnIly 67
201 A 201
|
67 s 67

seq_name: A_Geneseq_36:R28495

seq_documentation_block:

ID R28495 standard; Protein: 436 AA.
AC R28495;
DT 31-MAR-1993 (first entry)
DE Sequence of a soluble form of the Interferon (IFN) receptor

DE with a high affinity for IFN-alpha and -beta.
KW Interferon receptor; alpha-Interferon; beta-Interferon.
OS Synthetic.
PN WO9218626-A.
PD 29-OCT-1992.
PF 17-APR-1991; F00318.
PR 17-APR-1991; WO-F00318.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,
PI Tovey M, Uze G;
DR WPI: 92-382110/46.
DR N-PSDB: Q30532.
PT Water soluble polypeptide(s) strongly bind Interferon(s) alpha and beta - useful as immunosuppressants, for treating auto-immune PT diseases and transplant rejection
PS Claim 2: Fig 1: 58pp; English.
CC DNA encoding the water-soluble polypeptide with a high affinity for CC IFN-alpha and -beta is isolated by PCR, using appropriate CC oligonucleotides as primers and cloned cDNA as template. For example, CC bacteriophage lambda ZAP, containing the entire coding sequence of CC the IFN-alpha and -beta receptor (Q30533), was incubated with oligos CC Q30534 and Q30535. R28496 represents the complete receptor. R28495 CC lacks the transmembrane and cytoplasmic domains. Both forms bind CC IFN in the same way as antibodies so are immunosuppressants e.g. for CC treating autoimmune diseases and graft rejection. They lack the CC toxic side-effects of known immunosuppressants such as steroids.
SQ Sequence 436 AA;

alignment_scores:

Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x R28495 ..

Align seg 1/1 to: R28495 from: 1 to: 436

1 ATGATGCTGCTCTCTGGGCGGAGACCTAGTCTGTCGCCGTGGG 50
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
51 CCCATGGGTGTGTCGCCGAGCGAGTGAATAAATCTAAATCTCCCTC 100
|||||
17 yProtrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
51 AAAAGTAGAGGTGACATCATGATGACAACTTATCTGAGGTGGAAC 150
|||||
101 AAAAGTAGAGGTGACATCATGATGACAACTTATCTGAGGTGGAAC 150
|||||
34 InlYsValGluValAspIleIleAspAspAsnPhelIleLeuArgTrpAsn 50
151 AGGACGATGATGCTGTCGGGAATGTGACTTTTCATTCATTCATCAAA 200
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTrpGlnIly 67
201 A 201
|
67 s 67

seq_name: A_Geneseq_36:R17123

seq_documentation_block:

ID R17123 standard; Protein: 436 AA.
AC R17123;
DT 16-OCT-1995 (first entry)
DE IFN receptor extracellular domain.
KW IFN receptor; Interferon receptor; Interferon-alpha; Interferon-beta; monoclonal antibody; Immunomodulator; AIDS.
OS Homo sapiens.
PN WO9507716-A.
PD 23-MAR-1995.
PF 16-SEP-1994; E03114.
PR 17-SEP-1993; EP-402279.

PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
 PI Beniziri EJ, Tovey MG;
 DR WPI: 95-13187/17.
 DR N-PSDB: Q86457.
 PT Compn. of monoclonal antibodies against interferon receptor
 PT useful as immuno:modulator, eg. for treating AIDS
 PS Disclosure: Fig. 2A-2B; 105pp; English.
 CC A recombinant soluble form of the human interferon class I receptor
 CC protein extracellular domain, given in R71723, was expressed in
 CC either E. coli or COS cell hosts. The protein was used to raise
 CC immunomodulatory monoclonal antibodies.
 SO Sequence 436 AA;

Alignment_scores: Length: 67
 Quality: 340.00 Gaps: 0
 Ratio: 5.075
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-240-675-1_COPY_27_229 x R71723

Align seg 1/1 to: R71723 from: 1 to: 436

```

1 ATGATGTCGTCCTCCGCGCGAGACCCCTAGTCTCTCCGCGCGG 50
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
51 CCCATGGGTGTTGTCGCGAGCCGCGGTGGAATAATCTCTCTC 100
|||||
17 yProTyrPValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
101 AAAAGTGCATGTCATGATGATGATGATGATGATGATGATGATG 150
|||||
34 IntLysValGluValAspLeuLeuLeuLeuLeuLeuLeuLeuLeuArgTyrPsn 50
151 AGAGCGATGATGATGATGATGATGATGATGATGATGATGATG 200
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLys 67
201 A 201
67 s 67

```

seq_name: A_Geneseq_36:W21806

seq_documentation_block:

ID W21806 standard; Protein: 496 AA.
 AC W21806;
 DT 23-SEP-1997 (first entry)
 DE Spliced-deleted interferon alpha-receptor form 2.
 KM Interferon alpha-receptor: IFNAR.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT domain 1..419
 FT /label= "Extracellular_domain
 FT /note= "comprises amino acid residues 1-413 and
 FT 422-427 of transmembranal IFNAR"
 FT domain 420..496
 FT /label= "intracellular_domain
 FT /note= "comprises amino acids 481-557 of
 FT transmembranal IFNAR"
 PN A09475977-A.
 PD 11-MAY-1995.
 PF 20-OCT-1994; 075977.
 PR 24-OCT-1993; IL-107378.
 PA (VEDA) VEDA RES & DEV CO LTD.
 PA (ABRA/) ABRAMOVICH C.
 PI Abramovich C, Ratovitski E, Revel M;
 DR WPI: 95-200634/27.
 PT New mammalian soluble interferon alpha-receptor forms - used for
 PT inhibiting, modulating or modifying the activities of interferon(s)
 PS Example 3; fig 7; 46pp; English.

CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 2
 CC (W21806) is characterised by a double deletion when compared to
 CC transmembranal IFNAR (W21804). The extracellular domain is
 CC shortened by 6 amino acid residues and is followed by a truncated
 CC intracellular domain. There is no transmembrane region. The amino
 CC acid sequence is predicted from a cDNA clone (see also: T73521) ctd.
 CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR
 CC splice-deleted forms 1 (see also W21805) and 2 may regulate the
 CC response of human cells to IFNs, either by acting as IFN
 CC antagonists or by regulating IFN activities. They can be expressed
 CC in host cells and used to inhibit, modulate or modify the
 CC activities of IFNs alpha and beta in cells, tissues and organisms,
 CC or for diagnostic purposes.
 SO Sequence 496 AA;

alignment_scores: Length: 67
 Quality: 340.00 Gaps: 0
 Ratio: 5.075
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-240-675-1_COPY_27_229 x W21806

Align seg 1/1 to: W21806 from: 1 to: 496

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1 ATGATGTCGTCCTCCGCGCGAGACCCCTAGTCTCTCCGCGCGG 50
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
51 CCCATGGGTGTTGTCGCGAGCCGCGGTGGAATAATCTCTCTC 100
|||||
17 yProTyrPValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
101 AAAAGTGCATGTCATGATGATGATGATGATGATGATGATGATG 150
|||||
34 IntLysValGluValAspLeuLeuLeuLeuLeuLeuLeuLeuLeuArgTyrPsn 50
151 AGAGCGATGATGATGATGATGATGATGATGATGATGATGATG 200
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLys 67
201 A 201
67 s 67

```

seq_name: A_Geneseq_36:R11958

seq_documentation_block:

ID R11958 standard; Protein: 557 AA.
 AC R11958;
 DT 18-JUL-1991 (first entry)
 DE Human alpha-interferon receptor protein.
 KM Human alpha IFN; IFN agonists; antiviral; anti tumour agent;
 KW drug targeting.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT peptide 1..27
 FT /label= "signal peptide
 FT WO9105862-A.
 PD 02-MAY-1991.
 PF 19-OCT-1990; F00758.
 PR 20-OCT-1989; FR-013770.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 PI Mogensens KE, Uze G, Lutfalla G, Gresser I;
 DR WPI: 91-148740/20.
 DR N-PSDB: Q11701.
 PT New human alpha-interferon receptor protein - useful for testing
 PT interferon agonists and in treatment or diagnosis
 PS Disclosure: fig 4; 30pp; French.
 CC This recombinant human alpha interferon (IFN) receptor protein is
 CC useful for the testing of IFN agonists and for treatment and diag-
 CC nosis of viral diseases and tumours. Antibodies raised against

CC this protein can be used for blocking the receptor when required,
 CC eg where overexpression of alpha-IFN is harmful. The Abs are
 CC also useful for eg drug targeting. Variants of the protein,
 CC having residue 164 (Thr) replaced by Arg and an Asp inserted
 CC between residues 479 and 480, are also useful.
 SO Sequence 557 AA;

alignment_scores: Length: 67
 Quality: 340.00
 Ratio: 5.075
 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x R11958

Align seg 1/1 to: R11958 from: 1 to: 557

```

1  ATGATGTCGTCCTCCTGGCGCGACGACCTAGTCGTCGCGCGG 50
1  MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
51  CCCATGGGTGTGTCGCCGCGACCGCAGCTGAAAAATCTAAATCTCTC 100
17  yProtrpValLeuSerAlaAlaAlaGlyLysAsnLeuLysSerProG 34
101  AAAAGTAGAGTGCACATCATAGACAACTTTCTCTGAGGTGGAC 150
34  InLysValGluValAspIleIleAspAspAsnPhelLeuArgTrpAsn 50
151  AGGACGATGAGTGTGCGGAGTGTGACTTTTCATTCGATTATCAAAA 200
51  ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnly 67
201  A 201
67 s 67

```

seq_name: A_Geneseq_36:R14488

seq_documentation_block:

ID R14488 standard; Protein: 557 AA.
 AC R14488;
 DT 16-JAN-1992 (first entry)
 DE Complete interferon-alpha/beta receptor.
 KW IFN; autoimmune disease; graft rejection; histocompatibility.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT domain 437..457
 /label= transmembrane
 FT domain 458..557
 /label= cytoplasmic
 FT domain
 FN FR2657881-A.
 PN 09-AUG-1991.
 PE 05-FEB-1990: 001298.
 PR 05-FEB-1990: FR-001298.
 PA (EUBI-) LAB EURO BIOTECHNO.
 PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE;
 PI Tovey M, Uze G;
 PI WPI: 91-319778/44.
 DR N-PSDB: Q14240.
 PT New water-soluble polypeptide(s) with affinity for IFN-alpha and
 PT beta - used to treat e.g. lupus erythematosus, Behcet's disease,
 PT aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.
 PS Disclosure: Page 47; 52pp; French.
 CC The invention covers derivatives of the interferon-alpha and/or beta
 CC receptor obtained by deleting the transmembrane and cytoplasmic domains
 CC of the native receptor or by substitution. Potentially immunogenic
 CC epitopes are eliminated and the deriv. can be secreted from
 CC transformed cells. Soluble deriv.s block the activity of IFN alpha/beta
 CC and can be used to treat autoimmune diseases or to inhibit graft
 CC rejection. See also Q14239.
 SO Sequence 557 AA;

alignment_scores: Length: 67
 Quality: 340.00
 Ratio: 5.075
 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x R14488

Align seg 1/1 to: R14488 from: 1 to: 557

```

1  ATGATGTCGTCCTCCTGGCGCGACGACCTAGTCGTCGCGCGG 50
1  MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
51  CCCATGGGTGTGTCGCCGCGACCGCAGTGTGAAAAATCTAAATCTCTC 100
17  yProtrpValLeuSerAlaAlaAlaGlyLysAsnLeuLysSerProG 34
101  AAAAGTAGAGTGCACATCATAGACAACTTTCTCTGAGGTGGAC 150
34  InLysValGluValAspIleIleAspAspAsnPhelLeuArgTrpAsn 50
151  AGGACGATGAGTGTGCGGAGTGTGACTTTTCATTCGATTATCAAAA 200
51  ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnly 67
201  A 201
67 s 67

```

seq_name: A_Geneseq_36:R28496

seq_documentation_block:

ID R28496 standard; Protein: 557 AA.
 AC R28496;
 DT 31-MAR-1993 (first entry)
 DE Sequence of a soluble form of the interferon (IFN) receptor
 DE with a high affinity for IFN-alpha and -beta.
 KW Interferon receptor; alpha-interferon; beta-interferon.
 OS Synthetic.
 PN MO9218626-A.
 PD 29-OCT-1992.
 PE 17-APR-1991; F00318.
 PR 17-APR-1991; WO-F00318.
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
 PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,
 PI Tovey M, Uze G;
 PI WPI: 92-382110/46.
 DR N-PSDB: Q30533.
 PT Water soluble polypeptide(s) strongly bind interferon(s) alpha
 PT and beta - useful as immunosuppressants, for treating autoimmune
 PT diseases and transplant rejection
 PS Claim 3; Fig 2; 58pp; English.
 CC DNA encoding the water-soluble polypeptide with a high affinity for
 CC IFN-alpha and -beta is isolated by PCR, using appropriate
 CC oligonucleotides as primers and cloned cDNA as template. For example,
 CC bacteriophage lambda ZAP, containing the entire coding sequence of
 CC the IFN-alpha and -beta receptor (Q30533), was incubated with oligos
 CC Q30534 and Q30535. R28496 represents the complete receptor. R28495
 CC lacks the transmembrane and cytoplasmic domains. Both forms bind
 CC IFN in the same way as antibodies so are immunosuppressants e.g. for
 CC treating autoimmune diseases and graft rejection. They lack the
 CC toxic side-effects of known immunosuppressants such as steroids.
 SO Sequence 557 AA;

alignment_scores: Length: 67
 Quality: 340.00
 Ratio: 5.075
 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x R28496

Align seg 1/1 to: R28496 from: 1 to: 557

```

1 ATGATGCTGCTCTCTGGGCGGAGACCCCTAGTGTCTGCTGCCGTGG 50
1 MetMetValValLeuLeuGlyAlaThrThrLeuValAlaValAlaG1 17
51 CCCATGGGTGTCTCCGAGCCGAGGTGGAATAATCTAAATCTCCCTC 100
17 yProTriPValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
101 AAAAAGTAGAGGTGACATCATAGATGACAACTTATCTGAGGTGGAAC 150
34 InLysValGluValAspIleIleAspAspAsnPhelIleuArgTriPasn 50
151 AGGACCGATGAGTCTGTGGGAAATGTGACTTTTCATTGATTATCAAAA 200
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLys 67
201 A 201
1
67 s 67

```

seq_name: A_Geneseq_36:R42635

seq_documentation_block:

ID R42635 standard; Protein: 557 AA.

```

AC R42635;
DT 20-APR-1994 (first entry)
DE Human interferon receptor.
KW IFN-R; extracellular domain; monoclonal antibody; viral infection;
KW cell proliferation; allograft rejection; systemic lupus erythematosus;
KW psoriasis; multiple sclerosis; Behcet's disease; aplastic anaemia;
KW immunodeficiency; measles virus; interferon-alpha-beta.
OS Homo sapiens.
FH key Location/Qualifiers
FT domain 1..436
FT /label= extracellular domain
FT /note= "soluble, immunogenic form of IFN-R"
PD EP-563487-A.
PD 06-OCT-1993.
PF 31-MAR-1992; 400902.
PR 31-MAR-1992; EP-400902.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
PI Benoit P. Maguire D, Meyer F, Plavec I, Tovey MG.
PI WPI: 93-312951/40.
DR P-PSDB: R42635.
PT Monoclonal antibody to human interferon type-I receptor - having
PT neutralising activity against human type I interferon, used for
PT therapy and diagnosis
PS Disclosure; Fig 3; 21pp; English.
CC Monoclonal antibodies produced against soluble forms of the human
CC interferon alpha-beta receptor based on the full-length human IFN-R
CC sequence are claimed. The antibodies are useful for treatment and
CC prophylaxis of disorders involving cell proliferation and/or viral
CC infection.
SQ Sequence 557 AA;

```

alignment_scores:

Quality: 340.00 Length: 67
 Ratio: 5.075 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x R42635

Align seg 1/1 to: R42635 from: 1 to: 557

```

1 ATGATGCTGCTCTCTGGGCGGAGACCCCTAGTGTCTGCTGCCGTGG 50
1 MetMetValValLeuLeuGlyAlaThrThrLeuValAlaValAlaG1 17
51 CCCATGGGTGTCTCCGAGCCGAGGTGGAATAATCTAAATCTCCCTC 100
17 yProTriPValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
101 AAAAAGTAGAGGTGACATCATAGATGACAACTTATCTGAGGTGGAAC 150
34 InLysValGluValAspIleIleAspAspAsnPhelIleuArgTriPasn 50
151 AGGACCGATGAGTCTGTGGGAAATGTGACTTTTCATTGATTATCAAAA 200

```

seq_name: A_Geneseq_36:R75356

seq_documentation_block:

ID R75356 standard; Protein: 557 AA.

```

AC R75356;
DT 16-OCT-1995 (first entry)
DE Human IFN receptor.
KW IFN receptor; interferon receptor; interferon-alpha;
KW interferon-beta; monoclonal antibody; immunomodulator; AIDS.
OS Homo sapiens.
FH key Location/Qualifiers
FT domain 1..436
FT /label= Extracellular_domain
FT MO507716-A.
PD 16-SEP-1995.
PF 16-SEP-1994; E03114.
PR 17-SEP-1993; EP-402279.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
PI Beniziri EJ, Tovey MG.
PI WPI: 95-131187/17.
DR N-PSDB: 086458.
PT Compsn. of monoclonal antibodies against interferon receptor -
PT useful as immunomodulator, eg. for treating AIDS
PS Disclosure; Fig 3A-2B; 105pp; English.
CC The amino acid sequence of human interferon class I receptor is
CC given in R75356. A recombinant soluble form of the extracellular
CC domain of this receptor (R71723) has been used to raise
CC immunomodulatory monoclonal antibodies.
SQ Sequence 557 AA;

```

alignment_scores:

Quality: 340.00 Length: 67
 Ratio: 5.075 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x R75356

Align seg 1/1 to: R75356 from: 1 to: 557

```

1 ATGATGCTGCTCTCTGGGCGGAGACCCCTAGTGTCTGCTGCCGTGG 50
1 MetMetValValLeuLeuGlyAlaThrThrLeuValAlaValAlaG1 17
51 CCCATGGGTGTCTCCGAGCCGAGGTGGAATAATCTAAATCTCCCTC 100
17 yProTriPValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
101 AAAAAGTAGAGGTGACATCATAGATGACAACTTATCTGAGGTGGAAC 150
34 InLysValGluValAspIleIleAspAspAsnPhelIleuArgTriPasn 50
151 AGGACCGATGAGTCTGTGGGAAATGTGACTTTTCATTGATTATCAAAA 200

```

51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnIu 67

201 A 201

67 s 67

seq_name: A_Geneseq_36:W21804

seq_documentation_block:

ID W21804 standard; Protein: 557 AA.

AC W21804:

DE 23-SEP-1997 (first entry)

DE Transmembrane Interferon alpha-receptor.

KW Interferon alpha-receptor; IFNAR.

OS Homo sapiens.

FT Key Location/Qualifiers

FT domain 1..436

FT domain /label= Extracellular_domain

FT domain 437..457

FT domain /label= Transmembrane_domain

FT domain 458..557

FT domain /label= Intracellular_domain

PN A09475977-A.

PD 11-MAY-1995.

PE 20-OCT-1994: 075977.

PR 24-OCT-1993: IL-107378.

PA (YEDA) YEDA RES & DEV CO LTD.

PA (ABRA/) ABRAMOVICH C.

PI Abramovich C, Ratovitski E, Revel M;

DR WPI: 95-200634/27.

PT New mammalian soluble interferon alpha-receptor forms - used for

PT inhibiting, modulating or modifying the activities of interferon(s)

PS Disclosure: Fig 7: 46pp; English.

CC Human transmembrane Interferon alpha receptor (IFNAR) (W21804)

CC includes a 21-amino acid transmembrane region. Novel, splice-

CC deleted IFNAR forms 1 (W21805) and 2 (W21806) have been detected

CC that lack this transmembrane domain. These, soluble non-membrane

CC bound polypeptides can be expressed in host cells and used to

CC inhibit, modulate or modify the activities of interferons alpha

CC and beta in cells, tissues and organisms, or for diagnostic

CC purposes.

SO Sequence 557 AA:

alignment_scores:

Quality: 340.00

Ratio: 5.075

Percent Similarity: 100.000

Percent Identity: 100.000

Length: 67

Gaps: 0

US-09-240-675-1_COPY_27_229 x W21804

Align seg 1/1 to: W21804 from: 1 to: 557

1 ATGATGGTCCTCCTCGGCGGAGACCCCTAGTCTCCTCGCCGCGG 50

1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaG 17

51 CCCATGGGTCTTGTCCGACCCGAGGTGAAAAATCTAAATCTCTC 100

17 yPrrTrrValLeuSerAlaAlaGlyLysAsnLeuLysSerProG 34

101 AAAAAGAGAGTGCACATCATGATGACAACTTATCCGAGGTGAAC 150

34 InLysValGluValAspIleIleAspAspAsnPhelIleLeuArgTyrPasn 50

151 AGGAGGATAGTCTGTGCGGAATGTGACTTTTCATTGATTATCAAAA 200

51 ArgSerAspLysSerValGlyAsnValThrPheSerPheAspTyrGlnIu 67

201 A 201

67 s 67

seq_name: A_Geneseq_36:W93941

seq_documentation_block:

ID W93941 standard; Protein: 1429 AA.

AC W93941:

DE 30-JUN-1999 (first entry)

DE Human bix protein

KW Bix protein; breast cancer; nuclear receptor-binding auxiliary protein;

KW anti-cancer; anti-proliferative; mitogen; transcription factor; human;

KW tumour suppressor; ovarian cancer; proliferative disorder; treatment;

KW immune tissue; prevention; reproductive tissue.

OS Homo sapiens.

PN W0991554-A1.

PD 01-APR-1999.

PE 23-SEP-1998: U19782.

PR 23-SEP-1997: US-059621.

PA (DRIG/) DRIGERS P H.

PA (RUBI/) RUBINO D M.

PA (SEGE/) SEGERS J.

PI Driggers PH, Rubino DM, Segers J;

DR WPI: 99-254688/21.

DR N-PSDB: X24044.

PT Breast cancer gene encoding a nuclear receptor-binding auxiliary

PT protein, bix

PS Claim 1b: Page 58-62; 69pp; English.

CC This invention describes a novel human breast cancer gene encoding a

CC nuclear receptor-binding auxiliary protein, bix. The bix encoded protein

CC has anti-cancer, anti-proliferative and mitogenic activity and acts as a

CC transcription factor and tumour suppressor. Levels of expression of Bix

CC can be detected using the primers, probes and antibodies (contained in

CC the kit) to determine a predisposition to breast and ovarian cancer and

CC other proliferative disorders of immune tissues. Vectors containing the

CC Bix gene can be used for prevention of cancers and

CC proliferative diseases of mammalian reproductive and immune tissues.

SO Sequence 1429 AA:

alignment_scores:

Quality: 75.00

Ratio: 1.923

Percent Similarity: 52.703

Percent Identity: 41.892

Length: 74

Gaps: 5

US-09-240-675-1_COPY_27_229 x W93941

Align seg 1/1 to: W93941 from: 1 to: 1429

3 GATGGTCGTCCTCCTGCGGCGGAGACCCCTAGTCTCCTCGCCGCGGCC 52

1230 AspGlyArgProSerTrrP.....ProSerAlaArgArgGlyCysE 1243

53 CATGGGTGTGTCGCCAGCCGAGGTGAAAAATCTAAATCTCTCTCA 102

1243 rArgGly.....SerArgThrTrrPlySarGserGlyArgSerSers 1257

103 AAAGTAGAGGTGCACATCATGATGACAACT..... 134

1257 eArgArgArgAlaHisSerGlnTrrAspLeuGluArgLeuArgAla 1273

135TATCTGAGGTGAGAACAGGAGGAGTCTGTGCGGAATGTA 178

1274 GlnLysGlnLeuGluArgGlnGlnHis...ValArgArgGluAlaG 1289

179 CTTTTCATTGATTATCAAAA 200

1289 u.....ArgLeuSerGln 1293

seq_name: A_Geneseq_36:W93962

seq_documentation_block:

ID W93962 standard; Protein: 30 AA.

AC W93962;

seq_name: A_Geneseq_36:W93962

seq_documentation_block:

ID W93962 standard; Protein: 30 AA.

AC W93962;

seq_name: A_Geneseq_36:W93962

seq_documentation_block:

ID W93962 standard; Protein: 30 AA.

AC W93962;

seq_name: A_Geneseq_36:W93962

seq_documentation_block:

ID W93962 standard; Protein: 30 AA.

AC W93962;

DT 30-JUN-1999 (first entry)
DE Human brx immunogenic peptide 1.
KW Bx protein; breast cancer; nuclear receptor-binding auxiliary protein;
KW anti-cancer; anti-proliferative; mitogen; transcription factor; human;
KW tumour suppressor; ovarian cancer; proliferative disorder; treatment;
KW immune tissue; prevention; reproductive tissue; immunogenic.
OS Homo sapiens.
PN WO915344-A1.
PD 01-APR-1999.
PF 23-SEP-1998; U19782.
PR 23-SEP-1997; US-059621.
PA (DRIC/) DRIGERS P H.
PA (RUBI/) RUBINO D M.
PI Driggers PH, Rubino DW, Segers J;
DR MPI: 99-254688/21.
PT Breast cancer gene encoding a nuclear receptor-binding auxiliary
PT protein, brx
PS Disclosure: Page 29; 69pp; English.
CC This invention describes a novel human breast cancer gene encoding a
CC nuclear receptor-binding auxiliary protein, brx. The brx encoded protein
CC has anti-cancer, anti-proliferative and mitogenic activity and acts as a
CC transcription factor and tumour suppressor. Levels of expression of brx
CC can be detected using the primers, probes and antibodies (contained in
CC the kit) to determine a predisposition to breast and ovarian cancer and
CC other proliferative disorders of immune tissues. Vectors containing the
CC brx gene can be used for prevention and treatment of cancers and
CC proliferative diseases of mammalian reproductive and immune tissues.
SQ Sequence 30 AA:

alignment_scores:
Quality: 62.00 Length: 33
Ratio: 3.263 Gaps: 2
Percent Similarity: 57.576 Percent Identity: 54.545

alignment_block:

US-09-240-675-1_COPY_27_229 x W93962 ..

Align seg 1/1 to: W93962 from: 1 to: 30

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|||||
3 AspGlyArgProSerTrp.....ProSerAlaArgArgArgCysSe 16
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53 CATGGGTGTGTCCGACGAGGTGAAAAAATCTAAATCTCTCA 101
|||||
16 TArgGly.....SerArgThrTrpLysArgSerGlyArgSerSer 29
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seq_name: A_Geneseq_36:W52296

seq_documentation_block:

ID W52296 standard; Protein; 325 AA.

AC W52296;
DT 23-JUN-1998 (first entry)
DE CRFB4 protein.
KW CRFB4; interleukin-10; IL-10; IL-10 receptor; allograft rejection;
KW vaccine; photosensitivity; inflammation; autoimmune disease;
KW septic shock; immune response; organ rejection; gene therapy.
OS Homo sapiens.
PN WO9802342-A1.
PD 22-JAN-1998.
PF 17-JUL-1997; U12455.
PR 17-JUL-1996; US-683743.
PA (UYNE-) UNIV NEW JERSEY.
PI KOTenko SV, Pestka S;
DR MPI: 98-110590/10.
PT New recombinant DNA - comprises sequences encoding interleukin-10
PT and CRFB4 linked to operator, useful, e.g. preventing allograft
PT rejection
PS Claim 2: Page 7; 79pp; English.
CC This sequence is the human CRFB4 sequence, DNA encoding it is used in the

CC recombinant DNA (I) of the invention. (I) comprises a sequence (S1)
CC encoding the interleukin-10 (IL-10) receptor (IL10R) and a sequence (S2)
CC encoding CRFB4, both operably linked to expression control sequences.
CC Cells containing (I) may be used to identify agonists/antagonist of
CC IL-10. Agonists are potentially useful, e.g. for preventing allograft
CC rejection, as vaccine adjuvants, for treatment of photosensitivity,
CC inflammation, autoimmune disease and septic shock, while antagonists are
CC potentially useful for increasing immune responses against tumours,
CC viruses, bacteria and parasites (especially intracellular pathogens) and
CC for preventing organ rejection. A vector containing (I) is used to
CC restore, e.g. by gene therapy, IL-10 sensitivity to a cell that expresses
CC a dysfunctional IL10R and is able to bind IL-10 but not to transduce a
CC signal. Antisense CRFB4 sequences (especially ribozymes), can inhibit
CC IL-10 activity in cells. Antibodies specific for CRFB4 are used to
CC measure and localise CRFB4, for diagnosis of defective IL-10 activity.
CC Fragments of (I) are used as primers or probes to assay CRFB4-specific
CC RNA. Agonists/antagonists may be administered parenterally, orally or
CC rectally especially by intravenous injection or directly into a tumour or
CC allograft.
SQ Sequence 325 AA:

alignment_scores:
Quality: 61.50 Length: 54
Ratio: 1.922 Gaps: 1
Percent Similarity: 59.259 Percent Identity: 29.630

alignment_block:

US-09-240-675-1_COPY_27_229 x W52296 ..

Align seg 1/1 to: W52296 from: 1 to: 325

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55 TGGGTGTGTTCGCGGACGAGTGAATAATCTAAATCT..... 96
|||||
3 TrpSerLeuGlySerTrpLeuGlyGlyCysLeuLeuValSerAlaLeuG1 19
|||||
97 .....CTCAAAAGTAGAGTGCACATCATGATGACAACT 133
|||||
19 YMetValProProGluAsnValArgMetAsnSerValAsnPhelysa 36
|||||
134 TTATCCGAGGTGACACGAGCGATGAGTCTGCGGATGATGACTTT 183
|||||
36 snIleLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe 52
|||||
184 TCATTCGATTAT 195
|||
53 ThrAlaGlnTrp 56
|||
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seq_name: A_Geneseq_36:W07702

seq_documentation_block:

ID W07702 standard; Protein; 543 AA.

AC W07702;
DT 06-APR-1997 (first entry)
DE Mouse ETS2 repressor factor (ERF).
KW ETS2 repressor factor; ERF; transcriptional repressor;
KW tumour suppressor; tumour; cancer; oncoprotein; therapy.
OS Mus sp.
FH Key Location/Qualifiers
FT domain 21..98 /label= DNA_binding_domain
FT /note= "ets-like DNA binding domain"
FT domain 466..525 /label= Active_repressor_domain
PN WO9639517-A1.
PD 12-DEC-1996.
PF 04-JUN-1996; U010177.
PR 05-JUN-1995; US-469412.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PI Athanasiou MA, Beal GJ, Blair DG, Fisher RJ, Mavrothalassitis GJ;
DR MPI: 97-043139/04.
N-PSDB: T47200.

PT New DNA encoding ETS2 repressor factor - useful for reducing
 PT tumourigenicity, esp. oncogene associated tumour cells
 PS Disclosure: Page 70-72: 101pp: English
 CC Murine ETS2 repressor factor (ERF) (W07702) is a member of the ETS
 CC family and acts as a transcriptional repressor in mammalian cells.
 CC Its amino acid sequence was deduced from the murine ERF gene
 CC (T47198). Human ERF (see also W07700) has also been identified.
 CC ERF has tumour suppressor activity. Chimeric molecules comprising
 CC the ERF repressor domain in combination with a heterologous
 CC transcription factor having a binding domain can be used to reduce
 CC tumourigenicity associated with inappropriate expression of
 CC transcription factors.
 SO Sequence 543 AA;

alignment_scores: 1
 Quality: 61.00 Length: 24
 Ratio: 3.389 Gaps: 0
 Percent Similarity: 75.000 Percent Identity: 45.833

alignment_block:

US-09-240-675-1_COPY_27_229/rev x W07702 ..

Align seg 1/1 to: W07702 from: 1 to: 543

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82 TTCACCTGCGCGGACACACACCATGCGCCCGCGGAGAGACT 33
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367 PheLysPheLysLeuGlnProProLeuGlyArgArgGlnArgAla1 383
32 AGGTCGTGCGCGCCCGAGAGAGA 11
|||:|||||: |||:|||||:
383 agLgIuLysAlaProGlyGly 390
    
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34 InlysvaIGluValAspIleIleAspAspAsnPhelIleuArgTrpAsn 50
151 AGCAGCATGAGTCTGTGGGAAATGCAATTTTCATTGCATTACCAAA 200
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnIly 67
201 A 201
67 s 67
seq_name: /cgn2_6/prodata/1/1aa/5B-COMB.pep:US-08-307-588-2
seq_documentation_block:
; Sequence 2, Application US/08307588
; Patent No. 5919453
; GENERAL INFORMATION:
; APPLICANT: BENOIT, Patrick
; APPLICANT: MEYER, Francois
; APPLICANT: MACUIRE, Deborah
; APPLICANT: PLAVEC, Ivan
; APPLICANT: TOVEY, Michael G.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO).
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/307,588
; FILING DATE: 05-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00770
; FILING DATE: 30-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92400902.0
; FILING DATE: 31-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 17283/117/GUPL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 436 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-307-588-2
alignment_scores:
Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-240-675-1_COPY_27_229 x US-08-307-588-2 ..
Align seg 1/1 to: US-08-307-588-2 from: 1 to: 436
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1 MetheValValLeuLeuGlyAlaThrThrLeuValValAlaValGI 17
51 CCCATGGGTGTTGCCGAGCCGAGGTGGAATAATCTAAATCTCTCTC 100
17 yPrtIrrAlaLeuSerAlaAlaAlaGlyGlyAsnLeuYsserProG 34
101 AAAAGTAGAGTCGACATCATAGATGACAATTATCTGAGGTGGAAC 150
34 InlysvaIGluValAspIleIleAspAspAsnPhelIleuArgTrpAsn 50
151 AGCAGCATGAGTCTGTGGGAAATGCAATTTTCATTGCATTACCAAA 200
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnIly 67
201 A 201
67 s 67
seq_name: /cgn2_6/prodata/1/1aa/5A-COMB.pep:US-08-328-256-12
seq_documentation_block:
; Sequence 12, Application US/08328256
; Patent No. 5643749
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: ABRAMOVICH, Carolina
; APPLICANT: RATOVIJSKI, Edward
; TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,256
; FILING DATE: 24-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 107378
; FILING DATE: 24-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: REVEL-13
; REFERENCE/DOCKET NUMBER: 25,618
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELE: 248633
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 496 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-328-256-12
alignment_scores:
Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-240-675-1_COPY_27_229 x US-08-328-256-12 ..
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51 CCCATGGGTGTGTCGCCAGCCGAGGTGGAATAATCTAAATCTCTC 100
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17 yProTPrValleuSerAlaAlaAlaGlyGlyAsnleuLysSerProG 34
101 AAAAGTAGAGTGCATCATAGTACAACTTATCTTGAGGTGGAAC 150
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34 InLysValGluValAspIleIleAspAsnPhelIleuAgtPrasn 50
151 AGGAGCGATGAGTCTGTCGGAATGTGACTTTTCATTCGATTATCAA 200
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51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnly 67
201 A 201
67 s 67
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seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-328-256-10

seq_documentation_block:

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; Sequence 10, Application US/08328256
; Patent No. 5643749
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: ABRAMOVICH, Carolina
; APPLICANT: RABOVITSKI, Edward
; TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,256
; FILING DATE: 24-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 107378
; FILING DATE: 24-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: REVEL-13
; REFERENCE/DOCKET NUMBER: 25,618
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-328-256-10
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alignment_scores: Quality: 340.00

Length: 67

Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

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|||||
17 yProTPrValleuSerAlaAlaAlaGlyGlyAsnleuLysSerProG 34
101 AAAAGTAGAGTGCATCATAGTACAACTTATCTTGAGGTGGAAC 150
|||||
34 InLysValGluValAspIleIleAspAsnPhelIleuAgtPrasn 50
151 AGGAGCGATGAGTCTGTCGGAATGTGACTTTTCATTCGATTATCAA 200
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51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnly 67
201 A 201
67 s 67
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seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-471-454-2

seq_documentation_block:

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; Sequence 2, Application US/08471454
; Patent No. 5731169
; GENERAL INFORMATION:
; APPLICANT: MOGENSEN, Knud E.
; APPLICANT: UZE, Gilles
; APPLICANT: LOTFALFA, Georges
; APPLICANT: GRESSER, Ion
; TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
; TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,454
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/900,642
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: FR 89/13770
; FILING DATE: 20-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 960-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
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LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-454-2

alignment_scores:
Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

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Align seg 1/1 to: US-08-471-454-2 from: 1 to: 557

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|||||
17 yProTrpValLeuSerAlaAlaAlaGlyLysAsnLeuLysSerProG 34
101 AAAAAGTAGAGTCGACATCATGACAACTTATCTGAGGTGGAAC 150
|||||
34 IntyValGIValAlaSpIleIleAspAspAsnPhelleuAlaArgTyrpsn 50
151 AGAGCGATGAGTCGTGCGGAATGTGACTTTTTCATTGATATCAAAA 200
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51 ArgSerAspGluSerValGIyAsnValThrPheserPhespyrGlnly 67
201 A 201
67 s 67
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seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-466-974-2

seq_documentation_block:

Sequence 2, Application US/08466974
Patent No. 5861258
GENERAL INFORMATION:
APPLICANT: MOGENSEN, Knud E.
APPLICANT: UZE, Gilles
APPLICANT: LUTFALLA, Georges
APPLICANT: GRESSER, Ion
TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P. C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,974
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/300,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989

ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-466-974-2

alignment_scores:
Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x US-08-466-974-2 ..

Align seg 1/1 to: US-08-466-974-2 from: 1 to: 557

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51 CCCATGGGTCTTGTCCGCGACCGGAGTGGAAAAATCTAAATCTCTC 100
|||||
17 yProTrpValLeuSerAlaAlaAlaGlyLysAsnLeuLysSerProG 34
101 AAAAAGTAGAGTCGACATCATGACAACTTATCTGAGGTGGAAC 150
|||||
34 IntyValGIValAlaSpIleIleAspAspAsnPhelleuAlaArgTyrpsn 50
151 AGAGCGATGAGTCGTGCGGAATGTGACTTTTTCATTGATATCAAAA 200
|||||
51 ArgSerAspGluSerValGIyAsnValThrPheserPhespyrGlnly 67
201 A 201
67 s 67
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seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-471-453-2

seq_documentation_block:

Sequence 2, Application US/08471453
Patent No. 586153
GENERAL INFORMATION:
APPLICANT: MOGENSEN, Knud E.
APPLICANT: UZE, Gilles
APPLICANT: LUTFALLA, Georges
APPLICANT: GRESSER, Ion
TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P. C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,453
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-453-2

alignment_scores:
Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-240-675-1_copy_27_229 x US-08-471-453-2 ..

Align seg 1/1 to: US-08-471-453-2 from: 1 to: 557

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1 ATGATGTCCTCTCTCGGCGGCGACCCCTAGTGTCTGCGCCGTCGG 50
|||||
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValAl 17
51 CCCATGGGTGTTCGCCGACGCCGAGGTGGAATAAATCTAAATCTCTC 100
|||||
17 yProTrpValLeuSerAlaAlaAlaGlyGlyAsnLeuLysSerProG 34
101 AAAAGTAGAGTCGACATCATAGATGACACTTATCTAGGTGGAAC 150
|||||
34 InLysValGluValAspLeuLeuLeuAspAsnPheLeuArgTrpAsn 50
151 AGGAGCGATGAGTCTGTGCGGAGATGTGACTTTTCATTCGATTATCA 200
|||||
51 ArgSerAspGlnSerValGlyAsnValThrPheSerPheAspTyrGln 67
201 A 201
|
67 s 67
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seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-307-588-4

seq_documentation_block:

Sequence 4, Application US/08307588
Patent No. 5919453
GENERAL INFORMATION:
APPLICANT: BENOIT, Patrick
APPLICANT: MEYER, Francois
APPLICANT: MAGUIRE, Deborah
APPLICANT: PLAVEC, Ivan
APPLICANT: TOVEY, Michael G.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
TITLE OF INVENTION: INTERFERON
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
ZIP: 20007

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00770
FILING DATE: 30-MAR-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92400902.0

FILING DATE: 31-MAR-1992

ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernard D.
REGISTRATION NUMBER: 28,665

REFERENCE/DOCKET NUMBER: 17283/117/GUPL

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5399

TELEFAX: (202)672-5399

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-307-588-4

alignment_scores:
Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-240-675-1_copy_27_229 x US-08-307-588-4 ..

Align seg 1/1 to: US-08-307-588-4 from: 1 to: 557

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1 ATGATGTCCTCTCTCGGCGGCGACCCCTAGTGTCTGCGCCGTCGG 50
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1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValAl 17
51 CCCATGGGTGTTCGCCGACGCCGAGGTGGAATAAATCTAAATCTCTC 100
|||||
17 yProTrpValLeuSerAlaAlaAlaGlyGlyAsnLeuLysSerProG 34
101 AAAAGTAGAGTCGACATCATAGATGACACTTATCTAGGTGGAAC 150
|||||
34 InLysValGluValAspLeuLeuLeuAspAsnPheLeuArgTrpAsn 50
151 AGGAGCGATGAGTCTGTGCGGAGATGTGACTTTTCATTCGATTATCA 200
|||||
51 ArgSerAspGlnSerValGlyAsnValThrPheSerPheAspTyrGln 67
201 A 201
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67 s 67
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seq_name: /cgn2_6/ptodata/1/1aa/PCtUS_COMB.pep:PCT-US94-14277-3

seq_documentation_block:

Sequence 3, Application PC/TUS9414277
GENERAL INFORMATION:
APPLICANT: Agnet, Michel
APPLICANT: Bohnl, Ruth

APPLICANT: Hemmi, Silvio
 TITLE OF INVENTION: Receptor Subunit Polypeptides
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: path (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/14277
 FILING DATE: 07-DEC-1994
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/164596
 FILING DATE: 09-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Love, Richard B.
 REGISTRATION NUMBER: 34,659
 REFERENCE/DOCKET NUMBER: 866PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-5530
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 202 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

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alignment_scores:
  Quality: 112.00
  Ratio: 3.613
  Percent Similarity: 79.487
  Length: 39
  Gaps: 0
  Percent Identity: 48.718
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alignment block:
US-09-240-675-1_COPY_27_229 x PCT-US94-14277-3    ..
Align seg 1/1  to: PCT-US94-14277-3  from: 1  to: 2022

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[illegible]

seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-683-743-4

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: seq_documentation_block:
: Sequence 4, Application US/08683743
: Patent No. 5843697
:
: GENERAL INFORMATION:
:
: APPLICANT: Pestka, Sydney
:
: TITLE OF INVENTION: CYCLOXINE RECEPTOR SIGNAL TRANSDUCTION
:
: TITLE OF INVENTION: CHAIN
:
: NUMBER OF SEQUENCES: 25
:
: CORRESPONDENCE ADDRESS:
:
: ADDRESSEE: David A. Jackson, Esq.

```

STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
City: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,743
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601-1-050
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
type: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE:
US-08-683-743-4

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alignment_scores:
    Quality: 61.50      Length: 54
    Ratio: 1.922       Gaps: 1
Percent Similarity: 59.259   Percent Identity: 29.630
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alignment_block:
US-09-240-675-1_COPY_27_229 x US-08-683-743-4 .

Align seg 1/1 to: US-08-683-743-4 from: 1 to: 325

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55 TGGGTTTTCGCCGACCCGACGCTGGAAAAATTAATAAT ..... 96
      |||:||||: ||||| ||| |||
3  TrpSerLeuLysSerTrpLeuLysIleuValSerAlaLeuG1 19
      |||:||||: ||||| ||| |||
97 ..... CCTCAAAAAGTAGAGCTGCATCATAGATGACACT 133
      |||:||||: ||||| ||| |||
19 yMetValProProGluAsnValArgMetAsnSerValAsnHeuYsA 36
      |||:||||: ||||| ||| |||
134 TTAATCTGAGTGGAAACACGACCGATGAGCTGTGGGAAATGATCTTTT 183
      |||:||||: ||||| ||| |||
36 snLeuGlnTrpGlnSerProAlaPheAlaLysGlyAsnLeuThrPhe 52
      |||:||||: ||||| ||| |||
184 TCATTCGATTAT 195
      |||:||||: ||||| ||| |||
53 ThrAlaGlnTrp 56

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seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-469-412A-7

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seq_documentation_block :
: Sequence 7, Application US/08469412A
: Patent No. 5856125
:
: GENERAL INFORMATION:
:
: APPLICANT: Mavrothalassitis, George J.
:
: APPLICANT: Blair, Donald G.
:
: APPLICANT: Fisher, Robert J.
:
: APPLICANT: Beal Jr., Gregory J.
:
: APPLICANT: Athanasiou, Metropi A.
:
: APPLICANT: Souras, Dionysios N.
:
: TITLE OF INVENTION: The ERP Genetic Locus and Its Products

```


NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,412A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Mackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 015280-229000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 543 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..543
OTHER INFORMATION: /note="murine ERF amino acid sequence
OTHER INFORMATION: (first 8 amino acids from first exon not
included)"
US-08-469-412A-7

alignment_scores:
Quality: 61.00 Length: 24
Ratio: 3.389 Gaps: 0
Percent Similarity: 75.000 Percent Identity: 45.833

alignment_block:
US-09-240-675-1_COPY_27_229/rev x US-08-469-412A-7 ..
Align seg 1/1 to: US-08-469-412A-7 from: 1 to: 543

seq_documentation_block:
; Sequence 64, Application US/08317310A
; Patent No. 5858701
; GENERAL INFORMATION:
; APPLICANT: WHITE, Morris F.
; APPLICANT: SUN, Xiao Jian
; APPLICANT: PIERCE, Jacalyn H.
; TITLE OF INVENTION: THE IRS FAMILY OF GENES
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston

seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-317-310A-64

82 TTCACCTGCGGCTGCGACACACCATGGCCGCGGAGGAGCACT 33
||| :|||:||||| :|||:|||||
367 PhelypheyleuylglnProProleuGlyArgArglnArgAlaAl 383
|||:||||| :|||:|||||
32 AGGCTGCTGCGCGCCGAGGAGA 11
|||:||||| :|||:|||||
383 aglygluLyAlaProGlyGly 390

STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,310A
FILING DATE: 03-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: JDP-022
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 1321 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-317-310A-64

alignment_scores:
Quality: 61.00 Length: 29
Ratio: 2.652 Gaps: 1
Percent Similarity: 79.310 Percent Identity: 51.724

alignment_block:
US-09-240-675-1_COPY_27_229/rev x US-08-317-310A-64 ..
Align seg 1/1 to: US-08-317-310A-64 from: 1 to: 1321

98 GGAGATTTTGAATTTTTCACCTGCGGCTGCGGAGACACCATGGGCC 49
|||:||||| :|||:||||| :|||:||||| :|||:|||||
1029 GlyAspLeuYrArgLeuProProAlaSerAlaAlaThrSerGlnGlyr 1045
|||:||||| :|||:||||| :|||:||||| :|||:|||||
48 CACGGCGAGCAGCATAGGCTGCTGCGGCCGAGGA 14
|||:||||| :|||:||||| :|||:||||| :|||:|||||
1045 ornAlaGlySerSerMet.SerSerGluProGly 1056

seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-323-170B-2

seq_documentation_block:
; Sequence 2, Application US/08323170B
; Patent No. 5733772
; GENERAL INFORMATION:
; APPLICANT: Williamson, Kim C.
; APPLICANT: KASLOW, David C.
; TITLE OF INVENTION: Cloning and Expression of Plasmodium
; TITLE OF INVENTION: falciiparum Transmission-Blocking Target Antigen, PfS230
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,170B
; FILING DATE: 13-OCT-1994
; CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/010,409
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Quine, Jonathan A.
REGISTRATION NUMBER: P-41,261
REFERENCE/DOCKET NUMBER: 015280-113100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-323-170B-2

Alignment_scores:
Quality: 59.00 Length: 51
Ratio: 1.844 Gaps: 3
Percent Similarity: 62.745 Percent Identity: 37.255

Alignment_block:
US-09-240-675-1_COPY_27_229 x US-08-323-170B-2 ..

Align seg 1/1 to: US-08-323-170B-2 from: 1 to: 3135

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64 TCCGACGCCGAGGTGGA.....AAAATCTAAATCTCTCA 101
|||||
787 SerGIspIleGlyIleLeuPheProLysAsnIleLysSerThrTh 803
|||
102 AAAAGTAGAGTCGACATCATGACACTTATCTCTGAGGTGGAACA 151
|||||
803 rCySpheIu...GIuMetIleProTyAsnLysGIuIleLysTrpAsnL 819
152 GGAGCGAGTAGCTGTGCGGAAT...GTGACTTTTTCATTGCAATTACA 198
|||||
819 ySGIuAsnLysSerLeuGIuLysLeuValAsnAsnSerValItyrAsn 835
199 AAA 201
|||
836 Lys 836
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seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-252-626A-2

seq_documentation_block:

Sequence 2, Application US/08252626A
Patent No. 5585269
GENERAL INFORMATION:
APPLICANT: Earp, Henry S.
APPLICANT: Graham, Douglas K.
APPLICANT: Dawson, Thomas L.
APPLICANT: Mullaney, David L.
APPLICANT: Snodgrass, Hiram R.
TITLE OF INVENTION: Isolated DNA Encoding C-MER
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 5585269th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,626A

FILING DATE: 02-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-81
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 881-3140
TELEFAX: (919) 881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 999 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-252-626A-2

Alignment_scores:
Quality: 58.00 Length: 37
Ratio: 2.417 Gaps: 1
Percent Similarity: 64.865 Percent Identity: 35.135

Alignment_block:
US-09-240-675-1_COPY_27_229 x US-08-252-626A-2 ..

Align seg 1/1 to: US-08-252-626A-2 from: 1 to: 999

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43 GCCGTGGGCCCATGGTGTGTCCGACGCCGAGTGAATAATCTAA 92
|||||
369 AlaValSerProTrpIleLeuAlaSerThrThcIuGIyAlaProSerVa 385
|||||
93 ATCTCTCAAAAAGTAGAGTCGACATCATGAT.....GACAACTTA 136
|||||
385 lAlaProLeuAsnValThrValPheLeuAsnGluSerSerAspAsnValA 402
137 TCCGAGGCTGG 147
402 spleaArgTrp 405
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seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-505-218-4

seq_documentation_block:

Sequence 4, Application US/08505218
Patent No. 5914447
GENERAL INFORMATION:
APPLICANT: ARAYA, ALEJANDRO
APPLICANT: MOURAS, ARMAND
TITLE OF INVENTION: TRANSGENIC PLANTS INCLUDING A HYBRID
TITLE OF INVENTION: NUCLEIC ACID SEQUENCE, COMPRISING AN UNEDITED
TITLE OF INVENTION: MITOCHONDRIAL GENE FRAGMENT FROM HIGHER PLANTS AND PROCESS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/505,218
FILING DATE: 03-NOV-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: KRAUS, ERIC J
REGISTRATION NUMBER: 36,190

REFERENCE/DOCKET NUMBER: 1169-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 684-1111
TELEFAX: (703) 684-1124
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-505-218-4

alignment_scores:
Quality: 57.50 Length: 74
Ratio: 1.438 Gaps: 3
Percent Similarity: 54.054 Percent Identity: 29.730

alignment_block:
US-09-240-675-1_COPY_27_229 x US-08-505-218-4 ..

Align seg 1/1 to: US-08-505-218-4 from: 1 to: 335

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10  GTCTCTCTGGCGGAGACCTAGTCTGTCGCCGTGGGCCCATGGGT 59
    |||||
103  ValLeuTyrMetLeuLeuThrValValLeuValPheLeuPhePheVal 119
    |||||
60  GTGTCCGACGCGCAGTGTGAAATAATCTTAATCTCTCAAAAGTAG 109
    |||||
119  lValThrLysLysGlyGlyLysSerValProAsnAlaTrpGlnSerL 136
    |||||
110  AGGTGACATCATAGATGACAACTTATCTGAGGTGGAACAGGACGAT 159
    |||||
136  euValGluLeuIleTyrAsp...PheValLeu.....AsnLeuValAsn 149
    |||||
160  GAGTCTCTCGGG..... 171
    |||||
150  GluGlnIleGlyGlyLeuSerGlyAsnValLysGlnLysPhePheProAr 166
    |||||
172  ....AATGACATTTCATTTC 189
    |||||
166  gLleSerValThrPheThrPhe 173
    |||||

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C:Species: Bos primigenius taurus (cattle)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C:Accession: S27387; S33770
 R:Kouchel-Viehn, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G.
 FEBS Lett. 313, 255-259, 1992
 A:Title: Specific antiviral activities of the human alpha interferons are determined at
 A:Reference number: S27387; MUID:93076908
 A:Accession: S27387
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-560 <M0U>
 A:Cross-references: EMBL:X68443; NID:9431; PIDN:CAA48484.1; PID:9432
 A:Experimental source: MDBK cells
 R:Lim, J.K.; Langer, J.A.
 Biochim. Biophys. Acta 1173, 314-319, 1993
 A:Title: Cloning and characterization of a bovine alpha interferon receptor.
 A:Reference number: S33770; MUID:93305725
 A:Accession: S33770
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-421, 'V', 423-560 <LIM>
 A:Cross-references: EMBL:L06320; NID:9163187; PIDN:AAA02571.1; PID:9163188
 A:Experimental source: Lung
 C:Keywords: antiviral; cytokine receptor; transmembrane protein
 F:1.24/Domain: signal sequence #status predicted <SIG>
 F:25-560/Product: Interferon alpha receptor type 1 #status predicted <MAT>

alignment_scores:
 Quality: 209.00 Length: 65
 Ratio: 3.800 Gaps: 2
 Percent Similarity: 84.615 Percent Identity: 69.231

alignment_block:
 US-09-240-675-1_copy_27_229 x S27387

Align seg 1/1 to: S27387 from: 1 to: 560

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4 ATGGTCGCTCTCTGGCGCGAGACCCCTAGTCGTCGCGCGCCGCC 53
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 MetLeuAlaLeuLeuLcylAlaThrLeuMetLeuValAla...GlyAr 16

54 ATGGGTGTCTCCGCGAGCGAGGTGGAATAAATCTAAATCTCTCAAA 103
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
16 GtrPAlleuProAlaAlaSerGlyGluAlaAsnLeuLys...ProGluA 32

104 AAGTAGAGCTGCATCATATGACACACTTATCTGAGGTGGAACAGC 153
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
32 snValGluLeuLeuLcylAlaAspAsnPhaPheLeuLysTrpAsnSer 48

154 AGCGATGACTCTGCGGAATGTGACTTTTTCATTGATATCAAA 198
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
49 SerSerGluSerValLysAsnValThrPheSerAlaAspTyrGln 63

```

seq_name: p1r2:A45283

seq_documentation_block:

Interferon alpha/beta receptor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
 C:Accession: A45283; I48423; I48425; I48426; I48427; I48428; I48429
 R:Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E.
 Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992
 A:Title: Behavior of a cloned murine interferon alpha/beta receptor expressed in homosp
 A:Reference number: A45283; MUID:92262522
 A:Accession: A45283
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-590 <UZE>
 A:Cross-references: GB:M89641; NID:9194111; PIDN:AAA37890.1; PID:9194112
 A:Note: Sequence extracted from NCBI backbone (NCBIN:102354, NCBI:P:102357)
 R:Lutfalla, G.; Uze, G.
 Gene 148, 343-346, 1994

A:Title: Structure of the murine interferon alpha/beta receptor-encoding gene: high-
 A:Reference number: I48423; MUID:95047447
 A:Accession: I48423
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 118-125 <RES>
 A:Cross-references: EMBL:U06237; NID:9497103; PIDN:AAA65003.1; PID:9755810
 A:Accession: I48424
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 127-224 <RE2>
 A:Cross-references: EMBL:U06238; NID:9497104; PIDN:AAC01749.1; PID:9755811
 A:Accession: I48425
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 243-264 <RE3>
 A:Cross-references: EMBL:U06239; NID:9497106; PIDN:AAA65004.1; PID:9510261
 A:Accession: I48426
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 265-375 <RE4>
 A:Cross-references: EMBL:U06240; NID:9497108; PIDN:AAA65005.1; PID:9510262
 A:Accession: I48427
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 397-424 <RE5>
 A:Cross-references: EMBL:U06241; NID:9497110; PIDN:AAA65006.1; PID:9755812
 A:Accession: I48428
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 426-445 <RE6>
 A:Cross-references: EMBL:U06242; NID:9497112; PIDN:AAA65007.1; PID:9755813
 A:Accession: I48429
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 473-590 <RE7>
 A:Cross-references: EMBL:U06244; NID:9497114; PIDN:AAA65008.1; PID:9510265
 C:Genetics:
 A:Gene: IFNAR
 A:Insertions: 177/3; 331/1
 C:Keywords: cytokine receptor; transmembrane protein

alignment_scores:
 Quality: 198.00 Length: 65
 Ratio: 3.536 Gaps: 0
 Percent Similarity: 86.154 Percent Identity: 55.385

alignment_block:
 US-09-240-675-1_copy_27_229 x A45283

Align seg 1/1 to: A45283 from: 1 to: 590

```

4 ATGGTCGCTCTCTGGCGCGAGACCCCTAGTCGTCGCGCGCCGCC 53
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 MetLeuAlaValAlaGlyAlaAlaLeuValLeuValAlaGlyAlaAr 17

54 ATGGGTGTCTCCGCGAGCGAGGTGGAATAAATCTAAATCTCTCAAA 103
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 GtrPAlleuProSerAlaAlaGlyGluAlaAsnLeuLysProGluA 34

104 AAGTAGAGCTGCATCATATGACACACTTATCTGAGGTGGAACAGC 153
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 snIleAspValTyrLleLeuAspAsnTyrThrLeuLysTrpSerSer 50

154 AGCGATGACTCTGCGGAATGTGACTTTTTCATTGATATCAAA 198
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51 HisGlyGluSerMetGlySerValThrPheSerAlaGlyTyrArg 65

```

seq_name: p1r2:T09357

seq_documentation_block:

hypothetical protein F33K16.40 - Arabidopsis thaliana

A:Reference number: A45731; MUID:93015705
A:Accession: A45731
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-141 <SAS>
A:Cross-references: GB:M89919; NID:9215829; PIDN:AAA32485.1; PID:9215832
C:Genetics:
A:Gene: comC alpha
A:Map position: 5,848-6,274
A:Superfamily: phage T4 comC-alpha protein
C:Keywords: transcription regulation

alignment_scores:
Quality: 62.50 Length: 50
Ratio: 2.155 Gaps: 3
Percent Similarity: 58.000 Percent Identity: 34.000

alignment_block:
US-09-240-675-1_COPY_27_229 x A45731 ..
Align seg 1/1 to: A45731 from: 1 to: 141

16 CTGGGGCGCGACCCAGTGCCTGCGCCGCGCCATGGGTGTC 65
||||| ||| : : : : : : : : : : : : : : : : : :
49 LeuGlyArgProThrLysIleMetThrSerIleGly.....ValLeuLys 63
66 CGAGCCCGCGAGTGTGAAAAATCTAAATCTCCCAAAAAGTAGAGTCG 115
:
63 sarGCSAlaGlyGly.....A 69
116 ACATCATAGTACACACTTATCTCGTAGAGAGAGAGAGAGAGTCT 165
||||| : : : : : : : : : : : : : : : : : :
69 spleuAspGluAsnPhenile.....TrrleuSerThrAsnGluAla 83

seq_name: p1r2:154418

seq_documentation_block:
MHC class I histocompatibility antigen HLA-B7 alpha chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C:Accession: 154418
R:SOOD, A.K.: Pan, J.; Biro, P.A.; Pereira, D.; Srivastava, R.; Reddy, V.B.; Duceaman, B.
Immunogenetics 22, 101-121, 1985
A:Title: Structure and polymorphism of class I MHC antigen mRNA.
A:Reference number: 154418; MUID:85287366
A:Accession: 154418
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-361 <SOD>
A:Cross-references: GB:M16102; NID:9187693; PIDN:AAA59622.1; PID:9307217
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

alignment_scores:
Quality: 62.50 Length: 61
Ratio: 1.645 Gaps: 2
Percent Similarity: 62.295 Percent Identity: 24.590

alignment_block:
US-09-240-675-1_COPY_27_229 x 154418 ..
Align seg 1/1 to: 154418 from: 1 to: 361

4 ATGGTCCTCTCTGGCGCGACCCAGTGCCTGTCGCGCCGCGCC 53
||||| : : : : : : : : : : : : : : : : : :
1 MetLeuValMetAlaProArgThrValLeuLeuLeuLeuSer...GlyPr 16
54 ATGGGCTGTTCGCGACCCAGTGTGAAAAATCTAAAA..... 93
||||| : : : : : : : : : : : : : : : : : :
16 ofTrpLeuThrGluThrTrpAlaGlySerHisSerMetAlaGlyTrpPheTyrT 33
94TCTCTCAAAAAGTAGAGGTGAC 117

33 hrSerValSerArgPro*****GlyGluProArgPheIleSerValGly 49
118 ATCATGATGACACTTATCTCGAGGTGAGAC 150
:
50 TyrValAspAspThrGlnPheValArgPheAsp 60

seq_name: p1r2:A26391

seq_documentation_block:
Phospholipase C (EC 3.1.4.3) - Pseudomonas aeruginosa
N:Alternate names: lecithinase C; lipophospholipase I
C:Species: Pseudomonas aeruginosa
C:Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 08-Oct-1999
C:Accession: A26391
R:Pritchard, A.E.; Vasil, M.L.
J. Bacteriol. 167, 291-298, 1986
A:Title: Nucleotide sequence and expression of a phosphate-regulated gene encoding
A:Reference number: A26391; MUID:86250607
A:Accession: A26391
A:Molecule type: DNA
A:Residues: 1-730 <PRI>
A:Cross-references: GB:M13047; NID:9151492; PIDN:AAA25966.1; PID:9151493
C:Keywords: phosphoric diester hydrolase

alignment_scores:
Quality: 62.00 Length: 69
Ratio: 1.824 Gaps: 4
Percent Similarity: 49.275 Percent Identity: 26.087

alignment_block:
US-09-240-675-1_COPY_27_229 x A26391 ..
Align seg 1/1 to: A26391 from: 1 to: 730

37 CTGTCGCGCGTGGCGCCATGGGTGTTGCCGCGCAGTGTGAAAAA 86
||||| : : : : : : : : : : : : : : : : : :
404 LeuIleAlaIleSerProTrp.....SerLysGlyGly..... 414
87 TCRAAATCTCTCCCAAAAAGTAGAGTGCATCATCATGACACTTAA 136
||||| : : : : : : : : : : : : : : : : : :
415LysValSerAlaGluValPheAspHisThrSerV 426
137 TCCTGAGG..... 144
426 AlLeuArgPheLeuGluArgArgPheGlyLeuValGluGluAsnIleSer 442
145TGGACAGAGCGAGTGTCTGTGCGGAATGTGACTTTTCATTGCA 191
||||| : : : : : : : : : : : : : : : : : :
443 TrpTrpArgArgAla.....ValCysGlyAspLeuThrSerLeuPheAs 457
192 TTATCA 198
: : : : : : : : : : : : : : : : : :
457 PheGln 459

seq_name: p1r2:G01418

seq_documentation_block:
Cytokine receptor family II, member 4 - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
C:Accession: G01418
R:Lutfalla, G.
submitted to the EMBL Data Library, April 1994
A:Reference number: G06935
A:Accession: G01418
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-273 <LUT>
A:Cross-references: EMBL:U08988; NID:9571295; PID:9571296
C:Genetics:
A:Gene: GDB:CRFB4; CRF2-4

OM of: US-09-240-675-1_COPY_27_229 to: SwissProt_38.* out_format : pfs
 Date: Jun 1, 2000 12:37 AM

About: Results were produced by the GeneCore software, version 4.5.
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Command line parameters:
 -MODEL=frame+asp.model -DEV=xip
 -O=CGN2_1/USPRO.spool/US09240675/runat_30052000_164313_24686/app_query.fasta.1
 -DB=SwissProt_38 -QWRT=fastan -SUFFIX=modif.rsp -GAPOP=12.000
 -GAPOP4=4.000 -MIMATCH=0.100 -LOOPEL=0.000 -LOOPEXT=0.000
 -OGAPOP4=5.000 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=dlcosum62
 -TRANS=human40.cdt -LIST=45 -DOCALIGN=200 -THR_SCORE=pcr
 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NOM=ext -MILEN=0
 -MALEN=1000000 -USER=US09240675 -NCPU=6 -ICPU=3 -NO_XLPHY -WAIT
 -THREADS=1

Search information block:

Query: US-09-240-675-1_COPY_27_229

Query length: 203

Database: SwissProt_38.*

Database sequences: 83857

Database length: 30454973

Search time (sec): 45.030000

Score list:

Sequence	Strd Orig	Zscore	Escore	Len	Documentation
SwissProt_38:INRL_HUMAN	340.00	743.63	1.4e-14	557	P17181 homo sapiens (human)
SwissProt_38:INRL_BOVIN	209.00	449.62	3.4e-18	560	P04790 bos taurus (bovine)
SwissProt_38:INRL_SHEEP	204.00	438.40	1.4e-17	560	P28588 ovis aries (sheep)
SwissProt_38:INRL_MOUSE	158.00	424.50	8.0e-17	590	P33896 mus musculus (mouse)
SwissProt_38:IN53_HUMAN	65.00	118.37	3.61	1475	P49790 homo sapiens (human)
SwissProt_38:CNMA_BPT4	62.50	132.43	6.21	141	Q01438 bacteriophage t4, comc
SwissProt_38:PHGC_PSEAE	62.00	117.53	8.12	730	P06200 pseudomonas aeruginosa
SwissProt_38:CPH4_HUMAN	61.50	123.19	8.82	325	P08833 homo sapiens (human)
SwissProt_38:ERF_MOUSE	61.00	117.64	10.60	551	P70459 mus musculus (mouse)
SwissProt_38:IRK2_MOUSE	61.00	110.31	11.31	1321	P81122 mus musculus (mouse)
SwissProt_38:SPF2_CHICK	60.00	123.05	13.20	221	P30352 gallus gallus (chicken)
SwissProt_38:CCMA_RABIT	60.00	102.98	15.79	2424	P27884 oryctolagus cuniculus
SwissProt_38:S230_PLAFO	59.50	109.43	17.04	982	P28594 anabena sp. (strain)
SwissProt_38:CAPR_HUMAN	59.00	120.81	17.60	221	P01130 homo sapiens (human)
SwissProt_38:HXAA_HUMAN	59.00	114.03	18.70	496	P31260 homo sapiens (human)
SwissProt_38:RPOA_STRCO	58.50	98.58	21.46	315	P08372 plasmodium falciparum
SwissProt_38:FLIL_BACSU	58.00	116.10	20.98	339	P23404 streptomyces coelicolor
SwissProt_38:Y288_METJA	58.00	122.39	22.68	140	P23452 bacillus subtilis, fl
SwissProt_38:SPVIR	58.00	120.38	23.09	178	P05736 methanococcus jannasch
SwissProt_38:ATPD_WHEAT	57.50	115.03	24.22	337	P15893 spiroplasma virus svp1
SwissProt_38:TP6_DROME	57.50	112.77	28.25	386	P20359 tritium aestivum (w)
SwissProt_38:TPD_BACSU	57.50	111.41	28.32	398	P01867 drosophila melanogaster
SwissProt_38:AK3_BACSU	57.50	109.05	29.21	454	P94417 bacillus subtilis, ptc
SwissProt_38:PEHX_RHCH	57.50	107.42	29.64	602	P15922 ewinia chrysanthemi
SwissProt_38:DEAD_KLEPM	57.00	107.17	33.96	731	P28719 zymomonas mobilis, dr
SwissProt_38:RE_BACSU	56.50	115.35	36.09	659	P33906 klebsiella pneumoniae
SwissProt_38:RRPL_RVYZ	56.50	108.41	38.40	217	P03457 bacillus subtilis, ftd
SwissProt_38:RRPL_RVYZ	56.50	96.14	42.84	497	P50736 human papillomavirus v
SwissProt_38:SER3_HUMAN	56.00	116.58	40.81	164	P23152 homo sapiens (human)
SwissProt_38:GRI1_RAT	56.00	107.37	44.31	492	P1167 rat mus musculus (rat)
SwissProt_38:SECY_MYCGA	56.00	107.27	44.35	498	P03235 mycoplasma gallisepti
SwissProt_38:IRK_CAVPO	55.00	99.33	47.64	1300	P14617 homo sapiens (human)
SwissProt_38:IRK_HUMAN	55.00	114.77	47.64	178	P20800 homo sapiens (human)
SwissProt_38:AMPN_LACIC	55.50	101.72	53.27	845	P17897 lactococcus lactis (s
SwissProt_38:IF2_ECOLI	55.50	101.28	53.48	890	P02995 escherichia coli, tran
SwissProt_38:GUNT_CLOSR	55.50	100.42	53.89	1486	P23659 clostridium stercoar
SwissProt_38:RHSD_ECOLI	55.00	97.33	55.40	1466	P16919 escherichia coli, rh
SwissProt_38:MOV1_TMYTO	55.00	110.34	56.39	264	P03588 tobacco mosaic virus
SwissProt_38:MOV1_TMYTO	55.00	110.34	56.39	264	P28719 tobacco mosaic virus
SwissProt_38:WNTA_ALOVA	54.50	115.83	61.40	120	P28099 atopias vulpinus (th)

seq_name: SwissProt_38:INRL_HUMAN

seq_documentation_block:

ID	INRL_HUMAN	STANDARD	PRT	557 AA
AC	P17181			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	15-FEB-2000 (Rel. 39, Last annotation update)			
DE	INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).			
GN	IFNAR1 OR IFNAR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 90124632.			
RA	Uze G., Lutfalla G., Gresser I.;			
RT	"Genetic transfer of a functional human interferon alpha receptor			
RT	into mouse cells: cloning and expression of its cDNA.";			
RL	Cell 60:225-234(1990).			
RN	(2)			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 92129376.			
RA	Lutfalla G., Gardiner K., Proudhon D., Vleth E., Uze G.;			
RT	"The structure of the human interferon alpha/beta receptor gene.";			
RL	J. Biol. Chem. 267:2802-2809(1992).			
RN	(3)			
RP	PHOSPHORYLATION BY TYR2.			
RX	MEDLINE: 95059042.			
RA	Colamonicl O., Yan H., Domanski P., Handa R., Smalley D.,			
RA	Mullersman J., Witte M., Krishnan K., Krolewski J.;			
RT	"Direct binding to and tyrosine phosphorylation of the alpha subunit			
RT	of the type I interferon receptor by p135tyk2 tyrosine kinase.";			
RL	Mol. Cell. Biol. 14:8133-8142(1994).			
CC	- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE			
CC	I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS			
CC	INCLUDING JAKS, TYR2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-			
CC	SUBUNTS THEMSELVES.			
CC	- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	- TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALL TISSUES AND			
CC	EVEN ON THE SURFACE OF MOST IFN-RESISTANT CELLS.			
CC	- PFM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYR2 TYROSINE KINASE.			
CC	- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.			
CC	-----			
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CC	-----			
DR	EMBL: J03171; AA5230.1; -			
DR	EMBL: X60459; CA442992.1; -			
DR	PIR: A32694; A32694.			
DR	PIR: S17112; S17112.			
DR	MIM: 107450; -			
KW	Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism;			
PT	Phosphorylation.			
FT	SIGNAL	1	27	POTENTIAL.
FT	CHAIN	28	557	INTERFERON-ALPHA/BETA RECEPTOR ALPHA
FT	CHAIN	28	557	CHAIN.
FT	DOMAIN	28	436	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	437	457	POTENTIAL.
FT	DOMAIN	458	557	CYTOPLASMIC (POTENTIAL).
FT	DISULFD	79	87	BY SIMILARITY.
FT	DISULFD	199	220	BY SIMILARITY.

```

FT MOD RES 466 466 PHOSPHORYLATION (BY TYK2) (PROBABLE).
FT MOD RES 481 481 PHOSPHORYLATION (BY TYK2) (PROBABLE).
FT CARBOHYD 50 50 POTENTIAL.
FT CARBOHYD 58 58 POTENTIAL.
FT CARBOHYD 81 81 POTENTIAL.
FT CARBOHYD 88 88 POTENTIAL.
FT CARBOHYD 110 110 POTENTIAL.
FT CARBOHYD 172 172 POTENTIAL.
FT CARBOHYD 254 254 POTENTIAL.
FT CARBOHYD 313 313 POTENTIAL.
FT CARBOHYD 314 314 POTENTIAL.
FT CARBOHYD 376 376 POTENTIAL.
FT CARBOHYD 416 416 POTENTIAL.
FT CARBOHYD 433 433 POTENTIAL.
FT VARIANT 168 168 POTENTIAL.
FT /FTID-VAR_002717.
FT CONFLICT 17 17 G -> A (IN REF. 2).
SQ SEQUENCE 557 AA; 63525 MW; 0F674C8A1ADB73 CRC64;

```

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alignment_scores:
Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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alignment_block:

US-09-240-675-1_COPY_27_229 x INRL_HUMAN ..

Align seg 1/1 to: INRL_HUMAN from: 1 to: 557

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1 ATGATGTCCTCTCTGCGCGACGACCTAGTCTGTCGCGGCGG 50
|||||
1 MethetvalvalleuleuglYAlathrleuvalleuvalalvalalgi 17
51 CCATGCGTGTGTCGCCGCGGAGGTGGAATAATCTAAATCTCC 100
|||||
17 yprotipalleasealalaalaglyGlyshnleuylsserprog 34
101 AAAAGTAGAGTGCATCATAGATGACACTTATCTGAGGCGAAC 150
|||||
34 InlysvaIgluvalaspilleleaspaspaspheileleuargtrpash 50
151 AGGAGCGATGCTGTCGCGGAGTGTATTCATTCGATTCACAAA 200
|||||
51 ArggerspIuservalIglYasnvalThrpheserpheserptglnly 67
201 A 201
67 s 67

```

seq_name: SwissProt_38:INRL_BOVIN

seq_documentation_block:

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ID INRL_BOVIN STANDARD; PRT; 560 AA.
AC 004790;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
GN IFNARI OR IFNAR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
RN 11;
RP SEQUENCE FROM N.A.
RC TISSUE-LUNG;
RX MEDLINE: 93076908.
RA Mouchel-Vielh E., Lutfalla G., Mogensen K.E., Uze G.;
RT "Specific antiviral activities of the human alpha interferons are
determined at the level of receptor (IFNAR) structure.";
RL FBS Lett. 313:255-259(1992).
RN [2]

```

```

RP SEQUENCE FROM N.A.
RX MEDLINE: 93305725.
RA Lim J.-K., Langer J.A.;
RT "Cloning and characterization of a bovine alpha interferon receptor.";
RL Biochim. Biophys. Acta 1173:314-319(1993).
CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
CC I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-ALPHA AND BETA-
CC SUBUNITS THEMSELVES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC EMBL: X68443; CAA48484.1; -.
CC EMBL: L06320; AAA02571.1; -.
CC PIR: S33770; S33770.
CC PIR: S27387; S27387.
CC PIR: PF00041; fn3; 1.
CC Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24 BY SIMILARITY.
FT CHAIN 25 560 INTERFERON-ALPHA/BETA RECEPTOR ALPHA
FT DOMAIN 25 437 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 438 458 POTENTIAL.
FT DOMAIN 459 560 CYTOPLASMIC (POTENTIAL).
FT DISULFID 76 84 BY SIMILARITY.
FT DISULFID 199 220 BY SIMILARITY.
FT CARBOHYD 47 47 POTENTIAL.
FT CARBOHYD 55 55 POTENTIAL.
FT CARBOHYD 85 85 POTENTIAL.
FT CARBOHYD 109 109 POTENTIAL.
FT CARBOHYD 172 172 POTENTIAL.
FT CARBOHYD 254 254 POTENTIAL.
FT CARBOHYD 313 313 POTENTIAL.
FT CARBOHYD 377 377 POTENTIAL.
FT CARBOHYD 434 434 POTENTIAL.
FT CONFLICT 422 422 F -> V (IN REF. 2).
SQ SEQUENCE 560 AA; 63818 MW; 66D76B72861E1D11 CRC64;

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alignment_scores:
Quality: 209.00 Length: 65
Ratio: 3.800 Gaps: 2
Percent Similarity: 84.615 Percent Identity: 69.231

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alignment_block:

US-09-240-675-1_COPY_27_229 x INRL_BOVIN ..

Align seg 1/1 to: INRL_BOVIN from: 1 to: 560

```

4 ATGATGTCCTCTCTGCGCGGAGCGACCTAGTCTGTCGCGGCGCC 53
|||||
1 MethleuvalleuleuglYAlathrThrleuMetleuValala...Glytr 16
54 ATGGGCTTGTCCGCGAGCGCGAGTGGAAAAATCTAAATCTCCACAA 103
|||||
16 gtrpvalleuProIalaleaserIgluIalaenleuys...Proglua 32
104 AAGTAGAGTGCATCATAGATGACAACTTATCTGAGGCGAGCAGG 153
|||||
32 snvalIgluIleHisIleIleaspaspaspheheleuylstrpanser 48
154 AGCGATGATGCTGTCGCGGAGTGTGACTTTTCATTCGATTCACAA 198
|||||
49 SerSerIuservalIglYasnvalThrpheserIalaspptgln 63

```

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seq_name: SwissProt_38:INRL_SHEEP
seq_documentation_block:
ID INRL_SHEEP STANDARD: PRT: 560 AA.
AC 028569: 095205:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC)
DE (INTERFERON ALPHA/BETA RECEPTOR-1).
GN IFNARI OR IFNAR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Caprinae; Ovis.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-ENDOMETRIUM;
RX MEDLINE: 97135690.
RA Kaluz S., Fisher P.A., Kaluzova M., Sheldrick E.L., Flint A.P.F.;
RT *Structure of an ovine interferon receptor and its expression in
RT endometrium.*
RL J. Mol. Endocrinol. 17:207-215(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-ENDOMETRIUM;
RX MEDLINE: 98006426.
RA Han C.-S., Mathalagan N., Klemann S.W., Roberts R.M.;
RT *Molecular cloning of ovine and bovine type I interferon receptor
RT subunits from uteri, and endometrial expression of messenger
RT ribonucleic acid for ovine receptors during the estrous cycle and
RT pregnancy.*
RL Endocrinology 138:4757-4767(1997).
CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
CC I FENS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
CC SUBUNITS THEMSELVES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT
CC CONCEPTUS AT DAY 15 OF PREGNANCY.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X05939: CAA65183.1: -
CC EMBL: U65978: AAB84231.1: -
CC EMBL: P00041: fn3.1: -
CC KW Receptor; Transmembrane; Glycoprotein; Signal.
CC FT SIGNAL 1 24
CC FT CHAIN 25 560
CC FT DOMAIN 25 437
CC FT TRANSMEM 438 458
CC FT DOMAIN 459 560
CC FT DISULFID 76 84
CC FT DISULFID 199 220
CC FT CARBOHYD 47 47
CC FT CARBOHYD 55 55
CC FT CARBOHYD 85 85
CC FT CARBOHYD 108 108
CC FT CARBOHYD 109 109
CC FT CARBOHYD 172 172
CC FT CARBOHYD 222 222
CC FT CARBOHYD 285 285
CC FT CARBOHYD 313 313

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FT CARBOHYD 359 359 POTENTIAL.
FT CARBOHYD 377 377 POTENTIAL.
FT CARBOHYD 434 434 POTENTIAL.
FT CONFLICT 352 352 S -> G (IN REF. 2).
FT CONFLICT 522 522 A -> D (IN REF. 2).
SQ SEQUENCE 560 AA: 63918 MW: E7198A1905D4805C CRC64:

alignment_scores:
Quality: 204.00 Length: 65
Ratio: 3.778 Gaps: 2
Percent Similarity: 83.077 Percent Identity: 69.231

alignment_block:
US-09-240-675-1_COPY_27_229 x INRL_SHEEP ..
Align seg 1/1 to: INRL_SHEEP from: 1 to: 560

4 ATGTCGCTCCTCGGGCGGACGACCTAGTCTGCTGCGCGCCG 53
||||: |||||||||
1 MetLeuSerLeuLeuGlyAlaThrThrLeuMetLeuValAla...GlyAr 16
54 ATGGCTGTCTCGCGACGCGCAGGTGGAATAATCTAAATCCCTCA 103
||||||| |||||||
16 gtrpValLeuProAlaIaIaSerGlyGluAlaAsnLeuLysSer...GluA 32
104 AAGTAGAGCTGACATCATGATGACAACTTTATCTGAGTGGAACAG 153
||||||| |||||||||
32 snValGluIleHsIleIleAspAspAspAspAspAspAspAspAsp 48
154 AGCGATGATGCTGCTGGGAAATGACTTTTATTCATTCATTAACA 198
||||||| |||||||
49 SerSerGluSerValArgAsnValThrPheSerAlaAspPyrgln 63

seq_name: SwissProt_38:INRL_MOUSE
seq_documentation_block:
ID INRL_MOUSE STANDARD: PRT: 590 AA.
AC P33896:
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
DE IFNARI OR IFNAR OR IFAR.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN
RP SEQUENCE FROM N.A.
RX MEDLINE: 92262522.
RA Uze G., Lutfalla G., Bandu M.T., Proudhon D., Mogenssen K.E.;
RT *Behavior of a cloned murine interferon alpha/beta receptor expressed
RT in homo-specific or hetero-specific background.*
RT Proc. Natl. Acad. Sci. U.S.A. 89:4774-4778(1992).
CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
CC I FENS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
CC SUBUNITS THEMSELVES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M89641: AAA37890.1: -
CC EMBL: PIR: A45283; A45283.
CC MGD: MGI:107658; IFNAR.

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CC -----
DR EMBL: M89919; AAA32485.1; -
DR PIR: A45731; A45731.
KW Transcription regulation.
SQ SEQUENCE 141 AA; 16682 MW; 96C9EFA8C673C479 CRC64;

alignment_scores:
  Quality: 62.50      Length: 50
  Ratio: 2.155      Gaps: 3
  Percent Similarity: 58.000      Percent Identity: 34.000

alignment_block:
US-09-240-675-1_COPY_27_229 x COMA_BPT4 ..
Align seg 1/1 to: COMA_BPT4 from: 1 to: 141

16 CTGGGCGCGAGACCTGCTGCTGCGCGCCGCGCCGATGGTGTGTC 65
   |||||  ||  |||||  |||||  |||||  |||||  |||||
49 LeuDIyArpProthlyslleMetHrSerlely.....ValleuLy 63
66 CGCAGCGCGAGGTGGAAAAATCTAAATCTCCCAAAAGTAGAGTCG 115
   :  |||||  |||||  |||||  |||||  |||||  |||||
63 sArGcYsAlaGlyLy.....A 69

116 ACATCATAGATGACACTTATCTCTGAGTGGAACAGAGGAGTACT 165
   |||||  |||||  |||||  |||||  |||||  |||||
69 spleuAuApGluAsnPhelle.....TrrleuSerThrAsnGluAla 83

seq_name: SwissProt_38:PHLC_PSEAE

seq_documentation_block:
ID PHLC_PSEAE STANDARD; PRT; 730 AA.
AC P06200;
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE HEMOLYTIC PHOSPHOLIPASE C PRECURSOR (EC 3.1.4.3) (HEAT LABILE-
GN HEMOLYSIN) (PHOSPHATIDYLCHOLINE CHOLINEPHOSPHOHYDROLASE).
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
OC Pseudomonas.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE: 86250607.
RA Pritchard A.E., Vasil M.L.;
RT "Nucleotide sequence and expression of a phosphate-regulated gene
RT encoding a secreted hemolysin of Pseudomonas aeruginosa."
RL J. Bacteriol. 167:291-298(1986).
RN (2)
RP REVISIONS.
RA Pritchard A.E.;
RL Submitted (Aug-1986) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: HYDROLYZES SPHINGOMYELIN IN ADDITION TO
CC PHOSPHATIDYLCHOLINE.
CC -1- CATALYTIC ACTIVITY: A PHOSPHATIDYLCHOLINE + H(2)O - 1,2-
CC DIACYLGLYCEROL + CHOLINE PHOSPHATE.
CC -1- SIMILARITY: 40% IDENTITY TO NON-HEMOLYTIC PHOSPHOLIPASE C.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M13047; AAA25966.1; -
DR PIR: A26391; A26391.
KW Hemolysis; Toxin; Hydrolyase; Signal.
FT SIGNAL 1
FT CHAIN 39
SQ SEQUENCE 730 AA; 82655 MW; F1D3695824445FBF CRC64;

alignment_scores:
  Quality: 62.00      Length: 69
  Ratio: 1.824      Gaps: 4
  Percent Similarity: 49.275      Percent Identity: 26.087

alignment_block:
US-09-240-675-1_COPY_27_229 x PHLC_PSEAE ..
Align seg 1/1 to: PHLC_PSEAE from: 1 to: 730

37 CTGTCGCGCGTGGCGCCATGGTGTGTCGCGAGCGCGAGTGA AAAA 86
   |||||  |||||  |||||  |||||  |||||  |||||
404 LeuIlAlAlleSerProTrp.....SerLyGlyLy..... 414
87 TCTAAATCTCTCAAAAAGTAGAGTCGACATCATGATGACACTTAA 136
   |||||  |||||  |||||  |||||  |||||  |||||
415 .....LysValSerAlaGluValAlaPheAspHisThrSerV 426
137 TCCTGAGG..... 144
426 AlLeuArpPheLeuGluArpArpGlyLeuValGluGluAsnIleSer 442
145 ...TGGAAGAGGAGCGATGCTGTGCGGAATGATCTTTTCATTGCA 191
   |||||  |||||  |||||  |||||  |||||  |||||
443 ProTrpArpArpAla.....ValCysGlyAspLeuThrSerIlePheAs 457
192 TTAACA 198
457 pPheGln 459

seq_name: SwissProt_38:CRF4_HUMAN

seq_documentation_block:
ID CRF4_HUMAN STANDARD; PRT; 325 AA.
AC Q08334;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE CYTOKINE RECEPTOR CLASS-II CRF2-4 PRECURSOR.
GN CRFB4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE: 93300510.
RA Lutfalla G., Gardiner K., Uze G.;
RT "A new member of the cytokine receptor gene family maps on chromosome
RT 21 at less than 35 kb from IFNAR."
RL Genomics 16:366-373(1993).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE: 96054036.
RA Lutfalla G., McInnis M.G., Antonarakis S.E., Uze G.;
RT "Structure of the human CRFB4 gene: comparison with its IFNAR
RT neighbor."
RL J. Mol. Evol. 41:338-344(1995).
CC -1- FUNCTION: IS PROBABLY INVOLVED IN THE INTERFERON SYSTEM.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -----
```

KN	11
RP	SEQUENCE FROM N.A.
RC	STRAIN-129/SVJ;

Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.

RP SEQUENCE FROM N.A.
PC TISSUE-BONE MARROW:
RX MEDLINE: 92212859.
RA Vellard M., Sureau A., Soret J., Martinerie C., Perbal B.;
RT "A potential splicing factor is encoded by the opposite strand of the
RL trans-spliced c-myc exon.";
RN Proc. Natl. Acad. Sci. U.S.A. 89:2511-2515(1992).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94134745.
RA Sureau A., Perbal B.;
RT "Several mRNAs with variable 3' untranslated regions and different
RL stability encode the human PR264/SC35 splicing factor.";
RN Proc. Natl. Acad. Sci. U.S.A. 91:932-936(1994).
[4]
RP SEQUENCE OF 1-34 FROM N.A.
RX MEDLINE: 93101590.
RA Sureau A., Soret J., Vellard M., Crochet J., Perbal B.;
RT "The PR264/c-myc connection: expression of a splicing factor
RL modulated by a nuclear protooncogene.";
RN Proc. Natl. Acad. Sci. U.S.A. 89:11683-11687(1992).
[5]
RP SEQUENCE OF 67-83.
RX MEDLINE: 92249775.
RA Zahler A.M., Lane W.S., Stolk J.A., Roth M.B.;
RT "SR proteins: a conserved family of pre-mRNA splicing factors.";
RN Genes Dev. 6:837-847(1992).
[6]
RP PROTEIN INTERACTIONS IN SPliceOSOME ASSEMBLY.
RX MEDLINE: 94084782.
RA Wu J.Y., Maniatis T.;
RT "Specific interactions between proteins implicated in splice site
RL selection and regulated alternative splicing.";
RN Cell 75:1061-1070(1993).
[7]
RP BINDING TO U1-70K.
RX MEDLINE: 94187841.
RA Korte J.D., Jamison S.F., Will C.L., Luo P., Luhrmann R.;
RT "Protein-protein interactions and 5'-splice-site recognition in
RL mammalian mRNA precursors.";
RN Nature 368:119-124(1994).
[8]
RP RNA BINDING SPECIFICITY.
RX MEDLINE: 95354672.
RA Tacke R., Manley J.L.;
RT "The human splicing factors ASF/SF2 and SC35 possess distinct,
RL functionally significant RNA binding specificities.";
RN EMBO J. 14:3540-3551(1995).
[9]
RP SPECIFICITY FOR BETA-GLOBIN MRNA.
RX MEDLINE: 93368668.
RA Fu X.-D.;
RT "Specific commitment of different pre-mRNAs to splicing by single SR
RL proteins.";
RN Nature 365:82-85(1993).
-1- FUNCTION: NECESSARY FOR THE SPLICING OF PRE-MRNA. IT IS REQUIRED
FOR FORMATION OF THE EARLIEST ATP-DEPENDENT SPLICING COMPLEX AND
INTERACTS WITH SPliceOSOMAL COMPONENTS BOUND TO BOTH THE 5' AND 3'
SPLICING SITES DURING SPliceOSOME ASSEMBLY. IT ALSO IS REQUIRED FOR
ATP-DEPENDENT INTERACTIONS OF BOTH U1 AND U2 SNRNPs WITH PRE-
MRNA. INTERACTS WITH OTHER SPliceOSOMAL COMPONENTS, VIA THE RS
DOMAINS, TO FORM A BRIDGE BETWEEN THE 5' AND 3' SPLICING SITE
BINDING COMPONENTS, U1 SNRNP AND U2AF. IN VITRO, BINDS SF2/ASF,
U1-70K AND THE 35 KD BUT NOT THE 65 KD SUBUNIT OF U2AF. BINDS TO
PURINE-RICH RNA SEQUENCES, EITHER 5'-AGSAGAGTA-3' (S-C OR G) OR
5'-GTTCGAGTA-3'. CAN BIND TO BETA-GLOBIN MRNA AND COMMIT IT TO THE
SPLICING PATHWAY.
-1- SUBCELLULAR LOCATION: NUCLEAR
-1- ALTERNATIVE PRODUCTS: DIFFERENT FORMS OF THE PROTEIN MAY BE
PRODUCED BY ALTERNATIVE SPLICING.
-1- PTM: EXTENSIVELY PHOSPHORYLATED ON SERINE RESIDUES IN THE RS
DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RNP).
CC -1- SIMILARITY: BELONGS TO THE SR FAMILY OF SPLICING FACTORS.
CC -----
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CC -----
DR EMBL: M90104; AAA60306.1; -
DR EMBL: X62447; CAA44307.1; -
DR EMBL: X75755; CAA53383.1; -
DR EMBL: L03693; AAA60162.1; -
DR PIR: S17328; S17328.
DR PIR: A42634; A42634.
DR HSP: P19339; ISXL.
DR MIM: 600813; -
DR PROSITE: PS00030; RNP_L; 1.
DR PRAM: PF00076; rtm_1.
KW Nuclear protein; RNA-binding; mRNA splicing; Alternative splicing;
KW Phosphorylation.
FT DOMAIN 16 21 RNA-BINDING (RNP2) (BY SIMILARITY).
FT DOMAIN 55 62 RNA-BINDING (RNP1) (BY SIMILARITY).
FT DOMAIN 111 116 GLY-RICH (HINGE REGION).
FT DOMAIN 117 221 ARG/SER-RICH (RS DOMAIN).
FT CONFLICT 38 38 R -> G (IN REF. 2 AND 3).
SQ SEQUENCE 221 AA; 25575 MW; 9D1B76BDB65701F5 CRC64;

alignment_scores:
Quality: 59.00 Length: 54
Percent Similarity: 2.185 Gaps: 2
Percent Identity: 50.000 Percent Identity: 35.185

alignment_block:
US-09-240-675-1_COPY_27_229 x SFR2_HUMAN ..

Align seg 1/1 to: SFR2_HUMAN from: 1 to: 221

6 GGTGCTCTCTCT.....GGGCGGACGACCTAGTCTGCTGCG 43
|||||||.....:|||||
93 GYARGPSPRODAPSPERHISHSERARGLGPYRPPRODARGAR 109
44 C.....CGTGGCCCATGGGTGTC 63
109 GYRGYGLYGLYGLYGLYRGYARGRGSERPRORARGARGA 126
64 TCCGACGCGGAGGTGGAATAATCTCAAAAGTAGAGGT 113
|||||||.....:|||||
126 RGRGSRGSRGSRGSRGSRGSRGSRGSRGSRGSRGSR 142
114 CGACATCATAGA 125
|||||
143 ARGTYRSEARG 146

seq_name: SwissProt_38:HXAA_HUMAN

seq_documentation_block:
ID HXAA_HUMAN STANDARD; PRT; 496 AA.
AC P31260; O15949;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE HOMOEOBOX PROTEIN HOX-A10 (HOX-1H) (HOX-1.8) (PL).
OS HOXA10 OR HOX1H.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 91288229.

OM of: US-09-240-675-1_COPY_27_229 to: SPTREMBL_12:*

out-format: pfs

Date: Jun 1, 2000 12:39 AM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

-MODEL=itame+_12p_model -DEV=xlp
-O=/cgn2.1/USPTO_sptol/US09240675/runat_30052000_164313_24664/app-query.fasta.1
-DB=SPTREMBL_12 -OEMT=fastan -SUFEX=modif.rspt -GAPOP=12.000
-GAPXT=4.000 -MINMATCH=0.100 -IOOPCL=0.000 -IOOEXT=0.000
-GAPOP=4.500 -GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELDP=6.000 -DELEX=7.000 -START=1 -MATRIX=blsum62
-TRANS=human400.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pc
-ALIGN=15 -MODE=LOCAL -OUTFM=ps -NORM=ext -MINLEN=0
-MAXLEN=1000000 -USER=US09240675 -NCPU=6 -ICPU=3 -NO_XLPHY -WAIT
-THREADS=1

Search information block:

Query: US-09-240-675-1_COPY_27_229
Query length: 203
Database: SPTREMBL_12:*Database sequences: 225878
Database length: 6933412
Search time (sec): 89.940000

Sequence	Strd Orig	ZScore	EScore	Len	Documentation
sp.vertbrate:09YHW0	+	108.50	226.67	2.0e-05	1569 09YHW0 gallus gallus (chicken).
sp.human:09Y5T6	+	75.00	144.00	0.3165	1429 09Y5T6 homo sapiens (human).
sp.invertebrate:076514	+	66.00	133.60	4.70	365 076514 caenorhabditis elegans
sp.human:013507	+	63.00	120.63	10.69	848 013507 homo sapiens (human).
sp.human:077699	+	62.00	132.87	16.11	117 077699 bos taurus (bovine).
sp.human:095927	+	62.00	126.22	15.25	290 095927 homo sapiens (human).
sp.rodent:088970	+	61.00	117.15	19.29	734 088970 mus musculus (mouse).
sp.human:09Y415	+	60.50	124.46	23.91	232 09Y415 homo sapiens (human).
sp.invertebrate:091232	+	60.50	121.66	23.36	340 P91232 caenorhabditis elegans
sp.plant:064410	+	60.00	122.21	27.40	270 064410 zea mays (maize).
sp.invertebrate:002424	+	60.00	120.00	26.90	365 002424 caenorhabditis elegans
sp.invertebrate:023047	+	60.00	119.73	26.84	379 023047 caenorhabditis elegans
sp.rodent:060805	+	60.00	112.64	23.32	994 060805 mus musculus (mouse).
sp.human:09Y519	+	60.00	104.64	23.70	2971 09Y519 homo sapiens (human).
sp.archaea:09YEB6	+	59.50	127.79	33.49	108 09YEB6 aeropyrum pernix. 108aa
sp.rodent:062143	+	59.50	123.89	32.43	184 062143 mus musculus (mouse).
sp.human:030849	+	59.50	119.01	31.15	358 030849 oryctolagus cuniculus (r
sp.human:09Y775	+	59.50	118.40	30.99	389 09Y775 candida tropicalis (yeas
sp.plant:008700	+	59.00	116.28	35.55	445 008700 brassica napus (rape).
sp.plant:09XFW6	+	59.00	116.28	35.55	445 09XFW6 brassica oleracea (cauli
sp.invertebrate:018109	+	59.00	115.04	35.19	527 018109 caenorhabditis elegans
sp.invertebrate:025994	+	59.00	101.98	31.60	3134 025994 plasmodium falciparum
sp.bacteria:086774	+	58.50	117.12	41.79	340 086774 streptomyces coelicolor.
sp.bacteria:09X4V6	+	58.50	117.12	41.79	340 09X4V6 streptomyces griseofolius
sp.plant:09XID0	+	58.50	106.47	38.27	1456 09XID0 arabidopsis thaliana (m
sp.plant:023740	+	58.00	113.25	47.25	494 023740 brassica oleracea (cauli
sp.plant:09XFW5	+	58.00	109.29	45.72	849 09XFW5 brassica oleracea (cauli
sp.human:012866	+	58.00	108.09	45.28	999 012866 homo sapiens (human).
sp.plant:065711	+	57.50	120.29	58.44	162 065711 arabidopsis thaliana (m
sp.virus:065450	+	57.50	116.00	56.41	291 065450 pestivirus type 3. nonst
sp.invertebrate:021784	+	57.50	115.07	55.98	330 021784 caenorhabditis elegans
sp.invertebrate:016867	+	57.50	113.70	55.35	398 016867 drosophila melanogaster
sp.invertebrate:021494	+	57.50	112.36	54.75	478 021494 caenorhabditis elegans
sp.fungi:008912	+	57.50	110.41	53.87	624 008912 saccharomyces cerevisiae
sp.rodent:088277	+	57.50	96.18	47.91	4351 088277 rattus norvegicus (rat)
sp.virus:081166	+	57.00	118.26	67.09	183 081166 hepatitis B virus. core
sp.invertebrate:09XYT5	+	57.00	117.32	66.57	208 09XYT5 cassiopea xamachana. s
sp.plant:023854	+	57.00	112.00	63.72	430 023854 brassica campestris (flg
sp.plant:064680	+	57.00	111.82	63.62	441 064680 arabidopsis thaliana (m
sp.human:075167	+	57.00	109.16	62.24	634 075167 homo sapiens (human).
sp.plant:023292	+	57.00	106.30	60.79	936 023292 arabidopsis thaliana (m

sp.invertebrate:045604	+	57.00	105.24	60.26	1083 045604 caenorhabditis
sp.bacteria:034557	+	56.50	115.88	76.79	217 034557 bacillus subtilis.
sp.plant:038704	+	56.50	111.36	73.98	402 038704 avena fatua. dna-b
sp.plant:039363	+	56.50	111.24	73.91	409 039363 brassica napus (ra

seq_name: sp.vertbrate:09YHW0

seq_documentation_block:

ID	Q9YHW0	PRELIMINARY	PRT	569 AA.
AC	Q9YHW0			
DT	01-MAY-1999 (TEMBLrel. 10, Created)			
DT	01-MAY-1999 (TEMBLrel. 10, Last sequence update)			
DT	01-MAY-1999 (TEMBLrel. 10, Last annotation update)			
DE	INTERFERON ALPHA/BETA RECEPTOR 1.			
GN	IFNAR1.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;			
OC	Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER;			
PA	REBOUL J., GARDINER K., MONNERON D., UZE G., LUTFALLA G.;			
RT	"Comparative genomic analysis of the interferon/interleukin-10			
RT	receptor gene cluster".			
RL	Genome Res. 0:0-0(1999).			
DR	EMBL; AF082664; AAD13659.1; ..			
KW	RECEPTOR.			
SO	SEQUENCE	569 AA;	64055 MW;	F99BC099 CRC32;

alignment_scores:

Quality:	108.50	Length:	60
Ratio:	2.712	Gaps:	1
Percent Similarity:	66.667	Percent Identity:	43.333

alignment_block:

US-09-240-675-1_COPY_27_229 x 09YHW0 ..

Align seg 1/1 to: 09YHW0 from: 1 to: 569

19	GGCGCAGACGACCTGCTGCTGCGCGCCGATGCTGCTGCGC	68
9	GLYRGLGUALAVALLEULEUCYSVALLEUVALVALLEISRAAGCY	25
69	AGCGCAGGTGAGAAAATCTAAATCTCTCAAAAAGTAGAGTCGACA	118
25	scysALGLYGLNthrasnleuYsserProGlnaspIleGlnvalTYRA	42
119	TCATAGATGACACTTATCTCTGAGTGAGAACAGAGCGATGATGTC	168
42	lavalasnrthrasPheThrLeuMettrpansrYrthrglyaspGlyThr	58
169	GGGAATGTGACTTTTCATTCGATTCAAA	198
59	..AsnValthrPheSerAlaGlnTYrGln	67

seq_name: sp.human:09Y5T6

seq_documentation_block:

ID	Q9Y5T6	PRELIMINARY	PRT	1429 AA.
AC	Q9Y5T6			
DT	01-NOV-1999 (TEMBLrel. 12, Created)			
DT	01-NOV-1999 (TEMBLrel. 12, Last sequence update)			
DT	01-NOV-1999 (TEMBLrel. 12, Last annotation update)			
DE	BREAST CANCER NUCLEAR RECEPTOR-AUXILIARY PROTEIN.			
GN	BRX.			
OS	homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Catarrhini; Homiidae; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=TESTIS.			
RX	MEDLINE; 98288806.			

RA RUBINO D., DRIGERS P., ARBIT D., KEMP L., MILLER B., COSO O.,
 RA PAGLIAI K., GRAY K., GUTKIND S., SEGARS J.;
 RT "Characterization of Brx, a novel DBI family member that modulates
 RT estrogen receptor action."
 RL Oncogene 16:2513-2526(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-TESTIS;
 RA RUBINO D.M., DRIGERS P.H., MILLER B., SEGARS J.H.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF126008; AAD21311.1;
 KW Receptor.
 SQ SEQUENCE 1429 AA; 161033 MW; 542B8C25 CRC32;

alignment_scores:
 Quality: 75.00 Length: 74
 Ratio: 1.923 Gaps: 5
 Percent Similarity: 52.703 Percent Identity: 41.892

alignment_block:

US-09-240-675-1_COPY_27_229 x Q9Y5T6

Align seg 1/1 to: Q9Y5T6 from: 1 to: 1429

```

3  CATGTCGCTCCTCGGCGGCGAGCACCCTAGTCTGCTGCGCGGCGGC 52
   |||||||
1230 AspGlyArgProSerTrp.....ProSerAlaArgArgArgCysSe 1243
   |||
53  CATGGGTGTGTGCCAGCCGAGGTGGAATAATCTAATCTCTCTCA 102
   |||
1243 rArgGly.....SerArgThrTrpArgSerGlyArgSerSers 1257
   |||
103  AAAGTAGAGGTGCACATCATATGACAACCT..... 134
   |||
1257 eArgArgArgAlaHisSerGlnTrpAspLeuGluArgLeuArgAla 1273
   |||
135  ....TATCCTAGGTGAGCAGACAGCATGATGCTGCGGAGTGTGA 178
   |||
1274 GlnLysGlnLeuGluArgGluGlnGlnHis...ValArgArgGluAla 1289
   |||
179  CTTTTCATTCGATTATCAAAA 200
   |||||||
1289 u.....ArgLeuSerGln 1293

```

seq_name: sp_invertebrate:076514

seq_documentation_block:

ID 076514 PRELIMINARY; PRT; 365 AA.
 AC 076514;
 DT 01-NOV-1998 (TREMblrel. 08, Created)
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
 DE 01-NOV-1999 (TREMblrel. 12, Last annotation update)
 GN CEF-1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
 OC Rhabditina; Rhabditioidea; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-N2;
 RA MORITA K., CHOW K.L., UENO N.;
 RT "Body Length and Male Tail Ray Pattern Formation of C. elegans are
 RT Regulated by a Member of TGF β Family."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF074395; AAC26791.1;
 DR HSSP; P18075; 1BMP.
 DR PFAM; PF00019; TGF-beta; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 SO SEQUENCE 365 AA; 41781 MW; 54051BEE CRC32;

alignment_scores:

Quality: 66.00 Length: 54
 Ratio: 1.941 Gaps: 2
 Percent Similarity: 62.963 Percent Identity: 31.481

alignment_block:

US-09-240-675-1_COPY_27_229 x 076514

Align seg 1/1 to: 076514 from: 1 to: 365

```

27  GACCCTAGTGCTGCTGCGCGGCGCCAGTGGTGTTCGCCAGCCGAG 76
   ::|||
228 GluProSerSerValArgArg.....LysArgSerArgG1 239
   |||
77  GTGGAATAATCTAATCTCTCTCAAAAAGTAGAGTCGACATCATGAT 126
   ::|||
239 nThrgLysnSerGlnArgLysnArgLysLysGlyArgLysHis. 255
   |||
127  GACAACCTTATCCGAGGTGGAACAGCAGCATGATGCTGCGGAGTGT 176
   ::|||
256 .....AsnThrgLysnSerGlnArgLysnSerGlnArgArgThr 267
   |||
177  GACTTTTCATT 188
   |||
268  AspPheTyVal 271

```

seq_name: sp_human:Q13507

seq_documentation_block:

ID Q13507 PRELIMINARY; PRT; 848 AA.
 AC Q13507; 000593;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DE 01-NOV-1999 (TREMblrel. 12, Last annotation update)
 GN TRANSIENT RECEPTOR POTENTIAL RELATED CHANNEL 3 PROTEIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 96234226.
 RX ZHU X., JIANG M., PEYTON M., BOULAY G., HURST R., STEFANI E.,
 RA BIRNBAUMER L.;
 RT "trp, a novel mammalian gene family essential for agonist-activated
 RT capacitative Ca2+ entry."
 RL Cell 85:661-671(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97358541.
 RA XU X.Z.S., LI H.S., GUGGINO W.B., MONTPELL C.;
 RT "Coassembly of TRP and TRPL produces a distinct store-operated
 RT conductance."
 RL Cell 89:1155-1164(1997).
 DR EMBL; U47050; AAC51653.1;
 DR EMBL; Y13758; CAA74083.1;
 DR PFAM; PF00023; ank; 2.
 DR PRINTS; PR01097; TRNSRCEPTRP.
 SO SEQUENCE 848 AA; 97354 MW; 78AC2E9D CRC32;

alignment_scores:

Quality: 63.00 Length: 75
 Ratio: 1.537 Gaps: 3
 Percent Similarity: 54.667 Percent Identity: 33.333

alignment_block:

US-09-240-675-1_COPY_27_229 x Q13507

Align seg 1/1 to: Q13507 from: 1 to: 848

```

4  ATGGTCGCTCCTCGGCGGCGAGCACCCTAGTCTGCTGCGCGGCGCC 53
   ::|||
351 LeuValValValValAlaLeuGlyLeuProPheLeuAlaIleGlyTy 367

```

```

54 ATGGGTGTTCTCCGACCCGAGTGGAAAAATCTAAATCTCTCAAA 103
   |||||  |||||  |||||  |||||  |||||  |||||
367 rtrpillealprocysersargleuglylleleuargserprohem 384
   |||||  |||||  |||||  |||||  |||||  |||||
104 AAGTAGAGCNC.....GACATCATAGATGACAATTCATCCG 141
   |||||  |||||  |||||  |||||  |||||  |||||
384 eltysphevalalahlalaleuargserphellelepheleuglyleu 400
   |||||  |||||  |||||  |||||  |||||  |||||
142 AGGTGACACAGAGCAGTGTCTGCGG.....AATGT 176
   |||||  |||||  |||||  |||||  |||||  |||||
401 valpheasmlaserasparpneuglyllethrthleuproasnll 417
   |||||  |||||  |||||  |||||  |||||  |||||
177 GACCTTTTCATTCGATTATCAAAA 201
   |||||  |||||  |||||  |||||  |||||  |||||
417 ethrvalthr...Asptryprolys 424

```

seq_name: sp_mammal:077699

```

seq_documentation_block:
ID 077699 PRELIMINARY: PRT: 117 AA.
AC 077699;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE TRP3 PROTEIN (FRAGMENT).
GN TRP3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RA WISENBACH U., PHILIPP S., FLOCKERZI V.;
RT "Cloning and analysis of trp channels."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL, AJ006781; CA07246.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 117 AA; 13295 MW; B9F9B808 CRC32;

```

alignment_scores:

Quality:	62.00	Length:	75
Ratio:	1.512	Gaps:	3
Percent Similarity:	54.667	Percent Identity:	33.333

alignment_block:

US-09-240-675-1_COPY_27_229 x 077699 ..

Align seg 1/1 to: 077699 from: 1 to: 117

```

4 ATGTCGTCCTCTGGCGGACGACCCCTAGTGTCTGCGCGGAGGCC 53
   |||||  |||||  |||||  |||||  |||||  |||||
25 leuvalvalleuvalalaleuuglyleuropheleuallieglyty 41
   |||||  |||||  |||||  |||||  |||||  |||||
54 ATGGGTGTTCTCCGACCCGAGTGGAAAAATCTAAATCTCTCAAA 103
   |||||  |||||  |||||  |||||  |||||  |||||
41 rtrpillealprocysersargleuglylleuargserprohem 58
   |||||  |||||  |||||  |||||  |||||  |||||
104 AAGTAGAGCNC.....GACATCATAGATGACAATTCATCCG 141
   |||||  |||||  |||||  |||||  |||||  |||||
58 eltysphevalalahlalaleuargserphellelepheleuglyleu 74
   |||||  |||||  |||||  |||||  |||||  |||||
142 AGGTGACACAGAGCAGTGTCTGCGG.....AATGT 176
   |||||  |||||  |||||  |||||  |||||  |||||
75 valpheasmlaserasparpneuglyllethrthleuproasnll 91
   |||||  |||||  |||||  |||||  |||||  |||||
177 GACCTTTTCATTCGATTATCAAAA 201
   |||||  |||||  |||||  |||||  |||||  |||||
91 ethrvalthr...ileasptyprolys 98

```

seq_name: sp_human:095927

```

seq_documentation_block:
ID 095927 PRELIMINARY: PRT: 290 AA.
AC 095927;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE D465N24.2.1 (PUTATIVE NOVEL PROTEIN) (ISOFORM 1).
GN D465N24.2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA WILSON S.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL031432; CAB37992.1; -.
SQ SEQUENCE 290 AA; 33613 MW; B59E0C18 CRC32;

```

alignment_scores:

Quality:	62.00	Length:	62
Ratio:	2.296 <td>Gaps:</td> <td>1 </td>	Gaps:	1
Percent Similarity:	43.548 <td>Percent Identity:</td> <td>29.032</td>	Percent Identity:	29.032

alignment_block:

US-09-240-675-1_COPY_27_229 x 095927 ..

Align seg 1/1 to: 095927 from: 1 to: 290

```

6 GGTGTCCTCTGGCGGACGACCCCTAGTGTCTGCGCGGAGGCCAT 55
   |||||  |||||  |||||  |||||  |||||  |||||
11 glyserproglnglulysaspserserthrsargserglyse 27
   |||||  |||||  |||||  |||||  |||||  |||||
56 GGTGTCCTCTGGCGGACGACCCCTAGTGTCTGCGCGGAGGCCAT 74
   |||||  |||||  |||||  |||||  |||||  |||||
27 rserargleuserargserargserargserargserargser 44
   |||||  |||||  |||||  |||||  |||||  |||||
75 .....AGGTGAAAAAATCT 89
   |||||  |||||  |||||  |||||  |||||  |||||
44 rserargleuserargserargserargserargserargser 60
   |||||  |||||  |||||  |||||  |||||  |||||
90 AAAATCTCTCAAAAAGTAGAGTGCACATCTAGA 125
   |||||  |||||  |||||  |||||  |||||  |||||
61 lysersargserargserargserargserargserargser 72

```

seq_name: sp_rodent:088970

seq_documentation_block:

ID 088970 PRELIMINARY: PRT: 734 AA.

```

AC 088970;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE INSULIN RECEPTOR SUBSTRATE-2 (FRAGMENT).
GN IRS2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA XU G., ULLMER W.T., WOLF B.A.;
RT "Partial genomic DNA sequence of mouse beta-cell IRS-2."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF090738; AAC61743.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 734 AA; 75251 MW; B3410CAF CRC32;

```

alignment_scores:

Quality:	61.00	Length:	29
Ratio:	2.652 <td>Gaps:</td> <td>1 </td>	Gaps:	1
Percent Similarity:	79.310 <td>Percent Identity:</td> <td>51.724</td>	Percent Identity:	51.724

alignment_scores:
 Quality: 59.50 Length: 35
 Ratio: 2.705 Gaps: 1
 Percent Similarity: 62.857 Percent Identity: 42.857

alignment_block:
 US-09-240-675-1_COPY_27_229 x Q9YEB6 ..

Align seg 1/1 to: Q9YEB6 from: 1 to: 108

```

12 CCGCCGCGGCGCGACACCTAGTCTGCTGCGCGCGCGCCCATGGGTCT 61
   |||||:::||||:::|||||:::|||||:::|||||
13 ProProSerArgProSerPro.....GlnArgGlyProGlnGly 26
62 TGTCCGCGCGCGCGAGGTGCAAAATCTAAATCTCCTCAAAAGTAGAG 111
   |:::||||:::|||||:::|||||
26 lphneGlyAlaCysArgGlyProGlnProLeuGlnSerArgArgSerArg 43
112 GTCGA 116
   |||||
43 lYArg 44
  
```

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 1, 2000, 00:40:13 ; Search time 42.08 Seconds
(without alignments)
128,900 Million cell updates/sec

Title: US-09-240-675-2_COPY_1_229

Perfect score: 1196
Sequence: 1 MMVVLGATTLVAVGPMV.....WKIGYSPVHCIKTVENEL 229

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1196	100.0	436	R14487	Soluble Interferon
2	1196	100.0	436	R28495	Sequence of a soul
3	1196	100.0	436	R17173	IFN receptor extra
4	1196	100.0	557	R11958	Human alpha-interf
5	1196	100.0	557	R14488	Complete Interfero
6	1196	100.0	557	R28496	Sequence of a soul
7	1196	100.0	557	R42635	Human Interferon r
8	1196	100.0	557	R75356	Human IFN receptor
9	1191	99.6	434	W21805	Spliced-deleted in
10	1191	99.6	496	W21806	Transmembranal int
11	1191	99.6	557	W21804	CRFB4 protein. New
12	222.5	18.6	325	W52296	IFN-gamma receptor
13	203	17.0	332	R75782	Cytot7 cytokine r
14	184.5	15.4	553	W79159	Human IFN-gamma ac
15	151.5	12.7	337	R71035	Human gamma recept
16	149.5	12.5	337	R75783	Human cytokine rec
17	140.5	11.7	574	W97861	Human gamma recept
18	131.5	11.0	211	W97864	Human gamma recept
19	117	9.8	227	R14642	Gamma interferon r
20	117	9.8	231	R14641	Gamma interferon r
21	117	9.8	473	R55749	Extracellular doma
22	117	9.8	489	R07469	Plasmd pBABE hu
23	117	9.8	942	R70113	Gamma-IFN-R-GBP 13
24	114.5	9.6	245	R62023	Soluble human inte
25	111	9.3	210	R14643	Gamma interferon r
26	95.5	8.0	575	W41803	Mouse IL-10 recept
27	95	7.9	578	R57138	Interleukin-10 rec
28	95	7.9	578	W41804	Human IL-10 recept
29	94.5	7.9	575	R57139	Interleukin-10 rec
30	93.5	7.8	219	W17734	Human truncated t1
31	93.5	7.8	263	W17725	Human tissue facto
32	92	7.7	251	R28067	Sequence encoded b
33	92	7.7	251	R42463	Truncated tissue f
34	92	7.7	251	W17746	Human truncated t1

35	92	7.7	251	W55781	Truncated tissue f
36	92	7.7	265	R80063	Human IFNAB-BPI en
37	92	7.7	295	P81503	Human tissue facto
38	92	7.7	295	P80504	Sequence encoded b
39	92	7.7	295	P80713	Complete sequence
40	92	7.7	295	R55178	Pre-hurph. Inhibit
41	92	7.7	295	W17716	Human tissue facto
42	92	7.7	295	W31532	Human tissue facto
43	92	7.7	295	W55780	Full length tissue
44	92	7.7	295	W59047	Human thromboplast
45	92	7.7	295	W98950	Human tissue facto

ALIGNMENTS

RESULT	ID	Query Match	Score	DB 1	Length	36
1	R14487	Standard: Protein: 436 AA.	100.0%	DB 1	436	
AC	R14487	16-JAN-1992 (first entry)				
DE	DT	Soluble Interferon-alpha/Beta receptor.				
KM	IFN; autoimmune disease; graft rejection; histocompatibility.					
OS	Homo sapiens.					
PN	FR2657881-A.					
PD	09-AUG-1991.					
PF	05-FEB-1990; 001298.					
PA	(EUBI-) LAB EURO BIOTECHNO.					
PI	Eld P. Gresser I, Lutfalla G, Meyer F, Mogensen KE;					
PI	Tovey MG, Dze G;					
DR	WPI; 91-319778/44.					
DR	N-PSDB; Q14239.					
PT	New water-soluble polypeptide(s) with affinity for IFN-alpha and					
PT	beta - used to treat e.g. lupus erythematosus, Behcet's disease,					
PT	aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.					
PS	Claim 2: Page 45; 52pp; French.					
CC	The transmembrane and cytoplasmic domains of the native IFN receptor					
CC	have been deleted to obtain a soluble, circulating form of the					
CC	receptor. Potentially immunogenic epitopes have thus been eliminated.					
CC	Derivatives obtained by substitution or deletion of this sequence					
CC	are also claimed as are hybrid molecules comprising the soluble					
CC	receptor (or deriv.) and an immunoglobulin such as IgG1.					
CC	See also Q14240.					
SQ	Sequence 436 AA;					
QY	1	MMVVLGATTLVAVGPMVLSAAGGKNDKSPQKVEVDIIDDNFIIRNRSDESVGNVT	100.0%	Score 1196;	DB 1;	Length 436;
		Best Local Similarity 100.0%; Pred No. 2.6e-115.				
		Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
DB	1	MMVVLGATTLVAVGPMVLSAAGGKNDKSPQKVEVDIIDDNFIIRNRSDESVGNVT				
QY	61	PSFYQGTGMDNWKLSGCONITSTKCNFSSKLINVEETKLRARAKENTSSYEVDSF				
DB	61	FSPFYQGTGMDNWKLSGCONITSTKCNFSSKLINVEETKLRARAKENTSSYEVDSF				
QY	121	TPFKKAIGPPEVLEADKAIVIHISPGTKDSYMAALDGLSTFYSLIKNNSGVPERI				
DB	121	TPFKKAIGPPEVLEADKAIVIHISPGTKDSYMAALDGLSTFYSLIKNNSGVPERI				
QY	181	ENISRKRIKYLSPETTYCKVKKALITSKIGYSPVHCIKTVENEL 229				
DB	181	ENISRKRIKYLSPETTYCKVKKALITSKIGYSPVHCIKTVENEL 229				
RESULT	2					
ID	R28495	Standard: Protein: 436 AA.				
AC	R28495					
DT	31-MAR-1993 (first entry)					

DE Sequence of a soluble form of the interferon (IFN) receptor
 DE with a high affinity for IFN-alpha and -beta.
 KW Interferon receptor; alpha-interferon; beta-interferon.
 OS Synthetic.
 PN WO9218626-A.
 PD 29-OCT-1992.
 PF 17-APR-1991; F00318.
 PR 17-APR-1991; WO-F00318.
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
 PI Eid P, Gresser I, Luftalla G, Meyer F, Mogensen KE,
 PI Tovey M, Uze G;
 DR MPI: 92-382110/46.
 DR N-PSDB: Q30532.
 PT Water soluble polypeptide(s) strongly bind interferon(s) alpha
 PT and beta - useful as immunosuppressants, for treating autoimmune
 PT diseases and transplant rejection
 PT Claim 2: Fig 1: 58pp: English.
 CC DNA encoding the water-soluble polypeptide with a high affinity for
 CC IFN-alpha and -beta is isolated by PCR, using appropriate
 CC oligonucleotides as primers and cloned cDNA as template. For example,
 CC bacteriophage lambda ZAP, containing the entire coding sequence of
 CC the IFN-alpha and -beta receptor (Q30533), was incubated with oligos
 CC Q30534 and Q30535. R28496 represents the complete receptor. R28495
 CC lacks the transmembrane and cytoplasmic domains. Both forms bind
 CC IFN in the same way as antibodies so are immunosuppressants e.g. for
 CC treating autoimmune diseases and graft rejection. They lack the
 CC toxic side-effects of known immunosuppressants such as steroids.
 SQ Sequence 436 AA.

Query Match 100.0%; Score 1196; DB 1; Length 436;
 Best Local Similarity 100.0%; Pred. No. 2,6e-115;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAVILGATTLVAVGAWVLSAAAGGNLSPKQVEVDIIDDNFILRNNSDSVGNVT 60
 DB 1 MAAVILGATTLVAVGAWVLSAAAGGNLSPKQVEVDIIDDNFILRNNSDSVGNVT 60
 QY 61 FSEDYQKTGMNWKILSGCONITSTKCNFSSKLNYEEIKLRIRAEKENTSSWYEVDSF 120
 DB 61 FSEDYQKTGMNWKILSGCONITSTKCNFSSKLNYEEIKLRIRAEKENTSSWYEVDSF 120
 QY 121 TPFRAQIGPPEVHLAEADKAIVHISPGTDSVMALDGLSFTYSLILMKNSSGVEERI 180
 DB 121 TPFRAQIGPPEVHLAEADKAIVHISPGTDSVMALDGLSFTYSLILMKNSSGVEERI 180
 QY 181 ENYSRHKIYKLSPTTYCLVKAKALLTSMKIGVSPVHCITTYVENEL 229
 DB 181 ENYSRHKIYKLSPTTYCLVKAKALLTSMKIGVSPVHCITTYVENEL 229

RESULT 3
 ID R71723 standard; Protein: 436 AA.
 AC R71723.
 DT 16-OCT-1995 (first entry)
 DE IFN receptor extracellular domain.
 KW IFN receptor; interferon receptor; interferon-alpha;
 KW interferon-beta; monoclonal antibody; immunomodulator; AIDS.
 OS Homo sapiens.
 PN MO9507716-A.
 PD 23-MAR-1994.
 PF 16-SEP-1994; E03114.
 PR 17-SEP-1993; EP-402279.
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
 PI Benizri EJ, Tovey MG;
 DR MPI: 95-131187/17.
 DR N-PSDB: Q86457.
 PT Composn. of monoclonal antibodies against interferon receptor -
 PT useful as immuno:modulator, eg. for treating AIDS
 CC Disclosure: Fig.2A-2B: 105pp: English.
 CC A recombinant soluble form of the human interferon class I receptor
 CC protein extracellular domain, given in R71723, was expressed in

CC either E. coli or COS cell hosts. The protein was used to raise
 CC immunomodulatory monoclonal antibodies.
 SQ Sequence 436 AA;

Query Match 100.0%; Score 1196; DB 1; Length 436;
 Best Local Similarity 100.0%; Pred. No. 2,6e-115;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAVILGATTLVAVGAWVLSAAAGGNLSPKQVEVDIIDDNFILRNNSDSVGNVT 60
 DB 1 MAAVILGATTLVAVGAWVLSAAAGGNLSPKQVEVDIIDDNFILRNNSDSVGNVT 60
 QY 61 FSEDYQKTGMNWKILSGCONITSTKCNFSSKLNYEEIKLRIRAEKENTSSWYEVDSF 120
 DB 61 FSEDYQKTGMNWKILSGCONITSTKCNFSSKLNYEEIKLRIRAEKENTSSWYEVDSF 120
 QY 121 TPFRAQIGPPEVHLAEADKAIVHISPGTDSVMALDGLSFTYSLILMKNSSGVEERI 180
 DB 121 TPFRAQIGPPEVHLAEADKAIVHISPGTDSVMALDGLSFTYSLILMKNSSGVEERI 180
 QY 181 ENYSRHKIYKLSPTTYCLVKAKALLTSMKIGVSPVHCITTYVENEL 229
 DB 181 ENYSRHKIYKLSPTTYCLVKAKALLTSMKIGVSPVHCITTYVENEL 229

RESULT 4
 ID R11958 standard; Protein: 557 AA.
 AC R11958.
 DT 18-JUL-1991 (first entry)
 DE Human alpha-interferon receptor protein.
 KW Human alpha-IFN; IFN agonists; antiviral; anti tumour agent;
 KW drug targeting.
 OS Homo sapiens.
 PN WO9105862-A.
 PD 02-MAY-1991.
 PF 19-OCT-1980; F00758.
 PR 20-OCT-1989; FR-013770.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 PI Mogensen KE, Uze G, Luftalla G, Gresser I;
 DR MPI: 91-148740/20.
 DR N-PSDB: Q11701.
 PT New human alpha-interferon receptor protein - useful for testing
 PT interferon agonists and in treatment or diagnosis
 PS Disclosure: Fig 4; 30pp: French.
 CC This recombinant human alpha interferon (IFN) receptor protein is
 CC useful for the testing of IFN agonists and for treatment and diag-
 CC nosis of viral diseases and tumours. Antibodies raised against
 CC this protein can be used for blocking the receptor when required,
 CC eg where overexpression of alpha-IFN is harmful. The Abs are
 CC also useful for eg drug targeting. Variants of the protein,
 CC having residue 164 (Thr) replaced by Arg and an Asp inserted
 CC between residues 479 and 480, are also useful.
 SQ Sequence 557 AA;

Query Match 100.0%; Score 1196; DB 1; Length 557;
 Best Local Similarity 100.0%; Pred. No. 3,7e-115;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAVILGATTLVAVGAWVLSAAAGGNLSPKQVEVDIIDDNFILRNNSDSVGNVT 60
 DB 1 MAAVILGATTLVAVGAWVLSAAAGGNLSPKQVEVDIIDDNFILRNNSDSVGNVT 60
 QY 61 FSEDYQKTGMNWKILSGCONITSTKCNFSSKLNYEEIKLRIRAEKENTSSWYEVDSF 120
 DB 61 FSEDYQKTGMNWKILSGCONITSTKCNFSSKLNYEEIKLRIRAEKENTSSWYEVDSF 120
 QY 121 TPFRAQIGPPEVHLAEADKAIVHISPGTDSVMALDGLSFTYSLILMKNSSGVEERI 180

Db 121 TPFKAOIGPEVHLEADKAIVHISPTKDSVMALDGLSFTYSLIKNNSGVEERI 180
|||||
Qy 181 ENISRRIKIKLSPETTYCLKVKAAALLTSWKIGVSPVHCIKITVENEL 229
|||||
Db 181 ENISRRIKIKLSPETTYCLKVKAAALLTSWKIGVSPVHCIKITVENEL 229

RESULT 5
R14488
ID R14488 standard; Protein: 557 AA.
AC R14488:
DT 16-JAN-1992 (first entry)
DE Complete Interferon-alpha/beta receptor.
KW IFN; autoimmune disease; graft rejection; histocompatibility.
OS Homo sapiens.
FH Key location/Qualifiers
FT domain 437..457
FT domain /label= transmembrane
FT domain 458..557
FT domain /label= cytoplasmic
FR2657881-A.
PN 09-AUG-1991.
PF 05-FEB-1990: 001298.
PA 05-FEB-1990: FR-001298.
PI (EUBI-) LAB EURO BIOTECHNO.
PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE;
PI Tovey MG, Uze G;
DR WPI: 91-319778/44.
DR N-PSDB: Q14240.
PT New water-soluble polypeptide(s) with affinity for IFN-alpha and
PT beta - used to treat e.g. lupus erythematosus, Behcet's disease,
PT aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.
PS Disclosure: Page 47: 52pp; French.
CC The invention covers derivatives of the interferon-alpha and/or beta
CC receptor obtained by deleting the transmembrane and cytoplasmic domains
CC of the native receptor or by substitution. Potentially immunogenic
CC epitopes are eliminated and the deriv. can be secreted from
CC transformed cells. Soluble deriv.s block the activity of IFN alpha/beta
CC and can be used to treat autoimmune diseases or to inhibit graft
CC rejection. See also Q14239.
SQ Sequence 557 AA:

Query Match 100.0%; Score 1196; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 3.7e-115;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMYVLLGATTLVYAVGPMWLSAAGGKNLSPQKEVDIIDNFIIRNRSDSVGNVT 60
|||||
Db 1 MMYVLLGATTLVYAVGPMWLSAAGGKNLSPQKEVDIIDNFIIRNRSDSVGNVT 60
|||||
Qy 61 FSPDYOKTGMDNWKILSGCONITSTKCNFSSKLNYEEIKLRIRAKENTSSMYEVSDF 120
|||||
Db 61 FSPDYOKTGMDNWKILSGCONITSTKCNFSSKLNYEEIKLRIRAKENTSSMYEVSDF 120
|||||
Qy 121 TPFKAOIGPEVHLEADKAIVHISPTKDSVMALDGLSFTYSLIKNNSGVEERI 180
|||||
Db 121 TPFKAOIGPEVHLEADKAIVHISPTKDSVMALDGLSFTYSLIKNNSGVEERI 180
|||||
Qy 181 ENISRRIKIKLSPETTYCLKVKAAALLTSWKIGVSPVHCIKITVENEL 229
|||||
Db 181 ENISRRIKIKLSPETTYCLKVKAAALLTSWKIGVSPVHCIKITVENEL 229
|||||

RESULT 6
R28496
ID R28496 standard; Protein: 557 AA.
AC R28496:
DT 31-MAR-1993 (first entry)
DE Sequence of a soluble form of the interferon (IFN) receptor
DE with a high affinity for IFN-alpha and -beta.
KW Interferon receptor; alpha-interferon; beta-interferon.

OS Synthetic.
PN W09218626-A.
PD 29-OCT-1992.
PF 17-APR-1991: F00318.
PR 17-APR-1991: WO-F00318.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,
PI Tovey M, Uze G;
DR WPI: 92-382110/46.
DR N-PSDB: Q30533.
PT Water soluble polypeptide(s) strongly bind interferon(s) alpha
PT and beta - useful as immunosuppressants, for treating autoimmune
PT diseases and transplant rejection
PS Claim 3; Fig 2; 58pp; English.
CC DNA encoding the water-soluble polypeptide with a high affinity for
CC IFN-alpha and -beta is isolated by PCR, using appropriate
CC oligonucleotides as primers and cloned cDNA as template. For example,
CC bacteriophage lambda ZAP, containing the entire coding sequence of
CC the IFN-alpha and -beta receptor (Q30533), was incubated with Q11905
CC Q30534 and Q30535. R28496 represents the complete receptor. R28495
CC lacks the transmembrane and cytoplasmic domains. Both forms bind
CC IFN in the same way as antibodies so are immunosuppressants e.g. for
CC treating autoimmune diseases and graft rejection. They lack the
CC toxic side-effects of known immunosuppressants such as steroids.
SQ Sequence 557 AA:

Query Match 100.0%; Score 1196; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 3.7e-115;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMYVLLGATTLVYAVGPMWLSAAGGKNLSPQKEVDIIDNFIIRNRSDSVGNVT 60
|||||
Db 1 MMYVLLGATTLVYAVGPMWLSAAGGKNLSPQKEVDIIDNFIIRNRSDSVGNVT 60
|||||
Qy 61 FSPDYOKTGMDNWKILSGCONITSTKCNFSSKLNYEEIKLRIRAKENTSSMYEVSDF 120
|||||
Db 61 FSPDYOKTGMDNWKILSGCONITSTKCNFSSKLNYEEIKLRIRAKENTSSMYEVSDF 120
|||||
Qy 121 TPFKAOIGPEVHLEADKAIVHISPTKDSVMALDGLSFTYSLIKNNSGVEERI 180
|||||
Db 121 TPFKAOIGPEVHLEADKAIVHISPTKDSVMALDGLSFTYSLIKNNSGVEERI 180
|||||
Qy 181 ENISRRIKIKLSPETTYCLKVKAAALLTSWKIGVSPVHCIKITVENEL 229
|||||
Db 181 ENISRRIKIKLSPETTYCLKVKAAALLTSWKIGVSPVHCIKITVENEL 229
|||||

RESULT 7
R42635
ID R42635 standard; Protein: 557 AA.
AC R42635:
DT 20-APR-1994 (first entry)
DE Human Interferon receptor.
KW IFN-R; extracellular domain; monoclonal antibody; viral infection;
KW cell proliferation; allograft rejection; systemic lupus erythematosus;
KW porphyrin; multiple sclerosis; Behcet's Disease; aplastic anaemia;
KW immunodeficiency; measles virus; interferon-alpha-beta.
OS Homo sapiens.
FH Key location/Qualifiers
FT domain 1..456
FT domain /label= extracellular-domain
FT domain /note= "soluble, immunogenic form of IFN-R"
PN EP-563487-A.
PD 06-OCT-1993.
PF 31-MAR-1992: 400902.
PR 31-MAR-1992: EP-400902.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
PI Benoit P, Maguire D, Meyer F, Plavec I, Tovey MG;
DR WPI: 93-312951/40.
DR P-PSDB: R42635.
PT Monoclonal antibody to human interferon type-I receptor - having
PT neutralising activity against human type I interferon, used for

PT therapy and diagnosis
 PS Disclosure: Fig 3: 21pp; English.
 CC Monoclonal antibodies produced against soluble forms of the human
 CC Interferon alpha-beta receptor based on the full-length human IFN-R
 CC sequence are claimed. The antibodies are useful for treatment and
 CC prophylaxis of disorders involving cell proliferation and/or viral
 CC infection.
 SQ Sequence 557 AA;

Query Match 100.0%; Score 1196; DB 1; Length 557;
 Best Local Similarity 100.0%; Pred. No. 3.7e-115;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MMVVLGATTLVAVGPNVLSAAGGNLSPQKVEVDIIDNFILRNRSDESGVNT 60
 DB 1 MMVVLGATTLVAVGPNVLSAAGGNLSPQKVEVDIIDNFILRNRSDESGVNT 60
 OY 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSLKLVYEIEIKLIRAEKENTSSWYEVDSF 120
 DB 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSLKLVYEIEIKLIRAEKENTSSWYEVDSF 120
 OY 121 TPFRAQIGPPEVHLEAEDEKAIIVHISPGTKDSVMALDGLSFTYSLILMKNSSGVEERI 180
 DB 121 TPFRAQIGPPEVHLEAEDEKAIIVHISPGTKDSVMALDGLSFTYSLILMKNSSGVEERI 180
 OY 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITTYENEL 229
 DB 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITTYENEL 229

RESULT 8
 ID R75356 standard; Protein: 557 AA.
 AC R75356:
 DT 16-OCT-1995 (first entry)
 DE Human IFN receptor.
 KW IFN receptor; Interferon receptor; Interferon-alpha;
 KW Interferon-beta; monoclonal antibody; Immunomodulator; AIDS.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT domain 1..436
 FT /label= Extracellular-domain
 PN W09507716-A.
 PD 23-MAR-1995.
 PF 16-SEP-1994; E03114.
 PR 17-SEP-1993; EP-402279.
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
 PI Benlert EJ, Tovey MG;
 DR N-PSDB: Q86458.
 PT Compn. of monoclonal antibodies against Interferon receptor
 PT useful as immuno-modulator, eg. for treating AIDS
 PS Disclosure: Fig. 3a-2b, 105pp; English.
 CC The amino acid sequence of human Interferon class I receptor is
 CC given in R75356. A recombinant soluble form of the extracellular
 CC domain of this receptor (R71723) has been used to raise
 CC immunomodulatory monoclonal antibodies.
 SQ Sequence 557 AA;

Query Match 100.0%; Score 1196; DB 1; Length 557;
 Best Local Similarity 100.0%; Pred. No. 3.7e-115;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MMVVLGATTLVAVGPNVLSAAGGNLSPQKVEVDIIDNFILRNRSDESGVNT 60
 DB 1 MMVVLGATTLVAVGPNVLSAAGGNLSPQKVEVDIIDNFILRNRSDESGVNT 60
 OY 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSLKLVYEIEIKLIRAEKENTSSWYEVDSF 120
 DB 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSLKLVYEIEIKLIRAEKENTSSWYEVDSF 120

OY 121 TPFRAQIGPPEVHLEAEDEKAIIVHISPGTKDSVMALDGLSFTYSLILMKNSSGVEERI 180
 DB 121 TPFRAQIGPPEVHLEAEDEKAIIVHISPGTKDSVMALDGLSFTYSLILMKNSSGVEERI 180
 OY 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITTYENEL 229
 DB 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITTYENEL 229

RESULT 9
 ID W21805 standard; Protein: 434 AA.
 AC W21805:
 DT 23-SEP-1997 (first entry)
 DE Spliced-deleted interferon alpha-receptor form 1.
 KW Interferon alpha-receptor; IFNAR.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT domain 1..427
 FT /label= Extracellular-domain
 FT /note= "comprises amino acids 1-427 of the
 FT transmembrane IFNAR"
 FT 428..434
 FT domain
 FT /label= S-domain
 PN A09475977-A.
 PD 11-MAY-1995.
 PF 20-OCT-1994; 075977.
 PR 24-OCT-1993; IL-107378.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PA (ABRAV/) ABRAMOVICH C.
 PI Abramovich C, Ratovitski E, Revel M;
 DR WPI: 95-200634/27.
 PT New mammalian soluble interferon alpha-receptor forms - used for
 PT inhibiting, modulating or modifying the activities of interferon(s)
 PS Example 2: Fig 7: 46pp; English.
 CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 1
 CC (W21805) is characterised by a new domain (S) which follows an
 CC end-deleted extracellular domain when compared to transmembrane
 CC IFNAR (W21804). There is no transmembrane domain. The amino acid
 CC sequence is predicted from a cDNA clone (see also R73520) obtd.
 CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR
 CC splice-deleted forms 1 and 2 (see also W21806) probably regulate
 CC the response of human cells to IFNs, either by acting as IFN
 CC antagonists or by regulating the activity of the multiple IFN
 CC subtypes. They can be expressed in host cells and used to inhibit,
 CC modulate or modify the activities of IFNs alpha and beta in cells,
 CC tissues and organisms, or for diagnostic purposes.
 SQ Sequence 434 AA;

Query Match 99.6%; Score 1191; DB 1; Length 434;
 Best Local Similarity .99.6%; Pred. No. 8.4e-115;
 Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MMVVLGATTLVAVGPNVLSAAGGNLSPQKVEVDIIDNFILRNRSDESGVNT 60
 DB 1 MMVVLGATTLVAVGPNVLSAAGGNLSPQKVEVDIIDNFILRNRSDESGVNT 60
 OY 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSLKLVYEIEIKLIRAEKENTSSWYEVDSF 120
 DB 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSLKLVYEIEIKLIRAEKENTSSWYEVDSF 120
 OY 121 TPFRAQIGPPEVHLEAEDEKAIIVHISPGTKDSVMALDGLSFTYSLILMKNSSGVEERI 180
 DB 121 TPFRAQIGPPEVHLEAEDEKAIIVHISPGTKDSVMALDGLSFTYSLILMKNSSGVEERI 180
 OY 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITTYENEL 229
 DB 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITTYENEL 229

RESULT 10
 W21806

ID W21806 standard: Protein: 496 AA.
AC W21806:
DT 23-SEP-1997 (first entry)
DE Spliced-deleted interferon alpha-receptor form 2.
KM Interferon alpha-receptor: IFNAR.
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 1..413
FT /label= Extracellular_domain
FT /note= "Comprises amino acid residues 1-413 and
422-427 of transmembrane IFNAR"
FT 420..496
FT domain /label= Intracellular_domain
FT /note= "comprises amino acids 481-557 of
transmembrane IFNAR"
PN A09475977-A.
PD 11-MAY-1995.
PF 20-OCT-1994: 075977.
PR 24-OCT-1993: IL-107378.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (ABRA/) ABRAMOVICH C.
PI Abramovich C, Ratovitski E, Revel M;
DR WPI: 95-200634/27.
PT New mammalian soluble interferon alpha-receptor forms - used for
PT inhibiting, modulating or modifying the activities of interferon(s)
PS Example 3; Fig 7; 46pp; English.
CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 2
CC (W21806) is characterised by a double deletion when compared to
CC transmembrane IFNAR (W21804). The extracellular domain is
CC shortened by 6 amino acid residues and is followed by a truncated
CC intracellular domain. There is no transmembrane region. The amino
CC acid sequence is predicted from a cDNA clone (see also T73521) obtd.
CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR
CC splice-deleted forms 1 (see also W21805) and 2 may regulate the
CC response of human cells to IFNs, either by acting as IFN
CC antagonists or by regulating IFN activities. They can be expressed
CC in host cells and used to inhibit, modulate or modify the
CC activities of IFNs alpha and beta in cells, tissues and organisms,
CC or for diagnostic purposes.
SQ Sequence 496 AA;

Query Match 99.6%; Score 1191; DB 1; Length 496;
Best Local Similarity 99.6%; Pred. No. 1e-114;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MMYVLLGATTLVAVGPMWLSAAGGNLKSPOKVEVDIIDDFILRMNSDESGVNT 60
DB 1 MMYVLLGATTLVAVGPMWLSAAGGNLKSPOKVEVDIIDDFILRMNSDESGVNT 60
QY 61 FSPDYOKTGMDNWKLSGCONITSTKCNFSSSLKLNVEEIKLRIRAKENTSSMYEVSF 120
DB 61 FSPDYOKTGMDNWKLSGCONITSTKCNFSSSLKLNVEEIKLRIRAKENTSSMYEVSF 120
QY 121 TPFKRAQIGPEVHLAEADKAIVIHISGTDVMAALDGLSFTYSLIKNNSGVEERI 180
DB 121 TPFKRAQIGPEVHLAEADKAIVIHISGTDVMAALDGLSFTYSLIKNNSGVEERI 180
QY 181 ENISYRHKIKYKLSPEETTCCLKVKKALLTSWKIGVSPVHCIKITVENEL 229
DB 181 ENISYRHKIKYKLSPEETTCCLKVKKALLTSWKIGVSPVHCIKITVENEL 229

RESULT 11
ID W21804
AC W21804 standard: Protein: 557 AA.
DT 23-SEP-1997 (first entry)
DE Transmembrane interferon alpha-receptor.
KM Interferon alpha-receptor: IFNAR.
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 1..436

FT domain /label= Extracellular_domain
FT 437..457
FT /label= Transmembrane_domain
FT 458..557
FT domain /label= Intracellular_domain
PN A09475977-A.
PD 11-MAY-1995.
PF 20-OCT-1994: 075977.
PR 24-OCT-1993: IL-107378.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (ABRA/) ABRAMOVICH C.
PI Abramovich C, Ratovitski E, Revel M;
DR WPI: 95-200634/27.
PT New mammalian soluble interferon alpha-receptor forms - used for
PT inhibiting, modulating or modifying the activities of interferon(s)
PS Disclosure; Fig 7; 46pp; English.
CC Human transmembrane interferon alpha receptor (IFNAR) (W21804)
CC includes a 21-amino acid transmembrane region. Novel, splice-
CC deleted IFNAR forms 1 (W21805) and 2 (W21806) have been detected
CC that lack this transmembrane domain. These, soluble non-membrane
CC bound polypeptides can be expressed in host cells and used to
CC inhibit, modulate or modify the activities of interferons alpha
CC and beta in cells, tissues and organisms, or for diagnostic
CC purposes.
SQ Sequence 557 AA;

Query Match 99.6%; Score 1191; DB 1; Length 557;
Best Local Similarity 99.6%; Pred. No. 1.2e-114;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MMYVLLGATTLVAVGPMWLSAAGGNLKSPOKVEVDIIDDFILRMNSDESGVNT 60
DB 1 MMYVLLGATTLVAVGPMWLSAAGGNLKSPOKVEVDIIDDFILRMNSDESGVNT 60
QY 61 FSPDYOKTGMDNWKLSGCONITSTKCNFSSSLKLNVEEIKLRIRAKENTSSMYEVSF 120
DB 61 FSPDYOKTGMDNWKLSGCONITSTKCNFSSSLKLNVEEIKLRIRAKENTSSMYEVSF 120
QY 121 TPFKRAQIGPEVHLAEADKAIVIHISGTDVMAALDGLSFTYSLIKNNSGVEERI 180
DB 121 TPFKRAQIGPEVHLAEADKAIVIHISGTDVMAALDGLSFTYSLIKNNSGVEERI 180
QY 181 ENISYRHKIKYKLSPEETTCCLKVKKALLTSWKIGVSPVHCIKITVENEL 229
DB 181 ENISYRHKIKYKLSPEETTCCLKVKKALLTSWKIGVSPVHCIKITVENEL 229

RESULT 12
ID W52296
AC W52296 standard: Protein: 325 AA.
DT 23-JUN-1998 (first entry)
DE CRFB4 protein.
KM CRFB4; Interleukin-10; IL-10; IL-10 receptor; allograft rejection;
KM vaccine; photosensitivity; inflammation; autoimmune disease;
KM septic shock; immune response; organ rejection; gene therapy.
OS Homo sapiens.
PN MO9802542-A1.
PD 22-JAN-1998.
PF 17-JUL-1997: U12455.
PR (UYNE-) UNIV NEW JERSEY.
PA Kotoenko SV, Pestka S;
PI WPI: 98-110590/10.
DR N-PSDB: V19874.
PT New recombinant DNA - comprises sequences encoding interleukin-10
PT and CRFB4 linked to operator, useful, e.g. preventing allograft
PT rejection.
PS Claim 2; Page -: 79pp; English.
CC This sequence is the human CRFB4 sequence, DNA encoding it is used in the
CC recombinant DNA (I) of the invention. (I) comprises a sequence (S1)
CC encoding the interleukin-10 (IL-10) receptor (IL10R) and a sequence (S2)

CC encodina CRPB4, both operably linked to expression control sequences.
CC Cells containing (1) may be used to identify agonists/antagonist of
CC IL-10. Agonists are potentially useful, e.g. for preventing allograft
CC rejection, as vaccine adjuvants, for treatment of photosensitivity,
CC inflammation, autoimmune disease and septic shock, while antagonists are
CC potentially useful for increasing immune responses against tumours,
CC viruses, bacteria and parasites (especially intracellular pathogens) and
CC for preventing organ rejection. A vector containing (1) is used to
CC restore, e.g. by gene therapy, IL-10 sensitivity to a cell that expresses
CC a dysfunctional IL10R and is able to bind IL-10 but not to transduce a
CC signal. Antisense CRPB4 sequences (especially ribozymes), can inhibit
CC IL-10 activity in cells. Antibodies specific for CRPB4 are used to
CC measure and localise CRPB4, for diagnosis of defective IL-10 activity.
CC Fragments of (1) are used as primers or probes to assay CRPB4-specific
CC RNA. Agonists/antagonists may be administered parenterally, orally or
CC rectally, especially by intravenous injection or directly into a tumour or
CC allograft. 325 AA:
CC Sequence

Query Match	18.6%	Score	222.5	DB	1	Length	325
Best Local Similarity	30.3%	Pred	No	4.7e-15			
Matches	66	Conservative	40	Mismatches	93	Indels	19
						Gaps	8

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QY      19  WYLSAAGGKNLKS-----PKAYEVDIIDNFIILRNRSDESGVNTFSFDYKXTGMD 71
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Db      3  WSLGSLGCGCLVSALGNVPPEVNRNNSVNFKNILQWESPAPAKGNLTFTAQY----LS 58

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09      72 NMIKSGCQNTSTKCNFSSLKLNYEEIKRIRAE-KENTSSWYEVDSFTPFRAQIGP 13
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Db 116 PGMQVEVLADSLHMRFLAPKIEENEYETWTMMNVNSNTYNVQYWKNGTDEKFQITPQYDF 177

Db 176 EVLRNLEPMTTCVQVGRGFLPRNRKAGEWSESPVCEQPT 213

ID	AC	Standard	Protein	332 AA
R75782				

DE IFN-gamma receptor beta-subunit.
KW Interferon-gamma receptor beta subunit; mIIFN;
KW interferon-gamma-antagonist.

Key	Location/Qualifiers
peptide	1..18
	/label= Sig-peptide
	10
	242

FT	domain	/label= Extracellular_domain
FT	domain	243..266
FT	domain	/label= Transmembrane_anchoring_domain
FT	domain	267..332

PN	MO9516036-A.	/rabel- cyclopiasmic_oumail
PD	15-JUN-1995.	
PF	07-DEC-1994; U14277.	

PA (AGUE/) AGUET M.
PA (BOEH/) BOEHNI R.
PA (HEMM/) HEMMI S.

DR WPI; 95-224321/29.
DR N-PSDB; Q90808.
PT Novel Interferon gamma receptor beta chain polypeptide - for treatment of inflammatory bowel disease and HIV disease

PT treatment of inflammatory bowel disease and liver damage
PS Claim 3; Fig. 2A; 86pp; English.
CC The IFN-gamma receptor beta-subunit encoded by a cDNA clone derived

CC from mouse B-cells is given in R75782. Recombinant beta-subunit,
CC pref. with the transmembrane anchoring domain deleted or
CC inactivated and with the cytoplasmic domain deleted, may be
CC may be used to treat pathological conditions associated with endogenous
CC IFN-gamma production.
50 Sequence 332 AA;

Query Match	17.0%	Score 203;	DB 1;	Length 332;
Best Local Similarity	30.1%	Pred. No. 4.9e-13;		
Matches 69; Conservative	38;	Mismatches 86;	Indels 36;	Gaps 13

Db
09
21
16
LGAASSPDSFSLAAPLNPRLILYNDQILTFEPPSPSNDPRVIVQVEYSF-----I 69

DB 70 DGSWHRLEPNCTDITERKCDLITGGGRUKLFPPPTFVLRVRAKRGNTLSKMWGLEPFOH 129

Db 130 YENVTGPKNKISVTPGKGLVHFSPPD---VFHGATFOYLVIHYEKSSETOOEVE 184

Db 185 GPKSKNSIVLGINKLPYRYCLOTEAOLILKNKKIRPHGLLSNVSCHETT 233

ID	RESULT
W79159	14
W79159	standard; Protein; 553 AA.
W79159	

DT 20-NOV-1998 (first entry)
DE zcyto17 cytokine receptor polypeptide.
KW zcyto7 cytokine receptor; ligand-binding polypeptide; kidney; pancreas; tissue;
KW type2 cytokine receptor family; CCR2; prostate; tissue; nervous tissue;

Key	Location/Qualifiers
AM	amniotic; cell proliferation; cell differentiation; fetal disease; human;
AN	anatomical; cell proliferation; cell differentiation; fetal disease; human;
AW	anatomical; cell proliferation; cell differentiation; fetal disease; human;
OS	osteoblast; cell proliferation; cell differentiation; fetal disease; human;
EH	endothelial; cell proliferation; cell differentiation; fetal disease; human;
Key	Location/Qualifiers

FT	Domain	275. .553	/note= "extracellular (ligand-binding) domain; sequence claimed in claim 1"
FT			
FT			
FT			

PN MO9837193-A1.
PD 27-AUG-1998
PE 18-FEB-1998; 003029.007

PR 20-FEB-1997; US-803305.
PA (ZYMO) ZYMOGENETICS INC.
PI Adams RL, Farrah TM, Jelmberg AC, Kho CJ, Lok S,
PI Whitmore TF.

DR W-1: 98-480756/41.
DR N-PSDB: V57515.
PT Novel human zcytor7 DNA encodes a type 2 cytokine receptor - useful for treating renal, neural, pancreatic and prostatic diseases

CC This represents the zcyto7 cytokine receptor. zcyto7 is a ligand-
CC binding receptor polypeptide and is a novel member of the type 2 cytokine
CC receptor family (CRF2). An expression vector containing the zcyto7

CC encoding a transmembrane and intracellular domain, or both, and a
CC transcriptional terminator can be used to transform host cells for the
CC recombinant production of the polypeptide. The sequences can be used to

CC also be used in the treatment of renal, pancreatic and prostatic cancer. Agonists of γ cyt β 7 can be used to stimulate proliferation and differentiation of cell in these organs. The antagonists and agonists can

CC also be used in the treatment of renal, neural, pancreatic and prostate
CC diseases. 553 AA;
CC Sequence

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 1, 2000, 04:17:54 ; Search time 23.82 Seconds

(Without alignments)
138,798 Million cell updates/sec

Title: US-09-240-675-2_COPY_1_229

Perfect score: 1196

Sequence: 1 MMVVLGATTLVAVGPMV.....WKIGVYSPVHCITVENEL 229

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 145308 seqs, 14437401 residues

Total number of hits satisfying chosen parameters: 145308

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCRTUS.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/Backfiles1.pep:*

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1196	100.0	434 1 US-08-328-256-11	Sequence 11, Appl
2	1196	100.0	436 2 US-08-307-588-2	Sequence 2, Appl
3	1196	100.0	496 1 US-08-328-256-12	Sequence 12, Appl
4	1196	100.0	557 1 US-08-328-256-10	Sequence 10, Appl
5	1196	100.0	557 2 US-08-471-454-2	Sequence 2, Appl
6	1196	100.0	557 2 US-08-466-974-2	Sequence 2, Appl
7	1196	100.0	557 2 US-08-471-453-2	Sequence 2, Appl
8	1196	100.0	557 2 US-08-307-588-4	Sequence 4, Appl
9	490.5	41.0	202 4 PCT-US84-14277-3	Sequence 4, Appl
10	222.5	18.6	325 2 US-08-683-743-4	Sequence 3, Appl
11	203	17.0	332 4 PCT-US94-14277-2	Sequence 4, Appl
12	192	16.1	223 4 PCT-US94-14277-6	Sequence 2, Appl
13	184.5	15.4	553 2 US-08-943-087-14	Sequence 2, Appl
14	184.5	15.4	553 2 US-08-943-087-12	Sequence 14, Appl
15	184.5	15.4	553 2 US-08-943-087-16	Sequence 16, Appl
16	184.5	15.4	553 2 US-08-943-087-18	Sequence 18, Appl
17	184.5	15.4	553 2 US-08-943-087-20	Sequence 20, Appl
18	184.5	15.4	553 2 US-08-943-087-22	Sequence 22, Appl
19	184.5	15.4	553 2 US-08-943-087-24	Sequence 24, Appl
20	184.5	15.4	553 2 US-08-943-087-26	Sequence 26, Appl
21	184.5	15.4	553 2 US-08-943-087-28	Sequence 28, Appl
22	184.5	15.4	553 2 US-08-943-087-30	Sequence 30, Appl
23	184.5	15.4	553 2 US-08-943-087-32	Sequence 32, Appl
24	184.5	15.4	553 2 US-08-943-087-34	Sequence 34, Appl
25	184.5	15.4	553 2 US-08-943-087-36	Sequence 36, Appl
26	184.5	15.4	553 2 US-08-943-087-38	Sequence 38, Appl
27	184.5	15.4	553 2 US-08-943-087-40	Sequence 40, Appl
28	184.5	15.4	553 2 US-08-943-087-42	Sequence 42, Appl
29	184.5	15.4	553 2 US-08-943-087-44	Sequence 44, Appl

30	184.5	15.4	553 2 US-08-943-087-46	Sequence 46, Appl
31	184.5	15.4	553 2 US-08-943-087-48	Sequence 48, Appl
32	174.5	14.6	221 2 US-08-943-087-56	Sequence 56, Appl
33	169.5	14.2	221 2 US-08-943-087-50	Sequence 50, Appl
34	168.5	14.1	221 2 US-08-943-087-52	Sequence 52, Appl
35	167.5	14.0	221 2 US-08-943-087-54	Sequence 54, Appl
36	165.5	13.8	221 2 US-08-943-087-58	Sequence 58, Appl
37	162.5	13.6	221 2 US-08-943-087-60	Sequence 60, Appl
38	149.5	12.5	337 4 PCT-US94-14277-8	Sequence 8, Appl
39	145	12.1	200 4 PCT-US94-14277-4	Sequence 4, Appl
40	140.5	11.7	574 2 US-08-906-713-2	Sequence 2, Appl
41	117.5	9.8	489 5 PCT-US93-11110-1	Sequence 1, Appl
42	117.5	9.8	489 5 PCT-US93-11110-1	Sequence 1, Appl
43	95.5	8.0	575 1 US-08-424-788-2	Sequence 2, Appl
44	95.5	8.0	575 1 US-08-110-683-4	Sequence 4, Appl
45	95.5	8.0	575 2 US-08-477-166-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-08-328-256-11

Sequence 11, Application US/08328256

Patent No. 5643749

GENERAL INFORMATION:

APPLICANT: REVEL, Michel

APPLICANT: ABRAMOVICH, Carolina

APPLICANT: RATOVITSKI, Edward

TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESS: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/328,256

FILING DATE: 24-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 107378

FILING DATE: 24-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: REVEL-13

REFERENCE/DOCKET NUMBER: 25,618

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 434 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-328-256-11

Query Match 100.0%; Score 1196; DB 1; Length 434;
Best Local Similarity 100.0%; Pred. No. 2,4e-126;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MMVLLGATTLVAVGPWVLSAAGGNLKSPOKVEVDIIDDNFILRNRSDESGVNT 60
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Db 61 FSPDYOKTGMNDWIKISGCONITSTKCNFSSSLKLVNVEIKLRIRAEKENTSSWYEVDSF 120
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Db 121 TPRKRAQIGPEVHLEADKAIVIHISPGTKDSVMALDGLSFTYSLILMKNSSGVEERI 180
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RESULT 2
US-08-307-588-2
; Sequence 2, Application US/08307588
; Patent No. 5919453
; GENERAL INFORMATION:
; APPLICANT: BENOIT, Patrick
; APPLICANT: MEYER, Francois
; APPLICANT: MAGUIRE, Deborah
; APPLICANT: PLAVEC, Ivan
; APPLICANT: TOVEY, Michael G.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/307,588
; FILING DATE: 05-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00770
; FILING DATE: 30-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92400902.0
; FILING DATE: 31-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 17283/117/GUPL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; INFORMATION FOR SEQ. ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 436 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-307-588-2

Query Match 100.0%; Score 1196; DB 2; Length 436;
Best Local Similarity 100.0%; Pred. No. 2,4e-126;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLLGATTLVAVGPWVLSAAGGNLKSPOKVEVDIIDDNFILRNRSDESGVNT 60
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Db 121 TPRKRAQIGPEVHLEADKAIVIHISPGTKDSVMALDGLSFTYSLILMKNSSGVEERI 180
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Db 181 ENIYSRHKIYKLSPEPTYCYLKVKAAALLTSWKIGVSPVHCICKITVENEL 229

RESULT 3
US-08-328-256-12
; Sequence 12, Application US/08328256
; Patent No. 5643749
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: ABRAMOVICH, Carolina
; APPLICANT: RATOVIJSKI, Edward
; TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,256
; FILING DATE: 24-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 107378
; FILING DATE: 24-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: REVEL-13
; REFERENCE/DOCKET NUMBER: 25,618
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ. ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 496 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-328-256-12

Query Match 100.0%; Score 1196; DB 1; Length 496;
Best Local Similarity 100.0%; Pred. No. 3e-126;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 121 TPFRAQOIGPEVHLEADKAIYHISPGTKDSVMALDGLSFTYSLIMKNSGVEERI 180
DB 121 TPFRAQOIGPEVHLEADKAIYHISPGTKDSVMALDGLSFTYSLIMKNSGVEERI 180
OY 181 ENIYSRHKIYKLSPEPTYCLVKAKALLTSWKIGVSPVHCITVENEL 229
DB 181 ENIYSRHKIYKLSPEPTYCLVKAKALLTSWKIGVSPVHCITVENEL 229

RESULT 4

US-08-328-256-10
Sequence 10 Application US/08328256
Patent No. 5643749
GENERAL INFORMATION:
APPLICANT: REVEL, Michel
APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
NUMBER OF SEQUENCES: 12
TITLE OF INVENTION: PREPARATION AND USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328, 256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: REVEL-13
REFERENCE/DOCKET NUMBER: 25, 618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-328-256-10

Query Match 100.0%; Score 1196; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 3, 6e-126;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 TPFRAQOIGPEVHLEADKAIYHISPGTKDSVMALDGLSFTYSLIMKNSGVEERI 180
OY 181 ENIYSRHKIYKLSPEPTYCLVKAKALLTSWKIGVSPVHCITVENEL 229

DB 181 ENIYSRHKIYKLSPEPTYCLVKAKALLTSWKIGVSPVHCITVENEL 229

RESULT 5

US-08-471-454-2
Sequence 2, Application US/08471454
Patent No. 5731169
GENERAL INFORMATION:
APPLICANT: MOGENSEN, Knud E.
APPLICANT: UZE, Gilles
APPLICANT: LOTFALLA, Georges
APPLICANT: GRESSER, Ion
TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,454
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-454-2

Query Match 100.0%; Score 1196; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 3, 6e-126;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MMYVLGATTLVLA VAGFWVLSAAGGNKLSPOKVEYDIIDNFI LRNRSDSVGNT 60
DB 1 MMYVLGATTLVLA VAGFWVLSAAGGNKLSPOKVEYDIIDNFI LRNRSDSVGNT 60
OY 61 FSPDQKGMNWKLSGCONITSTKCNFSLKLVNVEIKLRIRAEKNTSSWTEVDSF 120
DB 61 FSPDQKGMNWKLSGCONITSTKCNFSLKLVNVEIKLRIRAEKNTSSWTEVDSF 120
OY 121 TPFRAQOIGPEVHLEADKAIYHISPGTKDSVMALDGLSFTYSLIMKNSGVEERI 180
DB 121 TPFRAQOIGPEVHLEADKAIYHISPGTKDSVMALDGLSFTYSLIMKNSGVEERI 180
OY 181 ENIYSRHKIYKLSPEPTYCLVKAKALLTSWKIGVSPVHCITVENEL 229

DB 181 ENIYSHKIKYKSPETTYCLKVAALLTSMKIGVISPVCIKTTVENEL 229

RESULT 8

US-08-307-588-4

Sequence 4, Application US/08307588
Patent No. 5919453

GENERAL INFORMATION:

APPLICANT: BENOIT, Patrick

APPLICANT: MEYER, Francois

APPLICANT: MAGUIRE, Deborah

APPLICANT: PLAVEC, Ivan

APPLICANT: TOVEY, Michael G.

TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON

TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

ZIP: 20007

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/307,588

FILING DATE: 05-DEC-1994

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/00770

FILING DATE: 30-MAR-1993

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: EP 92400902.0

FILING DATE: 31-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: Saxe, Bernhard D.

REFERENCE/DOCKET NUMBER: 28,665

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 557 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-307-588-4

Query Match

Best Local Similarity 100.0%; Score 1196; DB 2; Length 557;

Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MMVVLGATTVLVANGPVVLSAAGKMLKSPQKVEVDIIDNFTLRNRSDESIGNV 60
DB 1 MMVVLGATTVLVANGPVVLSAAGKMLKSPQKVEVDIIDNFTLRNRSDESIGNV 60
DB 61 FSDYOKTGMDNMWIKLSCGONITSTKCNFSLKLVYEEIKLRIRAEKENTSSWYVDSF 120
DB 61 FSDYOKTGMDNMWIKLSCGONITSTKCNFSLKLVYEEIKLRIRAEKENTSSWYVDSF 120
DB 121 TPRRKAQIGPPEVHLAEADKAIVIHISPGTKDSVMALDGLSFTYSLLIMKNSSGVEERI 180
DB 121 TPRRKAQIGPPEVHLAEADKAIVIHISPGTKDSVMALDGLSFTYSLLIMKNSSGVEERI 180
DB 181 ENIYSHKIKYKSPETTYCLKVAALLTSMKIGVISPVCIKTTVENEL 229
DB 181 ENIYSHKIKYKSPETTYCLKVAALLTSMKIGVISPVCIKTTVENEL 229

RESULT 9

PCT-US94-14277-3

Sequence 3, Application PC/TUS9414277

GENERAL INFORMATION:

APPLICANT: Agnet, Michel

APPLICANT: Bohni, Ruth

APPLICANT: Hemmi, Silvio

TITLE OF INVENTION: Receptor Subunit Polypeptides

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/14277

FILING DATE: 07-DEC-1994

CLASSIFICATION:

APPLICATION NUMBER: 08/164596

FILING DATE: 09-DEC-1993

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.

REFERENCE/DOCKET NUMBER: 34,659

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-5530

TELEFAX: 415/952-9881

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 202 amino acids

TYPE: amino acid

TOPOLOGY: linear

PCT-US94-14277-3

Query Match

Best Local Similarity 41.0%; Score 490.5; DB 4; Length 202;

Matches 98; Conservative 34; Mismatches 69; Indels 1; Gaps 1;

DB 28 KNLKSPQKVEVDIIDNFTLRNRSDESIGNVTSFYDOKTGMDNMWIKLSCGONITSTK 87
DB 1 ENLKRPENIDXTIIDNFTLRNRSDESIGNVTSFYDOKTGMDNMWIKLSCGONITSTK 60
DB 88 NSSLKLVYEEIKLRIRAEKEN-TSSWYVDSFTPRKQIGPPEVHLAEADKAIVIH 146
DB 61 ESSLDTNXXIKTQPRVRAEENSTSMNVEDPFIPTAHMSPEVRLEREDKALIVH 120
DB 147 SPGTDOSVMALDGLSFTYSLLIMKNSSGVEERINISRAKITYLSPETTYCLKVAAL 206
DB 121 SPGDDGNMVALEKPSFSTIRIMQKSSDKKTINSTYVEKIPLLPBTYYCLEKAIH 180
DB 207 LPSWKIGVSPVHCIKTTVENE 228
DB 181 PSLKHSNVTXQCIISTIVANK 202

RESULT 10
US-08-683-743-4
Sequence 4, Application US/08683743
Patent No. 5843697
GENERAL INFORMATION:
APPLICANT: Pestka, Sidney

APPLICANT: Kotenko, Serguei
 TITLE OF INVENTION: CYTOKINE RECEPTOR SIGNAL TRANSDUCTION
 TITLE OF INVENTION: CHAIN
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David A. Jackson, Esq.
 STREET: 411 Hackensack Ave, Continental Plaza, 4th
 STREET: Floor
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/683,743
 FILING DATE: 17-JUL-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 601-1-050
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 201-343-1684
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 325 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 FRAGMENT TYPE:
 US-08-683-743-4

```

Query Match Similarity      18.6%: Score 222.5: DB 2: Length 325:
Best Local Similarity      30.3%: Pred No.5.6e-17:
Matches      66: Conservative      40: Mismatches      93: Indels      19: Gaps      8

QY      19  WVLAAAGCKNIKS-----PQKVEVDIIDNFIIRNRSDESGVNTFFSFYQKTGMD 71
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB      3  WSLGSLMGCLLYSALGWPPENVRMNSVFNKNIQLWQESPAFAGNLTFTAQY-----LS 58

QY      72  NWIKTSGGONITSTACNFSSSLKLNLYEEELKLIARAE-KENTISSWYEVDSFTPPRKAQIQP 130
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB      59  YRIFDCKCMNTTTLTCDYSS--LSKRYGHTLLVRAEFADSHSDWNI--TFCVDDTIITQP 115

QY      131 PEVLEA-EDKAIVYHIISPTKDSV-PMALDEL--SFTSLIIMKSSGVEERIEIENYSR 186
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB      116 PGMQVEVLADSLHMFAPAKRIENEVEYETIMKKNVYMSWITNYQWKNKGTIDEKQITPQIDPF 175

QY      187 HKIYKLSPEITTYCKLVKAAALLTSMTIGYSPVHCIKTT 224
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB      176 EVLRNLEPWTYYCVGRGFLPDRNRAGESVEPCEQT 213

RESULT  11
PCT-US94-1A277-2
: Sequence 2, Application PC/TUS941A277
: GENERAL INFORMATION:
: APPLICANT: Aguet, Michel
: APPLICANT: Bohnl, Ruth
: APPLICANT: Hemmi, Silvio
: TITLE OF INVENTION: Receptor Subunit Polypeptides
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd

```

CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 KB floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/14277
 FILING DATE: 07-DEC-1994
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/164596
 FILING DATE: 09-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Love, Richard B.
 REGISTRATION NUMBER: 34,659
 REFERENCE/DOCKET NUMBER: 866PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-5530
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 332 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

```

Query Match          17.0% Score 203; DB 4; Length 332;
Best Local Similarity 30.1%; Pred No. 9,le-15;
Matches    69; Conservative   38; Mismatches   86; Indels    36; Gaps     13.

QY      21 LSAAGG---KNKSPQKEVVDIIDNFI LRWNRSDS-----VGNVTFESFDYOKTGM 70
        ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db       16 LGAAASPDPSFSQLAPLNPRLHLYNDQLITWPESPSSNP RPVVYGVEYSF-----I 69
QY      71 D-NMIKL--SCCQNTSTXCNFSS---LKLVYE-EIKLRIRAEKEN-TSSMYEVDSTP 122
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Dd       70 DGSMRRLLEPNCTCIETEKCDLTGGGRKLPHPEFTVLRYRAKGNGNLTSKWVGLPTQH 129
QY      123 FRKAQIGPE-VHD EADKAIVIHISPECTKSVMALDGSEFYSLLIMKNSGVGEERIE 181
        : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db       130 YENVTVGPDPKIISTYPGKGS LVTHFSPEF----VFHGATFYOLVIHWKXSSETQQEOVE 184
QY      182 NIVERHKIY-KLSPETTYCLKVKRAL-LTSMKI--GYVPVHCIRT 224
        : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Dd       185 GFPMNSNIYLGNLKRPRYCLOTENQILLNKKRI RPHOLS NVSCHETT 233


RESULT 12
PCT-US94-14277-6
: Sequence 6, Application PC/TUS9414277
: GENERAL INFORMATION:
: APPLICANT: Aguet, Michel
: APPLICANT: Bohni, Ruth
: APPLICANT: Hemmi, Silvio
: TITLE OF INVENTION: Receptor Subunit Polypeptides
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
```

SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14277
FILING DATE: 07-DEC-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/164596
FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 866PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US94-14277-6

Query Match 16.1%; Score 192; DB 4; Length 223;
Best Local Similarity 29.6%; Pred. No. 8.5e-14;
Matches 64; Conservative 37; Mismatches 83; Indels 32; Gaps 12;

OY 30 LKSPQKEVDIIDNFIEMNRSDS-----VGNVTFSDYQKGM-D-NWIKL--SGGQ 80
DB 10 LARPLNRLHLNDGOILLWEPSSNDPRVYQVEISF-----IDSMHRLLEPNT 63
OY 81 NITKCNFSS---KLNYE-EIKLRIRAKEN-TSSWYEVDSFTPFKAQIGPE-VH 134
DB 64 DITEFKDLTGGRKLKLFHPFTVFLVRARAKGNLTSKMGVLEPQHYENVTGVPKXNS 123
OY 135 LEAEKAIYHISPTKDSVMALDGLSTYSLLIMKNSGVEERIENTYSHKTY--KL 192
DB 124 VPPGKSLVHNSPPED-----VFHGATFOYLWHYWEKSETOOEVEGPKSNSIVLGNL 178
OY 193 SPETTYCLKVKAAL-LTSMKI---GVYSPVHCITTT 224
DB 179 KPRVYCUTERQILIKKIKRPHGLLSNVSCHEIT 214

RESULT 13
US-08-943-087-2
Sequence 2, Application US/08943087
Patent No. 5945511

GENERAL INFORMATION:

APPLICANT: Lok, Si
APPLICANT: Kho, Choon J.
APPLICANT: Jelmsberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Fairah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943.087
FILING DATE:

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-943-087-2

Query Match 15.4%; Score 184.5; DB 2; Length 553;
Best Local Similarity 26.3%; Pred. No. 2.4e-12;
Matches 55; Conservative 38; Mismatches 95; Indels 21; Gaps 7;

OY 11 LVLVAVGPM--VLSAAGKNLKSPQKEVDIIDNFIEMNRSDSEVG-NVTFSPDYQK 67
DB 18 LLLLAAPMGAVPCVSGG--LPRKANITFSLINKNVLTPTPEGLOGVYVTTVOYFI 75
OY 68 TGMNWKRLSGCONITSTKCNFSSIKLVYEIKLRIRAKEN-TSSWYEVDSFTPFKA 126
DB 76 YGKKWLKSCBKNINRTYCDLSAETSDYEHQYAKVKAIMGTCOSKMAESGRFPFLET 135
OY 127 QIGPEVHLEAEKAIYHISPTK-----DSVMALDGLSTYSLLIMKNSGVE 177
DB 136 QIGPEVALITDEKISIVLTAPEKWKRPEDLPVSMOQIYSNLKYNVSVLNTKSNRTWS 195
OY 178 ERIENTYSHKTYK--LSPETTYCLKVKA 204
DB 196 QCVTN---HTLVLTWLEPNTLYCVHVES 220

RESULT 14
US-08-943-087-14
Sequence 14, Application US/08943087
Patent No. 5945511

GENERAL INFORMATION:

APPLICANT: Lok, Si
APPLICANT: Kho, Choon J.
APPLICANT: Jelmsberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Fairah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943.087
FILING DATE:
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-943-087-14

Query Match 15.4%; Score 184.5; DB 2; Length 553;
Best Local Similarity 26.3%; Pred. No. 2.4e-12;
Matches 55; Conservative 38; Mismatches 95; Indels 21; Gaps 7;
OY 11 LVLVAVGPW-VLSAAGGNLKSPOKVEVDIIDNFILRMNRSDSVG-NYTFSPDYOK 67
DB 18 LLLLAAPMGRAVPCVSGG--LPKPANITFLSINKKNVLOMTPEGLQGVKAVITVQYFI 75
OY 68 TGMQMWIKLSCGONITSTKCNFSSILKNVEEIKLRIRAEKENTSSWYEVDSFTPFKRA 126
DB 76 YGOKRWLNKSECRNINRTYCDLSAETSDEHQYAKAKAIWGTCKSKWAESGRFPFLET 135
OY 127 QIGPEVHLEADKAIVHISPGR-----DSVMALDGLSTFTYSLIMKNSGVE 177
DB 136 QIGPEVALTTDEKISIVLTAPKWKRNPEDLPVSMQIYSNLKYNVSLNTRKSNRTWS 195
OY 178 ERIENIYSRHKIYK--LSPETTYCLKVKA 204
DB 196 QCVTN---HTLVLTWLEPNTLYCVHVES 220

RESULT 15
US-08-943-087-16
Sequence 16, Application us/08943087
Patent No. 5945511
GENERAL INFORMATION:
APPLICANT: Lok, SI
APPLICANT: Kho, Choon J.
APPLICANT: Jelmeberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: us/08/943,087
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-943-087-16

Query Match 15.4%; Score 184.5; DB 2; Length 553;
Best Local Similarity 26.3%; Pred. No. 2.4e-12;
Matches 55; Conservative 38; Mismatches 95; Indels 21; Gaps 7;
OY 11 LVLVAVGPW-VLSAAGGNLKSPOKVEVDIIDNFILRMNRSDSVG-NYTFSPDYOK 67
DB 18 LLLLAAPMGRAVPCVSGG--LPKPANITFLSINKKNVLOMTPEGLQGVKAVITVQYFI 75
OY 68 TGMQMWIKLSCGONITSTKCNFSSILKNVEEIKLRIRAEKENTSSWYEVDSFTPFKRA 126
DB 76 YGOKRWLNKSECRNINRTYCDLSAETSDEHQYAKAKAIWGTCKSKWAESGRFPFLET 135
OY 127 QIGPEVHLEADKAIVHISPGR-----DSVMALDGLSTFTYSLIMKNSGVE 177
DB 136 QIGPEVALTTDEKISIVLTAPKWKRNPEDLPVSMQIYSNLKYNVSLNTRKSNRTWS 195
OY 178 ERIENIYSRHKIYK--LSPETTYCLKVKA 204
DB 196 QCVTN---HTLVLTWLEPNTLYCVHVES 220

Search completed: June 1, 2000, 04:17:55
Job time: 15449 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 1, 2000, 04:35:14 ; Search time 64.83 Seconds

(without alignments)
207,099 Million cell updates/sec

Title: US-09-240-675-2_COPY_1_229

Perfect score: 1196

Sequence: 1 MMYVLGATTLVAVGPMV.....WKIGVSPVHCITVENEL 229

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 168808 segs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : PIR_63:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1196	100.0	557	A32694	Interferon alpha/b
2	782.5	65.4	560	S27387	Interferon alpha r
3	600.5	50.2	590	A45283	Interferon alpha/b
4	227.5	19.0	273	G01418	Cytokine receptor
5	222.5	18.6	325	A47003	Cytokine receptor
6	220	18.4	349	JC6311	Interleukin-10 rec
7	203	17.0	332	A49947	Interferon gamma r
8	151.5	12.7	337	I38500	Interferon gamma r
9	117.5	9.8	489	A31555	Interferon gamma r
10	102.5	8.6	477	A34368	Interferon gamma r
11	97.5	8.2	6831	T27934	hypothetical prote
12	97.5	8.2	6839	S57242	twilchin - Caenor
13	97.5	8.2	7160	T27935	hypothetical prote
14	95.5	8.0	925	A49667	Interleukin-10 rec
15	95.5	8.0	925	T29585	hypothetical prote
16	95	7.9	578	I56315	Interleukin-10 rec
17	92.5	7.7	292	KFB03	tissue factor prec
18	92	7.7	295	KFB03	tissue factor prec
19	91.5	7.7	6805	S20901	titin - rabbit (fr
20	90.5	7.6	1304	A46546	leukocyte common a
21	90	7.5	315	S14222	chalcone reductase
22	89.5	7.5	880	JC4166	protein-tyrosine k
23	89.5	7.5	2033	T09123	hybrid receptor so
24	89.5	7.5	2215	T00348	Lrll protein - mou
25	89	7.4	331	A54295	Interferon alpha/b
26	89	7.4	331	S59501	Interferon recepto
27	89	7.4	515	S59502	Interferon recepto
28	89	7.4	1152	S20106	hypothetical prote
29	88.5	7.4	1220	S64816	probable membrane
30	88	7.4	515	I39073	Interferon alpha-b

31	87	7.3	639	2	JC1391	dnak-type molecula
32	87	7.3	1083	2	T23031	hypothetical prote
33	87	7.3	1120	2	S67208	hypothetical prote
34	87	7.3	26926	1	I38344	titin, cardiac mus
35	86.5	7.2	429	2	S59773	26S proteasome reg
36	86	7.2	2131	2	S01446	hypothetical prote
37	84.5	7.1	623	1	VGBE68	glycoprotein E - h
38	83.5	7.0	306	2	A25698	probable protein x
39	83.5	7.0	430	2	T14420	S-luciferase
40	83	6.9	335	2	JT0569	chondromodulin-I p
41	83	6.9	359	2	J50734	endo-1,4-beta-xyla
42	83	6.9	520	2	T04591	ferulate-5-hydroxy
43	82.5	6.9	378	2	T04239	hypothetical prote
44	82.5	6.9	406	2	B64432	capsular polysacch
45	82.5	6.9	1068	2	S01519	hypothetical prote

ALIGNMENTS

RESULT 1
A32694

Interferon alpha/beta receptor precursor - human

C:Species: Homo sapiens (man)

C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 22-Oct-1999

C:Accession: A32694; S17112

R:Uze, G.; Lutfalla, G.; Gresser, I.

Cell 60, 225-234, 1990

A:Title: Genetic transfer of a functional human interferon alpha receptor into mouse

A:Reference number: A32694; MUID:90124632

A:Accession: A32694

A:Molecule type: mRNA

A:Residues: 1-557 <UZE>

A:Cross-references: GB:J03171; MID:9184645; PID:AAA52730.1; PID:9306914

R:Luftalla, G.

submitted to the EMBL Data Library, July 1991

A:Description: The structure of the human interferon alpha/beta receptor gene.

A:Reference number: S17112

A:Accession: S17112

A:Molecule type: DNA

A:Residues: 1-16, 'V', '18-329, 'V', '343-557 <LUT>

A:Cross-references: EMBL:X60459; MID:932671

C:Genetics:

A:Gene: GDB:IFNARI; IFNAR; IFRC

A:Cross-references: GDB:120078; OMIM:107450

A:Map position: 21q22.1-21q22.1

A:Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3

C:Keywords: cytokine receptor; glycoprotein; transmembrane protein

F1-21/Domaln: transmembrane #status predicted <TRN2>

F:437-455/Domaln: transmembrane #status predicted

F:50,58,81,88,110,172,254,313,314,376,416,433,507,518,537/Binding site: carbohydrate

Query Match

Best Local Similarity

Matches 229; Conservative

100.0%; Score 1196; DB 2; Length 557;

100.0%; Pred. No. 5.5e-97;

Mismatches 0; Indels 0; Gaps 0;

1 MMYVLGATTLVAVGPMVLSAAGKRLKSPQKVEVDIIDNFTLRNRSDESGVNT 60

1 MMYVLGATTLVAVGPMVLSAAGKRLKSPQKVEVDIIDNFTLRNRSDESGVNT 60

1 MMYVLGATTLVAVGPMVLSAAGKRLKSPQKVEVDIIDNFTLRNRSDESGVNT 60

1 MMYVLGATTLVAVGPMVLSAAGKRLKSPQKVEVDIIDNFTLRNRSDESGVNT 60

1 MMYVLGATTLVAVGPMVLSAAGKRLKSPQKVEVDIIDNFTLRNRSDESGVNT 60

1 MMYVLGATTLVAVGPMVLSAAGKRLKSPQKVEVDIIDNFTLRNRSDESGVNT 60

1 MMYVLGATTLVAVGPMVLSAAGKRLKSPQKVEVDIIDNFTLRNRSDESGVNT 60

1 MMYVLGATTLVAVGPMVLSAAGKRLKSPQKVEVDIIDNFTLRNRSDESGVNT 60

1 MMYVLGATTLVAVGPMVLSAAGKRLKSPQKVEVDIIDNFTLRNRSDESGVNT 60

1 MMYVLGATTLVAVGPMVLSAAGKRLKSPQKVEVDIIDNFTLRNRSDESGVNT 60

1 MMYVLGATTLVAVGPMVLSAAGKRLKSPQKVEVDIIDNFTLRNRSDESGVNT 60

1 MMYVLGATTLVAVGPMVLSAAGKRLKSPQKVEVDIIDNFTLRNRSDESGVNT 60

1 MMYVLGATTLVAVGPMVLSAAGKRLKSPQKVEVDIIDNFTLRNRSDESGVNT 60

1 MMYVLGATTLVAVGPMVLSAAGKRLKSPQKVEVDIIDNFTLRNRSDESGVNT 60

```
RESULT 2
27387
Interferon alpha receptor type 1 precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S27387; S33770
R:Mouchel-Vielh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G.
FEBS Lett. 313, 255-259, 1992
A:Title: Specific antiviral activities of the human alpha interferons are determined at
A:Reference number: S27387; MUID:93076908
A:Accession: S27387
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-560 <MCU>
A:Cross-references: EMBL:X68443; NID:g4331; PIDN:CAA48484.1; PID:g4332
R:Lim, J.K.; Langer, J.A.
Biochim. Biophys. Acta 1173, 314-319, 1993
A:Title: Cloning and characterization of a bovine alpha interferon receptor.
A:Accession: S33770; MUID:93305725
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-421, 'V', 423-560 <LIN>
A:Cross-references: EMBL:I06320; NID:g163187; PIDN:AAA02571.1; PID:g163188
C:Keywords: antiviral; cytokine receptor; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-560/Product: Interferon alpha receptor type 1 #status predicted <MAY>

Query Match 65.4%; Score 782.5; DB 2; Length 560;
Best Local Similarity 67.1%; Pred. No. 6,5e-61;
Matches 155; Conservative 31; Mismatches 40; Indels 5; Gaps 5;

Oy 2 MVLIGATTLVAVGPNVLSAAGKNLSPQKVEVDIIDNFILRNKSDSVGNVF 61
Db 1 MLALIGATTLMLVA-GRWVLPASGEANLK-PENVEIHIIDNFFLNKSSSESVKNVTF 58

Oy 62 SFDOYKTMGMNWKILSGCONITSTKCNFSSILK-LNVEEILRLRAEK-ENTSSMYEVSF 119
Db 59 SADIQIIDLTDNMKRLSGCGHTSTKCNFSSVLEWVEKIELRLRAEGNNTSTWYVEP 118

Oy 120 FTPEKAOIGPPEVHLAEADKAIVIHIS-PGTKDSVMALDGLSTFYLLIMKNSGVVEE 178
Db 119 FVPELEAIGPPVHLAEADKAILISIPGTKDSIMAMDRSSFRYSVYIMKNSSLDE 178

Oy 179 RIENYSRHKIYKLSPEPTYCLKVAALLTSWKIGVSPVHCITTVENEL 229
Db 179 RTEVYPEDKIYKLSPEITYCLKVAELRLQSRVGCSPVYCINTTERHKV 229

RESULT 3
A45283
Interferon alpha/beta receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A45283; I48423; I48425; I48426; I48427; I48428; I48429
R:Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992
A:Title: Behavior of a cloned murine interferon alpha/beta receptor expressed in homosp
A:Reference number: A45283; MUID:92262522
A:Accession: A45283
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-590 <UZE>
A:Cross-references: GB:M8961; NID:g194111; PIDN:AAA37890.1; PID:g194112
R:Lutfalla, G.; Uze, G.
Gene 148, 343-346, 1994
A:Title: Structure of the murine interferon alpha/beta receptor-encoding gene: high-fre
A:Reference number: I48423; MUID:95047447
```

```
A:Accession: I48423
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 118-125 <RS>
A:Cross-references: EMBL:U06237; NID:g497103; PIDN:AAA65003.1; PID:g755810
A:Accession: I48424
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 127-224 <RE2>
A:Cross-references: EMBL:U06238; NID:g497104; PIDN:AAC01749.1; PID:g755811
A:Accession: I48425
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 243-264 <RE3>
A:Cross-references: EMBL:U06239; NID:g497106; PIDN:AAA65004.1; PID:g510261
A:Accession: I48426
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 265-375 <RE4>
A:Cross-references: EMBL:U06240; NID:g497108; PIDN:AAA65005.1; PID:g510262
A:Accession: I48427
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 397-424 <RE5>
A:Cross-references: EMBL:U06241; NID:g497110; PIDN:AAA65006.1; PID:g755812
A:Accession: I48428
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 426-445 <RE6>
A:Cross-references: EMBL:U06242; NID:g497112; PIDN:AAA65007.1; PID:g755813
A:Accession: I48429
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 473-590 <RE7>
A:Cross-references: EMBL:U06244; NID:g497114; PIDN:AAA65008.1; PID:g510265
C:Gene: IFNAR
A:Introns: 177/3; 331/1
C:Keywords: cytokine receptor; transmembrane protein

Query Match 50.2%; Score 600.5; DB 2; Length 590;
Best Local Similarity 52.0%; Pred. No. 6,4e-45;
Matches 119; Conservative 40; Mismatches 69; Indels 1; Gaps 1;

Oy 2 MVLIGATTLVAVGPNVLSAAGKNLSPQKVEVDIIDNFILRNKSDSVGNVF 61
Db 1 MLAVGAAALVAVAGAPWVLPASAGENLKPENIDVIYIIDNVTLLKSSHGSGSVTF 60

Oy 62 SFDOYKTMGMNWKILSGCONITSTKCNFSSILK-LNVEEILRLRAEK-NTSSMYEVSF 120
Db 61 SAERTKDEAKWLKVPQCGTTTTCCEFSILDINVIYIKFOFRABEGNNTSSMNEVDF 120

Oy 121 TPPEKAOIGPPEVHLAEADKAIVIHIS-PGTKDSVMALDGLSTFYLLIMKNSGVVEE 180
Db 121 IPFYTAMSPPEVHLAEADKAILIVHISPPGODNNMNALEPSPYIRIWKSSSDKRTI 180

Oy 181 ENIYSRHKIYKLSPEPTYCLKVAALLTSWKIGVSPVHCITTVENEL 229
Db 181 NSTIYKEIPELLEPTYCLEVKAHPSLKKHNSIVTCISTIVANKM 229

RESULT 4
G01418
Cytokine receptor family II, member 4 - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
C:Accession: G01418
R:Lutfalla, G.
submitted to the EMBL Data Library, April 1994
A:Reference number: G06935
A:Accession: G01418
A:Status: preliminary; translated from GB/EMBL/DBJ
```


OY 182 NIYSRHKIY--KLSPETTYCLKVKAAL.LTSNKI--GYSPVHCITKT 224
 DB 185 GPFKNSIIVGLNLRKPYRYVCIQTEAQLILKNKKIRPHGLLSVSCHEET 233

RESULT 8
 138500

Interferon gamma receptor accessory factor-1 precursor - human

C:Species: Homo sapiens (man)
 C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 05-Nov-1999

C:Accession: 138500; 138501
 R:Son, J.; Donnelly, R.J.; Kotenko, S.; Mariano, T.M.; Cook, J.R.; Wang, N.; Emanuel, S.

Cell 76, 793-802, 1994

A:Title: Identification and sequence of an accessory factor required for activation of

A:Reference number: A4946; MUID:941170380

A:Accession: 138500

A:Molecule type: mRNA

A:Residues: 1-337 <RES>

A:Cross-references: EMBL:U05875; NID:9463549; PIDN:AAA16955.1; PID:9463550

A:Experimental source: clone pSK1

A:Accession: 138501

A:Molecule type: mRNA

A:Residues: 1-63, 'Q', 65-337 <RES>

A:Cross-references: EMBL:U05877; NID:9463551; PIDN:AAA16956.1; PID:9463552

A:Experimental source: clone pJS3

C:Genetics:

A:Map position: 21

C:Keywords: cytokine receptor

Query Match 12.7%; Score 151.5; DB 2; Length 337;
 Best Local Similarity 24.6%; Pred. No. 7.3e-06;
 Matches 61; Conservative 44; Mismatches 94; Indels 49; Gaps 13;

OY 12 VLVANGPVLAAAG---KNLSPQKVEVDIIDNFILRW-----NRSDSVGNVTF 62

DB 9 LLLLLGVFAAAAPDPLSQLPAOHPIRLYNAEQVLSWEPVALNSTREVVYRVQFK 68

OY 63 FDYOKTGMNDWIKLS-----GCONITSTKCNFSS-----LKLNYEEIKLRIRAEK 108

DB 69 YIDSK-----WFTADIMSGVNCOTITATECFPTAASBAGPMDPNV---TLRLRAEL 119

OY 109 ENT-SSWEVDSFTPFRRKAGIPPEVHLE--AEDKAIYIHISPTKDSVMALDGLSFT 164

DB 120 GALHSAWMTMPWFQHYRNVTVGPPE-NIEVTEGEGSLIRFSSPDIDTSTAF---FC 174

OY 165 YSLLMKSSSGVEERIENTIYSRHKIY--KLSPETTYCLKVKAALTS---WKIGVYSPV 218

DB 175 YVVAHWE--KGGIQOVKGFPRNSISLNDLKPSSRYCLOVQQLLMKNSNIFRGHLSNI 232

OY 219 HCITKTV 226

DB 233 SCYETMAD 240

RESULT 9

A13555 Interferon gamma receptor precursor - human

C:Species: Homo sapiens (man)
 C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 23-Jul-1999

C:Accession: A13555

R:Aguet, M.; Dembic, Z.; Merlin, G.

Cell 55, 273-280, 1988

A:Title: Molecular cloning and expression of the human interferon-gamma receptor.

A:Reference number: A13555; MUID:89003065

A:Accession: A13555

A:Molecule type: mRNA

A:Residues: 1-489 <AG>

A:Cross-references: GB:J03143; NID:9184650; PIDN:AAA52731.1; PID:9306915

C:Genetics:

A:Gene: GDB:IFNGR1; IFNGR

A:Cross-references: GDB:120668; OMIM:107470

A:Map position: 6q23-6q24
 C:Superfamily: Interferon gamma receptor
 C:Keywords: cytokine receptor; transmembrane protein

Query Match 9.8%; Score 117.5; DB 2; Length 489;
 Best Local Similarity 22.6%; Pred. No. 0.011;
 Matches 52; Conservative 44; Mismatches 99; Indels 35; Gaps 8;

OY 3 VVLGATLVVANGPVLAA--AGCKNLKSPQKVEVDIIDNFILRMNNSDESQGVN-T 60

DB 1 MALFLPLVWQGVSRKEMGTADIGSSVPTPIVNTIESINMFIWYEW--QIMPOVPV 58

OY 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSSLKLNYEEIKLRIRAE--EKENTSSWYEV 117

DB 59 FTVEVKVYGVKNSWIMDIACINISHYCNINSDHGDPSNLMVRKAVGQKE--SAVAKS 116

OY 118 DSFTPFRRKAGIPPEVHLEEDKAIYTHI-----SFGTK-----DSVMW 136

DB 117 EEFAVCRDGRKIGPKLDIRKEEKOIMIDIRHPSVYVNGDEQVVDYDETCYIRVNVVY 176

OY 157 ALDGLSTYSLLIKWNSGVEERIENTIYSRHKIYKLSPEITTYCLKVKAAL 206

DB 177 RMNSETIQYKILTK-----EDCDEIQCOLAIPVSLNSQYCSAGCVL 221

RESULT 10

A34368 Interferon gamma receptor precursor - mouse

C:Species: Mus musculus (house mouse)
 C:Date: 08-Jun-1990 #sequence_revision 08-Jun-1990 #text_change 23-Jul-1999

C:Accession: A34368; A34369; A34423; A34508; A36224; 148941

R:Kumar, C.S.; Muthukumar, G.; Frost, L.J.; Noe, M.; Ahn, Y.H.; Mariano, T.M.; Pes

J.; Biol. Chem. 264, 17939-17946, 1989

A:Title: Molecular characterization of the murine interferon gamma receptor cDNA.

A:Reference number: A34368; MUID:90036866

A:Accession: A34368

A:Molecule type: mRNA

A:Status: preliminary

A:Residues: 1-477 <KMG>

A:Cross-references: GB:M25764; NID:9197962; PIDN:AAA39177.1; PID:9309393

R:Cofano, F.; Moore, S.K.; Tanaka, S.; Yuhki, N.; Landolfo, S.; Appella, E.

J. Biol. Chem. 265, 4064-4071, 1990

A:Title: Affinity purification, peptide analysis, and cDNA sequence of the mouse int.

A:Reference number: A34468; MUID:90154099

A:Accession: A34468

A:Molecule type: mRNA

A:Residues: 1-477 <COE>

A:Cross-references: GB:M28711; NID:9197964; PIDN:AAA39178.1; PID:9309394

R:Gray, P.W.; Leong, S.; Fennie, E.H.; Farrer, M.A.; Pingel, J.T.; Fernandez-Luna, J

Proc. Natl. Acad. Sci. U.S.A. 86, 8497-8501, 1989

A:Title: Cloning and expression of the cDNA for the murine interferon gamma receptor

A:Reference number: A34423; MUID:90046824

A:Accession: A34423

A:Molecule type: mRNA

A:Status: preliminary

A:Residues: 1-94, 'E', 96-477 <GRA>

A:Cross-references: GB:M28333; NID:9194126; PIDN:AAA37896.1; PID:9309330

R:Hemmi, S.; Peghnt, P.; Metzler, M.; Merlin, G.; Dembic, Z.; Aguet, M.

Proc. Natl. Acad. Sci. U.S.A. 86, 9901-9905, 1989

A:Title: Cloning of murine interferon gamma receptor cDNA: expression in human cells

A:Reference number: A34508; MUID:90093370

A:Accession: A34508

A:Molecule type: mRNA

A:Residues: 1-94, 'E', 96-477 <HEM>

A:Cross-references: GB:M28333; NID:9194131; PIDN:AAA37898.1; PID:9309331

R:Munro, S.; Maniatis, T.

Proc. Natl. Acad. Sci. U.S.A. 86, 9248-9252, 1989

A:Title: Expression cloning of the murine interferon gamma receptor cDNA.

A:Reference number: A36224; MUID:90083245

A:Accession: A36224

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 10-477 <MUN>
A:Cross-references: GB:M8995; NID:g194123; PIDN:AAA37895.1; PID:g309329
R:Ravall, P.; Obidci, S.; Russell, S.W.; Murphy, W.J.
Gene 154, 219-223, 1995
A:Title: Characterization of the 5' flanking region and gene encoding the mouse interferon
A:Reference number: I48941; MUID:95197006
A:Accession: I48941
A:Status: translation not shown; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-28 <RES>
A:Cross-references: EMBL:U05960; NID:9454092; PIDN:AAA0980.1; PID:9454093
C:Superfamily: interferon gamma receptor
C:Keywords: cytokine receptor; transmembrane protein

Query Match	8.68;	Score 102.5;	DB 2;	Length 477;
Best Local Similarity	22.98;	Pred. No. 0.23;		
Matches 54; Conservative	38;	Mismatches 87;	Indels 57;	Gaps 14;

```

0Y      ATTATLVAAGPWWYLSAAAGKNLKS-----PQVEVDIIDDNELIRAMNSDSGVAGTFESFD 64
      1  :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      7  AGRHILLVY--LMLSAKYGSGALSTEDPEPSPVATYNLILKSYNL-----NPVYCW 58
      1  :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
0Y      65  YQ-----KTGDMNMIKLSCGONITSTKCNFSKLANYEIR-----LRIR 105
      1  :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      59  YONNSQPTIFWQYKVVYSGSW--TDSCNINSDHCC-----NIGQIMPDVSAMARVK 109
      1  :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
0Y      106  AE-KENNSSWKEVDSFTPFKRAQIGPP--EYHLEAEDKAIYIHISP-----GTRDSYMAA 157
      1  :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      110  AKVQKESDYSRKSKEFLMCLCKGKVGPGPLEIRRKEEQOLSLVLFHPVYVNGESQGTMGFC 169
      1  :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
0Y      158  LDG---LSFTSLIMKNSGVEERIEINYSRHKIYRLSPETTYC-LKYKAAALTS 209
      1  :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      170  -DGSCTCTFDYTYVVEHNRSG-----ELIATKHRYVEKEECNETICELINISVSTLDS 219
      1  :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

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RESULT 11
T27934
hypothetical protein ZK617.1a - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T27934; T28030
R:White, S.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z20442
A:Accession: T27934
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6831 <NTL>
A:Cross-references: EMBL:Z278997; PIDN:CAA98064.1; GSPDB:GN00022; CESP:ZK617.1a
A:Experimental source: clone ZK617
R:Harris, B.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z20458
A:Accession: T28030
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6831 <NTL>
A:Cross-references: EMBL:Z278999; PIDN:CAA98081.1; GSPDB:GN00022; CESP:ZK617.1a
A:Experimental source: clone ZK629
C:Genetics:
A:Gene: CESP:ZK617.1a
A:Map position: 4
A:Introns: 10/3; 61/3; 135/2; 168/3; 256/2; 379/3; 405/2; 463/1; 508/3; 542/3; 574/3; 555/4/4/3; 6683/3; 6768/1; 6800/3

Query Match	8.2%	Score 97.5;	DB 2;	Length 6831;
Best Local Similarity	22.8%	Pred. No. 21;		
Matches 44;	Conservative 22;	Mismatches 74;	Indels 53;	Gaps 10

[illegible]

RESULT 12
S57242
twitchin - *Caenorhabditis elegans*

N:Contains: protein kinase (EC 2.7.1.1.)
C:Species: *Caenorhabditis elegans*
C:Date: 28-Oct-1995 #sequence_revision 24-Oct-1997 #extl_change 18-Jun-1999
C:Accession: S57242; S07571; S06797; S57218
R:Benian, G.M.; L'Hernault, S.W.; Morris, M.E.
submitted to the EMBL Data Library, February 1993
A:Description: Additional sequence complexity within twitching of *Caenorhabditis elegans*
A:Reference number: S57242
A:Accession: S57242
A:Molecule type: DNA
A:Residues: 1-6839 <BEN1>
A:Cross-references: EMBL:L10351
A:Experimental source: var. Bristol
R:Benian, G.
submitted to the EMBL Data Library, November 1989
A:Reference number: S07571

A: Molecule type: DNA
A: Residues: 792-6839 <BEN2>
A: Cross-references: EMBL:X15423; NID:g66997; PIDN:CA433463.1; PID:g6898
A: Experimental source: Var. Bristol
R: Benlian, G.M.; Kiff, J.E.; Neckelmann, N.; Moerman, D.G.; Waterston, R.H.
Nature 342, 45-50, 1989
A: Title: Sequence of an unusually large protein implicated in regulation of myosin
A: Reference number: 506797; MID:90044042
A: Accession: S06797
A: Status: nucleic acid sequence not shown
A: Molecule type: DNA
A: Residues: 806-1175; 1178-1998, 'Y', 2000-3040, 'I', 3042-3335, 'I', 3337-5693; 5696-6359
A: Cross-references: EMBL:X15423
A: Experimental source: Var. Bristol
R: Benlian, G.M.; L'Hernault, S.W.; Morris, M.E.
Genetics 134, 1097-1104, 1993
A: Title: Additional sequence complexity in the muscle gene, unc-22, and its encoded
A: Reference number: 557218; MID:93387864
A: Accession: 557218
A: Molecule type: DNA
A: Residues: 2-99; 108-194, 'O', 196-206; 374-468; 658-753 <BEN4>
A: Experimental source: Var. Bristol
A: Comment: Lack of unc-22 leads to a constant twitching of the body muscles.
A: Genetics:
A: Gene: unc-22
A: Map position: IV
A: Introns: 18/3; 69/3; 143/2; 176/3; 264/2; 387/3; 413/2; 471/1; 516/3; 550/3; 582/2;
152/3; 6691/3; 6776/1; 6808/3
A: Superfamily: twitchin, fibronectin type III repeat homology; Immunoglobulin homology;
C: Keywords: ATP; autophosphorylation; duplication; muscle; phosphotransferase; seric; phosphotransferase;
E: 806-888, 899-990, 991-1083, 1084-1175, 1178-1273, 1474-1567, 1770-1864, 2065-2158, 2358-2761, 2762-2858, 2859-2957, 2958-3057, 3058-3157, 3158-3257, 3258-3357, 3358-3457, 3458-3557, 3558-3657, 3658-3757, 3758-3857, 3858-3957, 3958-4057, 4058-4157, 4158-4257, 4258-4357, 4358-4457, 4458-4557, 4558-4657, 4658-4757, 4758-4857, 4858-4957, 4958-5057, 5058-5157, 5158-5257, 5258-5357, 5358-5457, 5458-5557, 5558-5657, 5658-5757, 5758-5857, 5858-5957, 5958-6057, 6058-6157, 6158-6257, 6258-6357, 6358-6457, 6458-6557, 6558-6657, 6658-6757, 6758-6857, 6858-6957, 6958-7057, 7058-7157, 7158-7257, 7258-7357, 7358-7457, 7458-7557, 7558-7657, 7658-7757, 7758-7857, 7858-7957, 7958-8057, 8058-8157, 8158-8257, 8258-8357, 8358-8457, 8458-8557, 8558-8657, 8658-8757, 8758-8857, 8858-8957, 8958-9057, 9058-9157, 9158-9257, 9258-9357, 9358-9457, 9458-9557, 9558-9657, 9658-9757, 9758-9857, 9858-9957, 9958-10057, 10058-10157, 10158-10257, 10258-10357, 10358-10457, 10458-10557, 10558-10657, 10658-10757, 10758-10857, 10858-10957, 10958-11057, 11058-11157, 11158-11257, 11258-11357, 11358-11457, 11458-11557, 11558-11657, 11658-11757, 11758-11857, 11858-11957, 11958-12057, 12058-12157, 12158-12257, 12258-12357, 12358-12457, 12458-12557, 12558-12657, 12658-12757, 12758-12857, 12858-12957, 12958-13057, 13058-13157, 13158-13257, 13258-13357, 13358-13457, 13458-13557, 13558-13657, 13658-13757, 13758-13857, 13858-13957, 13958-14057, 14058-14157, 14158-14257, 14258-14357, 14358-14457, 14458-14557, 14558-14657, 14658-14757, 14758-14857, 14858-14957, 14958-15057, 15058-15157, 15158-15257, 15258-15357, 15358-15457, 15458-15557, 15558-15657, 15658-15757, 15758-15857, 15858-15957, 15958-16057, 16058-16157, 16158-16257, 16258-16357, 16358-16457, 16458-16557, 16558-16657, 16658-16757, 16758-16857, 16858-16957, 16958-17057, 17058-17157, 17158-17257, 17258-17357, 17358-17457, 17458-17557, 17558-17657, 17658-17757, 17758-17857, 17858-17957, 17958-18057, 18058-18157, 18158-18257, 18258-18357, 18358-18457, 18458-18557, 18558-18657, 18658-18757, 18758-18857, 18858-18957, 18958-19057, 19058-19157, 19158-19257, 19258-19357, 19358-19457, 19458-19557, 19558-19657, 19658-19757, 19758-19857, 19858-19957, 19958-20057, 20058-20157, 20158-20257, 20258-20357, 20358-20457, 20458-20557, 20558-20657, 20658-20757, 20758-20857, 20858-20957, 20958-21057, 21058-21157, 21158-21257, 21258-21357, 21358-21457, 21458-21557, 21558-21657, 21658-21757, 21758-21857, 21858-21957, 21958-22057, 22058-22157, 22158-22257, 22258-22357, 22358-22457, 22458-22557, 22558-22657, 22658-22757, 22758-22857, 22858-22957, 22958-23057, 23058-23157, 23158-23257, 23258-23357, 23358-23457, 23458-23557, 23558-23657, 23658-23757, 23758-23857, 23858-23957, 23958-24057, 24058-24157, 24158-24257, 24258-24357, 24358-24457, 24458-24557, 24558-24657, 24658-24757, 24758-24857, 24858-24957, 24958-25057, 25058-25157, 25158-25257, 25258-25357, 25358-25457, 25458-25557, 25558-25657, 25658-25757, 25758-25857, 25858-25957, 25958-26057, 26058-26157, 26158-26257, 26258-26357, 26358-26457, 26458-26557, 26558-26657, 26658-26757, 26758-26857, 26858-26957, 26958-27057, 27058-27157, 27158-27257, 27258-27357, 27358-27457, 27458-27557, 27558-27657, 27658-27757, 27758-27857, 27858-27957, 27958-28057, 28058-28157, 28158-28257, 28258-28357, 28358-28457, 28458-28557, 28558-28657, 28658-28757, 28758-28857, 28858-28957,

F:5948-5956/Region: protein kinase ATP-binding motif
F:5971/Active site: Lys #status predicted

Query Match 8.2%; Score 97.5; DB 2; Length 6839;
Best Local Similarity 22.8%; Pred. No. 21;
Matches 44; Conservative 22; Mismatches 74; Indels 53; Gaps 10;
OY 30 LKSPK---VEV-DIIDNFIILNRNRSDSEVNTFSFDYK--TGMDNWKLSGCONI 82
DB 1864 LDRPSKPNGLPESVDFEDNLNLSKPPDDGDEPIEYVEKLDATGRWVP---CAKV 1920
OY 83 TSTKCNFSLKLNVEEIKLRIR-A-EKENTSSWYEDSFTPPRKAQIGPPEVHLAEADKA 141
DB 1921 KDTAKHIGLKKG--QYQFRKATNKEGASDALSTDIDTKAKNPYDEGRK----- 1971
OY 142 IVIHISPTKDSVMALDGLSFTYSLILW--KNSSGVEERIENTYSRHKIKYLSPEPTY 198
DB 1971 -----GTPPYVDMDADNRVS-----LEWEPPKSDG-----APITQY 2001
OY 199 CLKVKAALLTSWK 211
DB 2002 VIEKKGKHGRMO 2014

RESULT 13
T27935
hypotheetical protein ZK617.1b - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T27935; T28031
R:White, S.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z20442
A:Accession: T27935
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-7160 <M12>
A:Cross-references: EMBL:Z73897; PIDN:CAA98065.1; GSPDB:GN00022; CESP:ZK617.1b
A:Experimental source: clone ZK617
R:Haris, B.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z20458
A:Accession: T28031
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-7160 <M12>
A:Cross-references: EMBL:Z73899; PIDN:CAA98082.1; GSPDB:GN00022; CESP:ZK617.1b
A:Experimental source: clone ZK829
C:Genetics:
A:Gene: CESP:ZK617.1b
A:Map position: 4
A:Introns: 10/3; 61/3; 135/2; 168/3; 256/2; 379/3; 405/2; 463/1; 508/3; 542/3; 574/3; 59
3067/1; 3141/3; 3269/1; 6473/3; 7012/3; 7097/1; 7129/3

Query Match 8.2%; Score 97.5; DB 2; Length 7160;
Best Local Similarity 22.8%; Pred. No. 22;
Matches 44; Conservative 22; Mismatches 74; Indels 53; Gaps 10;
OY 30 LKSPK---VEV-DIIDNFIILNRNRSDSEVNTFSFDYK--TGMDNWKLSGCONI 82
DB 2185 LDRPSKPNGLPESVDFEDNLNLSKPPDDGDEPIEYVEKLDATGRWVP---CAKV 2241
OY 83 TSTKCNFSLKLNVEEIKLRIR-A-EKENTSSWYEDSFTPPRKAQIGPPEVHLAEADKA 141
DB 2242 KDTAKHIGLKKG--QYQFRKATNKEGASDALSTDIDTKAKNPYDEGRK----- 2292
OY 142 IVIHISPTKDSVMALDGLSFTYSLILW--KNSSGVEERIENTYSRHKIKYLSPEPTY 198
DB 2292 -----GTPPYVDMDADNRVS-----LEWEPPKSDG-----APITQY 2322
OY 199 CLKVKAALLTSWK 211

DB 2323 VIEKKGKHGRMO 2335

RESULT 14
A49667
Interleukin-10 receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: A49667
R:Ho, A.S.; Liu, Y.; Khan, T.A.; Hsu, D.H.; Bazan, J.F.; Moore, K.W.
Proc. Natl. Acad. Sci. U.S.A. 90, 11267-11271, 1993
A:Title: A receptor for interleukin 10 is related to interferon receptors.
A:Reference number: A49667; MUID:94068585
A:Accession: A49667
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-575 <RES>
A:Cross-references: GB:L12120; NID:g437615; PIDN:AAA16156.1; PID:g437616
C:Genetics:
A:Gene: IL10R
C:Keywords: cytokine receptor

Query Match 8.0%; Score 95.5; DB 2; Length 575;
Best Local Similarity 20.5%; Pred. No. 1.2;
Matches 51; Conservative 39; Mismatches 98; Indels 61; Gaps 10;

OY 13 LVAVGPVYLSAAGCKNKSPOKYVEDIIDNFIILR---NRSDSEVNTFSFDYK 68
DB 9 LVITSSLSLEFIAYGTLPSPSYVWFAPFOHILHMKPIPNQSESTYVEVAL---KQY 64
OY 69 GMDWMKLSGCONITSTKCNFSLKLNVEE---IKRIR-A-EKENTSSWYEDS-PTPF 123
DB 65 GNSTWMDHICRKAQALSCDITFTLDYHRSYVRARVANDSOYSNMTTTFRT-- 123
OY 124 RKAQIGPPEVHLAEADKAIVIHISPTKDSY-VMALDGLSFTYSLILWKNSSGVEERLEN 182
DB 123 -----VDEIL-----IVDSYTLKAMGIIIGTILHPPRPTTPAGDEVEQ 162
OY 183 IYSRHKIKYLS-----PBT-----TYCLKVKAALLTSWKIGYSP 217
DB 163 VFKDLRYKISIRFSELSKNATKRVKQETFTLVPIGVKFCVAVLPRLSIRINKAMWSE 222
OY 218 VHCITTYE 226
DB 223 EQCLITTE 231

RESULT 15
T29585
hypotheetical protein F55F8.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T29585
R:Gallung, S.; Scheel, P.; Kemp, K.
submitted to the EMBL data library, November 1996
A:Description: The sequence of C. elegans cosmid f55f8.
A:Reference number: Z20647
A:Accession: T29585
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-925 <CGAT>
A:Cross-references: EMBL:U80447; PIDN:AAH37807.1; GSPDB:GN00019; CESP:F55F8.3
A:Experimental source: strain Bristol N2; clone f55f8
C:Genetics:
A:Gene: CESP:F55F8.3
A:Map position: 1
A:Introns: 6/3; 44/2; 76/1; 109/2; 159/2; 204/3; 327/1; 469/3; 617/1; 775/1; 825/3;
Query Match 8.0%; Score 95.5; DB 2; Length 925;
Best Local Similarity 25.7%; Pred. No. 2.3;

	Matches	38,	Conservative	19,	Mismatches	70,	Indels	21,	Gaps	4,
OY	70	MDNMIKLSGCONIT--	STKCNFSSLKLNYEEI--	KLIRAREKENTSSMYEWDSEFTTPRK	125					
Db	1	MDTNRLKSNICITGYRDG	GVAFSKDGYSVISPIGNLKITFDLRNNTSKTLDIDCYNIKR	60						
OY	126	AOIGPPEVHLEADKAIVHI-----	SRGTDSDYMAALDGLSFYY----	SLI	168					
Db	61	LSISPSGYHLLASDEGVVH	FVHLLSEKITYFRSRNKPIGSLQWSPDAPRAVACIRENDKQ	120						
OY	169	IMKNSSGVEERIEINITYSR	RHKIKYKLSPET	196						
Db	121	IHEFGKSTENKYNPNP	SLSRITYKLSDS	148						

Search completed: June 1, 2000, 04:35:19
Job time: 14299 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 1, 2000, 04:38:52 ; Search time 34.71 Seconds

(without alignments)
200.927 Million cell updates/sec

Title: US-09-240-675-2_COPY_1_229

Perfect score: 1196
Sequence: 1 MMYVLGATTLVAVGPMV.....WKIGVSPHCIKTVENEL 229

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_38:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1196	100.0	557	1 INR1_HUMAN	P17181 homo sapien
2	782.5	65.4	560	1 INR1_BOVIN	O04730 bos taurus
3	765.5	64.0	560	1 INR1_SHEEP	Q28589 ovis aries
4	600.5	50.2	590	1 INR1_MOUSE	P33836 mus musculus
5	222.5	18.6	325	1 CRF4_HUMAN	O08334 homo sapien
6	151.5	12.7	337	1 INGS_HUMAN	P32600 homo sapien
7	117.5	9.8	489	1 INGR_HUMAN	P15260 homo sapien
8	102.5	8.6	477	1 INGR_MOUSE	P15261 mus musculus
9	95.5	8.0	575	1 I10R_MOUSE	O61172 mus musculus
10	95.5	8.0	925	1 PWP2_CAEEL	P31341 caenorhabdi
11	95.5	7.9	578	1 I10R_HUMAN	Q13651 homo sapien
12	92.5	7.7	292	1 TF_BOVIN	P30931 bos taurus
13	92.5	7.7	295	1 TF_HUMAN	P33726 homo sapien
14	90.5	7.6	1304	1 CD45_HUMAN	P08575 homo sapien
15	90.5	7.5	315	1 6DCS_SOYBN	P26690 glycine max
16	89.5	7.5	530	1 INR2_BOVIN	Q55141 bos taurus
17	89.5	7.5	880	1 TYO3_RAT	P51146 rattus norv
18	89.5	7.4	515	1 INR2_HUMAN	P48551 homo sapien
19	87.5	7.3	639	1 HS74_PARLI	O62408 paracentrot
20	86.5	7.2	2131	1 XCF2_SPIOL	P08973 spinnella ol
21	84.5	7.1	623	1 VGLR_VZVD	P09259 varicella-z
22	83.5	7.0	306	1 KI28_YEAST	P06242 saccharomyc
23	83.5	6.9	536	1 INR2_SHEEP	Q95207 ovis aries
24	83.5	6.9	335	1 CHM1_BOVIN	P17404 bos taurus
25	83.5	6.9	520	1 CP84_ARATH	Q42600 arabidopsis
26	82.5	6.9	1068	1 XCF0_MARPO	P12221 marichantia
27	82.5	6.9	515	1 T15R_MOUSE	P11183 mus musculus
28	82.5	6.9	517	1 KTR7_YEAST	P40504 saccharomyc
29	82.5	6.9	875	1 HIR2_YEAST	P32480 saccharomyc
30	81.5	6.8	292	1 TF_RABIT	P24055 oryctolagus
31	81.5	6.8	2054	1 XCF2_PINTH	P41653 pinus thunb
32	80.5	6.7	486	1 VN53_RORTH	P35424 human rotav
33	80.5	6.7	780	1 AFG2_YEAST	P32794 saccharomyc
34	80.5	6.7	878	1 IL3B_MOUSE	P26954 mus musculus

35	80	6.7	918	1 IL6B_HUMAN	P40189 homo sapien
36	80	6.7	993	1 EPB3_MOUSE	P54754 mus musculus
37	79.5	6.6	918	1 IL6B_RAT	P40190 rattus norv
38	79.5	6.6	442	1 THDF_MYCCE	P47254 mycoplasma
39	78.5	6.6	853	1 TGR3_RAT	P26342 rattus norv
40	78.5	6.6	896	1 CYRB_MOUSE	P26955 mus musculus
41	78.5	6.5	1124	1 T1E2_HUMAN	O02763 homo sapien
42	77.5	6.5	274	1 VC06_SPVKA	P32226 swinepox vi
43	77	6.4	377	1 MTC3_CHYNI	P10833 chlorella v
44	77	6.4	460	1 HEMO_RABIT	P20058 oryctolagus
45	77	6.4	537	1 IL2B_RAT	P26896 rattus norv

ALIGNMENTS

```

RESULT 1
ID INR1_HUMAN STANDARD: PRT; 557 AA.
AC P17181;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
GN IFNARI OR IFNAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
NC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90124632.
RA Use G., Lutfalla G., Gresser I.;
RT "Genetic transfer of a functional human interferon alpha receptor
RT into mouse cells: cloning and expression of its cDNA.";
RL Cell 60:225-234(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92129376.
RA Lutfalla G., Gardiner K., Proudhon D., Vieh E., Use G.;
RT "The structure of the human interferon alpha/beta receptor gene.";
RL J. Biol. Chem. 267:2802-2809(1992).
RN [3]
RP PHOSPHORYLATION BY TYK2.
RX MEDLINE: 95059042.
RA Colomancini O., Yan H., Domanski P., Handa R., Smalley D.,
RA Mollersman J., Witte M., Krishnan K., Krolewski J.;
RT "Direct binding to and tyrosine phosphorylation of the alpha subunit
RT of the type I interferon receptor by p135tyk2 tyrosine kinase.";
RL Mol. Cell. Biol. 14:8133-8142(1994).
CC - FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
CC I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
CC SUBUNITS THEMSELVES.
CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC - TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALL TISSUES AND
CC EVEN ON THE SURFACE OF MOST IFN-RESISTANT CELLS.
CC - PTM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYK2 TYROSINE KINASE.
CC - SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC - SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb.slb.ch).
CC -----
DR EMBL: J03171; AAA52730.1; -
DR EMBL: X60459; CAA42992.1; -
DR PIR: A32694; A32694.
DR PIR: S17112; S17112.
DR MTM: 107450; -

```

KW Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism;
 RM Phosphorylation.
 FT SIGNAL 1 27 POTENTIAL.
 FT CHAIN 28 557 INTERFERON-ALPHA/BETA RECEPTOR ALPHA
 FT 28 557 CHAIN.
 FT DOMAIN 28 436 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 437 457 POTENTIAL.
 FT DOMAIN 458 557 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 79 87 BY SIMILARITY.
 FT DISULFID 199 220 BY SIMILARITY.
 FT MOD_RES 466 466 PHOSPHORYLATION (BY TYR2) (PROBABLE).
 FT MOD_RES 481 481 PHOSPHORYLATION (BY TYR2) (PROBABLE).
 FT MOD_RES 50 50 POTENTIAL.
 FT CARBOHYD 58 58 POTENTIAL.
 FT CARBOHYD 81 81 POTENTIAL.
 FT CARBOHYD 88 88 POTENTIAL.
 FT CARBOHYD 110 110 POTENTIAL.
 FT CARBOHYD 172 172 POTENTIAL.
 FT CARBOHYD 254 254 POTENTIAL.
 FT CARBOHYD 313 313 POTENTIAL.
 FT CARBOHYD 314 314 POTENTIAL.
 FT CARBOHYD 376 376 POTENTIAL.
 FT CARBOHYD 415 415 POTENTIAL.
 FT CARBOHYD 433 433 POTENTIAL.
 FT VARIANT 168 168 L->V.
 FT VARIANT 168 168 /FTID-VAR_002717.
 FT CONFLICT 17 17 G->A (IN REF. 2).
 FT SEQUENCE 557 AA; 63525 MM; 0F6744C8A1ADB373 CRC64;

Query Match 100.0%; Score 1196; DB 1; Length 557;
 Best Local Similarity 100.0%; Pred. No. 1,le-98;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MMYVLLGATTLVAVGPMVLSAAGGKNLSPQKVEVDIIDNFIILMNSDESQVNT 60
 DB 1 MMYVLLGATTLVAVGPMVLSAAGGKNLSPQKVEVDIIDNFIILMNSDESQVNT 60
 OY 61 SFSDYQKGMNMIKLSGCONITSTKCNFSSSLKLVYEIKLRIRAKENTSSWYEDSF 120
 DB 61 SFSDYQKGMNMIKLSGCONITSTKCNFSSSLKLVYEIKLRIRAKENTSSWYEDSF 120
 OY 121 TPFRAQOIGPPVHLAEADKAIVIHISPGTKDSVMALDGSFTYSLIMKNSGVEERI 180
 DB 121 TPFRAQOIGPPVHLAEADKAIVIHISPGTKDSVMALDGSFTYSLIMKNSGVEERI 180
 OY 181 ENIYSRHKIYKLSPEITCYCLKVKAALLTSWKIGVSPVHCITVTENEL 229
 DB 181 ENIYSRHKIYKLSPEITCYCLKVKAALLTSWKIGVSPVHCITVTENEL 229
 RESULT 2
 INRL_BOVIN STANDARD: PRT: 560 AA.
 ID 004790; 93076908.
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
 GN IFNAR1 OR IFNAR.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
 OC Bovinae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LUNG;
 RX MEDLINE: 93076908.
 RA Mouchel-Viehl E., Lutfalla G., Mogensen K.E., Uze G.;
 RT "Specific antiviral activities of the human alpha interferons are
 determined at the level of receptor (IFNAR) structure.";
 RL FEBS Lett. 313:255-259(1992).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE: 9305725.
 RA Lam J.-K., Langer J.A.;
 RT "Cloning and characterization of a bovine alpha interferon receptor.";
 RL Biochim. Biophys. Acta 1173:314-319(1993).
 CC -I- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
 CC I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
 CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
 CC SUBUNITS THEMSELVES.
 CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -I- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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DR EMBL: X68443; CAA48484.1; -;
 DR EMBL: L06320; AAA02571.1; -;
 DR PIR: S33770; S33770.
 DR PIR: S27387; S27387.
 DR PIR: PF00041; fn3; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24 BY SIMILARITY.
 FT CHAIN 25 560 INTERFERON-ALPHA/BETA RECEPTOR ALPHA
 FT 25 560 CHAIN.
 FT DOMAIN 25 437 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 438 458 POTENTIAL.
 FT DOMAIN 459 560 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 76 84 BY SIMILARITY.
 FT DISULFID 199 220 BY SIMILARITY.
 FT CARBOHYD 47 47 POTENTIAL.
 FT CARBOHYD 47 47 POTENTIAL.
 FT CARBOHYD 55 55 POTENTIAL.
 FT CARBOHYD 85 85 POTENTIAL.
 FT CARBOHYD 109 109 POTENTIAL.
 FT CARBOHYD 172 172 POTENTIAL.
 FT CARBOHYD 254 254 POTENTIAL.
 FT CARBOHYD 313 313 POTENTIAL.
 FT CARBOHYD 377 377 POTENTIAL.
 FT CARBOHYD 434 434 POTENTIAL.
 FT CONFLICT 422 422 F->V (IN REF. 2).
 FT SEQUENCE 560 AA; 63818 MM; 66D76B7861E1D11 CRC64;

Query Match 65.4%; Score 782.5; DB 1; Length 560;
 Best Local Similarity 67.1%; Pred. No. 5,4e-62;
 Matches 155; Conservative 31; Mismatches 40; Indels 5; Gaps 5;

OY 2 MMYVLLGATTLVAVGPMVLSAAGGKNLSPQKVEVDIIDNFIILMNSDESQVNT 61
 DB 1 MMYVLLGATTLVAVGPMVLSAAGGKNLSPQKVEVDIIDNFIILMNSDESQVNT 61
 OY 62 SFSDYQKGMNMIKLSGCONITSTKCNFSSSLKLVYEIKLRIRAK-ENTSSWYEDS 119
 DB 59 SADYQIIGTDMNMIKLSGCONITSTKCNFSSSLKLVYEIKLRIRAK-ENTSSWYEDS 118
 OY 120 TPFRAQOIGPPVHLAEADKAIVIHIS-PTKDSVMALDGSFTYSLIMKNSGVEE 178
 DB 119 FVPLEAQIGPPVHLAEADKAIVIHIS-PTKDSVMALDGSFTYSLIMKNSGVEE 178
 OY 179 RIENIYSRHKIYKLSPEITCYCLKVKAALLTSWKIGVSPVHCITVTENEL 229
 DB 179 RIENIYSRHKIYKLSPEITCYCLKVKAALLTSWKIGVSPVHCITVTENEL 229

RESULT 3
 INRL_SHEEP STANDARD: PRT: 560 AA.
 ID 028389; 095206;
 AC 028389; 095206;

01-NOV-1997 (Rel. 35, Last sequence update)
 01-NOV-1997 (Rel. 35, Last sequence update)
 15-FEB-2000 (Rel. 39, Last annotation update)
 INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC)
 (INTERFERON ALPHA/BETA RECEPTOR-1).
 IFNARI OR IFNAR.
 Ovis aries (Sheep).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
 Caprinae; Ovis.
 [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE-ENDOMETRIUM;
 RA Kaluz S., Fisher P.A., Kaluzova M., Sheldrick E.L., Flint A.P.F.;
 RT "Structure of an ovine interferon receptor and its expression in
 RT endometrium";
 RL J. Mol. Endocrinol. 17:207-215(1996).
 [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE-ENDOMETRIUM;
 RX MEDLINE; 98006426.
 RA Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.;
 RT "Molecular cloning of ovine and bovine type I interferon receptor
 RT subunits from uteri, and endometrial expression of messenger
 RT ribonucleic acid for ovine receptors during the estrous cycle and
 RT pregnancy";
 RL Endocrinology 138:4757-4767(1997).
 CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
 CC I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
 CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
 CC SUBUNITS THEMSELVES.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT
 CC CONCEPTUS AT DAY 15 OF PREGNANCY.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
 CC -----
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 CC -----
 DR EMBL; X95939; CA65183.1; -;
 DR EMBL; U65978; AAB84231.1; -;
 DR PIR; PF00041; fn3; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24 BY SIMILARITY.
 FT CHAIN 25 560 INTERFERON-ALPHA/BETA RECEPTOR ALPHA
 FT DOMAIN 25 437 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 438 458 POTENTIAL.
 FT DOMAIN 459 560 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 76 84 BY SIMILARITY.
 FT DISULFID 199 220 BY SIMILARITY.
 FT CARBOHYD 47 47 POTENTIAL.
 FT CARBOHYD 55 55 POTENTIAL.
 FT CARBOHYD 85 85 POTENTIAL.
 FT CARBOHYD 108 108 POTENTIAL.
 FT CARBOHYD 109 109 POTENTIAL.
 FT CARBOHYD 172 172 POTENTIAL.
 FT CARBOHYD 222 222 POTENTIAL.
 FT CARBOHYD 285 285 POTENTIAL.
 FT CARBOHYD 313 313 POTENTIAL.
 FT CARBOHYD 359 359 POTENTIAL.
 FT CARBOHYD 377 377 POTENTIAL.
 FT CARBOHYD 434 434 POTENTIAL.
 FT CARBOHYD 434 434 POTENTIAL.
 FT CONFLICT 352 352 S -> G (IN REF. 2).
 FT CONFLICT 522 522 A -> D (IN REF. 2).
 FT SEQUENCE 560 AA: 63918 MW: 7198A1905D4805C CAC64;

Query Match 64.0%; Score 765.5; DB 1; Length 560;
 Best Local Similarity 66.2%; Pred. No. 1.8e-60;
 Matches 153; Conservative 32; Mismatches 41; Indels 5; Gaps 5;
 QY 2 MYVLGATTVLVAVGPMVLSAAGGKLNKSPQKVEVDIDDFILRMNKSDESGVNTF 61
 DB 1 MLSTLGLATITMLVA-GRWVLPASGEANLKS-ENVEIHIIDDFELKWNSSSESVRVTF 58
 QY 62 SEDYKTKGMNWKLSGCONITSPKCNFSSLUK-NVEEIKLRIRAEK-ENTSSWEVDS 119
 DB 59 SADYQIIGTDNMWKLPPCCOHITSSCKNFSSVELKQVFEKLEIRAREGNTSTWYVFP 118
 QY 120 FTTPRKAQIPPEVHLEAEADKAIVIHIS-PGTRDSVMALDGLSFTYSLILWNSSGYEE 178
 DB 119 FVPLFKAQIGPPDVHLEAEADKAILISISPPOTEDSIMALDRSSFRTSVYIWNSSSLEE 178
 QY 179 RIEENIRHRIKYKSPETTYCLKVKALLSWKIGVSPVHCITTYENEL 229
 DB 179 RTEVYEDKIKYKSPETTYCLKVKALLRQSRVGCSPYVCINTYRHRV 229
 RESULT 4
 INRL_MOUSE STANDARD; PRT; 590 AA.
 ID INRL_MOUSE
 AC P33896;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
 GN IFNARI OR IFNAR OR IFNAR.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92262522.
 RA Ue G., Luitalla G., Bandu M.T., Proudhon D., Mogensen K.E.;
 RT "Behavior of a cloned murine interferon alpha/beta receptor expressed
 RT in homospesific or heterospesific background";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:4774-4778(1992).
 CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
 CC I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
 CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
 CC SUBUNITS THEMSELVES.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
 CC -----
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 CC -----
 DR EMBL; M89641; AAA37890.1; -;
 DR PIR; A45283; A45283.
 DR WGI; MGI107658; IFNAR.
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 27 590 INTERFERON-ALPHA/BETA RECEPTOR ALPHA
 FT DOMAIN 27 429 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 430 449 POTENTIAL.
 FT DOMAIN 450 590 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 78 86 BY SIMILARITY.
 FT DISULFID 199 220 BY SIMILARITY.
 FT CARBOHYD 43 43 POTENTIAL.
 FT CARBOHYD 109 109 POTENTIAL.
 FT CARBOHYD 181 181 POTENTIAL.

FT CARBOHYD 214 214 POTENTIAL.
 FT CARBOHYD 314 314 POTENTIAL.
 FT CARBOHYD 370 370 POTENTIAL.
 FT CARBOHYD 409 409 POTENTIAL.
 FT CARBOHYD 413 413 POTENTIAL.
 SQ SEQUENCE 590 AA; 65776 MW; 7EC6DF370185D3A CRC64;

Query Match 50.2%; Score 600.5; DB 1; Length 590;
 Best Local Similarity 52.0%; Pred. No. 8,1e-46;
 Matches 119; Conservative 40; Mismatches 69; Indels 1; Gaps 1;

OY 2 MYVLLGATTLVVAQVPMVLSAAGGKLNLSPOKVEYDIIDNFIILRNRSDESGVNTF 61
 1 LMAVVGAAALVLAQVPMVLSAAGGKLNLSPOKVEYDIIDNFIILRNRSDESGVNTF 60
 OY 62 SFYQKGMNMIKSGCONITSTKCFSSKLNYEELIRAKEN-TSSWYEVDSF 120
 61 SAEYRTRDEAKMKLVPECCOHTTTKCEFFSLDINNYIKTOFRVAREGNSSTSMNEVD 120
 OY 121 TPRKKAQIGPEVHEAEDKAIYIHISPGTKDSVMALDGLSTYSLLIMKSSGVEER 180
 121 IPIYTHMSPEVRLAEEDKAIYIHISPGTKDSVMALDGLSTYSLLIMKSSGVEER 180
 OY 181 ENIYSRHKIKLSPETTYCLKVKAAALTSWKIGVSPVHCITKTVENEL 229
 181 NSIYVEKIPPELLPETTYCLEVKAHPSLKHGNSYVOCISTTVANKM 229
 DB 181 NSIYVEKIPPELLPETTYCLEVKAHPSLKHGNSYVOCISTTVANKM 229

RESULT 5
 CRF4_HUMAN STANDARD; PRT; 325 AA.

ID CRF4_HUMAN STANDARD; PRT; 325 AA.
 AC 008334;
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE CYTOKINE RECEPTOR CLASS-II CRF2-4 PRECURSOR.
 GN CRF4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE-FETAL BRAIN;
 RX MEDLINE: 93300510.
 RA Luftala G., Gardiner K., Uze G.;
 RT "A new member of the cytokine receptor gene family maps on chromosome
 21 at less than 35 kb from IFNAR.";
 RL Genomics 16:366-373(1993).
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 96054036.
 RA Luftala G., McInnis M.G., Antonarakis S.E., Uze G.;
 RT "Structure of the human CRF4 gene: comparison with its IFNAR
 neighbor.";
 RL J. Mol. Evol. 41:338-344(1995).
 CC -1- FUNCTION: IS PROBABLY INVOLVED IN THE INTERFERON SYSTEM.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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 CC
 CC EMBL: 217227; CAA78933.1;
 CC EMBL: U08988; AA86872.1;
 CC PIR: A47003; A47003.
 DR HSP; P13726; IDAN.

DR MIM:123889; -;
 KM Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 325 CYTOKINE RECEPTOR CLASS-II CRF2-4.
 FT DOMAIN 20 220 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 221 249 POTENTIAL.
 FT DOMAIN 250 325 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 66 74 BY SIMILARITY.
 FT DISULFID 188 209 BY SIMILARITY.
 FT CARBOHYD 49 49 POTENTIAL.
 FT CARBOHYD 68 68 POTENTIAL.
 FT CARBOHYD 102 102 POTENTIAL.
 FT CARBOHYD 161 161 POTENTIAL.
 FT CONFLICT 124 124 A -> D (IN REF. 2).
 FT CONFLICT 269 273 FLGH -> VGRME (IN REF. 2).
 FT CONFLICT 274 325 MISSING (IN REF. 2).
 SQ SEQUENCE 325 AA; 37011 MW; 66706C79F8514B23 CRC64;

Query Match 18.6%; Score 222.5; DB 1; Length 325;
 Best Local Similarity 30.3%; Pred. No. 1.3e-12;
 Matches 66; Conservative 40; Mismatches 93; Indels 19; Gaps 8;

OY 19 WYLSAAGGKLNLS-----POKVEYDIIDNFIILRNRSDESGVNTFSPYQKGM 71
 3 WELSGMLGCLLVLSALGWPPENRYMNSVNRKNILOWESPAFAKGNLFTAOY----LS 58
 DB 72 WKIKSGCONITSTKCNSSKLNYEELIRAKEN-KENTSSWYEVDSFPRKAOIGP 130
 59 YRIFODKCMNTLTRECDPSS--LSKYGDHLRVRAEFADSHDWNI-TFCVPVDITIGP 115
 OY 131 PEVHEA-EDKAIYIHISPGTKDSV-AMALDGL--SFYSLLIMKSSGVEERIENIYS 186
 116 PEMOVEVLADSLHMFLLPARKIENEYETMTKKNVSYMTYINQYKNGXDEKFOITPOYDF 175
 OY 187 HKIYLSSETTYCLKVKAAALTSWKIGVSPVHCITKTVENEL 224
 176 EVLRNLEPWTYCVQVGRFLPDNRKAGEMSEPVCEOTT 213
 DB 176 EVLRNLEPWTYCVQVGRFLPDNRKAGEMSEPVCEOTT 213

RESULT 6
 INGS_HUMAN STANDARD; PRT; 337 AA.
 ID INGS_HUMAN STANDARD; PRT; 337 AA.
 AC P38484;
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (INTERFERON-GAMMA
 DE RECEPTOR ACCESSORY FACTOR-1) (AF-1) (INTERFERON-GAMMA TRANSDUCER-1).
 GN IFNGR2 OR IFNGT1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE-LUNG FIBROBLAST;
 RX MEDLINE: 94170380.
 RA Soh J., Donnelly R.J., Korenko S., Maritano T.M., Cook J.R.,
 RA Wang N., Emanuel S.L., Schwartz B., Miki T., Pestka S.;
 RT "Identification and sequence of an accessory factor required for
 RT activation of the human interferon gamma receptor.";
 RL Cell 76:793-802(1994).
 CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERFERON GAMMA. REQUIRED FOR
 CC SIGNAL TRANSDUCTION. THIS ACCESSORY FACTOR IS AN INTEGRAL PART OF
 CC THE IFN-GAMMA SIGNAL TRANSDUCTION PATHWAY AND IS LINELY TO
 CC INTERACT WITH GAF, JAK1, AND/OR JAK2.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
 CC
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DR EMBL: U05875; AAA16955.1; -
DR EMBL: U05877; AAA16956.1; -
DR MIM: 147559; -
DR PFM: PF00041; fn3; 1.
RW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 337 INTERFERON-GAMMA RECEPTOR BETA CHAIN.
FT DOMAIN 28 247 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 248 268 POTENTIAL.
FT DOVAIN 269 337 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 56 56 POTENTIAL.
FT CARBOHYD 85 85 POTENTIAL.
FT CARBOHYD 110 110 POTENTIAL.
FT CARBOHYD 137 137 POTENTIAL.
FT CARBOHYD 219 219 POTENTIAL.
FT CARBOHYD 231 231 POTENTIAL.
FT VARIANT 64 R->O.
FT SEQUENCE 337 AA; 37834 MW; 18C61B10AD90E509 CRC64; /FTID-VAR.002718.

Query Match 12.78; Score 151.5; DB 1; Length 337;
Best Local Similarity 24.68; Pred. No. 2.7e-06;
Matches 61; Conservative 44; Mismatches 94; Indels 49; Gaps 13;

OY 12 VLAVNGPVLVLSAAGG---KNLKSPOKVEVDIDNFIKRW-----NRSDSVGNVTF 62
DB 9 LLLLVGPAALAAAPPDPLSQLPAPQHKIRLYNEQVLSWEPVALSNSTRPVYRVQFK 68
OY 63 FDYQKTDGMDNWKLS-----GCQNTSTKCNFS-----LKNLYEEIKLRRAEK 108
DB 69 YTDKR-----WFTADIMSGVCTQITATEDCTAASPSAGPMFNV-----TLRLREL 119
OY 109 ENT-SSWYEVDSFTPFRRQAQIPPEVHLE---AEDKAIVIHISPTKDSVMALDGLSFT 164
DB 120 GALHSAMVTMPFQHYRNVTVGPPE-NIEVTPGESLIRFSSPDIDTSTAF-----FC 174
OY 165 YSLIKWKSQVEEIEINISNKKY--KLSPETTYCKLVKALITS---WKIVYSPV 218
DB 175 YVHWWE---KGGIQOVKQPFRRSISLDLNRKSVRYCLOVQOLMKNNSNIFRVGHLSTNI 232
OY 219 HCKITVE 226
DB 233 SCYETMAD 240

RESULT 7
ID INGR_HUMAN STANDARD: PRT: 489 AA.
AC P15260; -
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDM119).
GN IFNGRI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89003065.
RA Aguet M., Dentic L., Meriin G.;
RT "Molecular cloning and expression of the human interferon-gamma
RL Cell 55:273-280(1988).
RN [2]
RP DISULFIDE BONDS, PARTIAL SEQUENCE, AND MUTAGENESIS.
RX MEDLINE: 93183911.

RA Stueber D., Friedlein A., Fountoulakis M., Iahn H.-W., Garotta G.;
RT "Alignment of disulfide bonds of the extracellular domain of the
RT Interferon gamma receptor and investigation of their role in
RT biological activity.";
RL Biochemistry 32:2423-2430(1993).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 26-248.
RX MEDLINE: 95342235.
RA Walter M.R., Windsor W.T., Nagabhushan T.L., Lundell D.J., Lunn C.A.,
RA Zanoudy P.J., Narula S.K.;
RT "Crystal structure of a complex between Interferon-gamma and its
RT soluble high-affinity receptor.";
RL Nature 376:230-235(1995).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 28-122 COMPLEX WITH ANTIBODY.
RX MEDLINE: 98035727.
RA Sogabe S., Stuart F., Henke C., Bridges A., Williams G., Birch A.,
RA Winkler F.K., Robinson J.A.;
RT "Neutralizing epitopes on the extracellular Interferon gamma receptor
RT (IFNGAMMAR) alpha-chain characterized by homolog scanning mutagenesis
RT and X-ray crystal structure of the A6 fab-IFNGAMMAR1-108 complex.";
RL J. Mol. Biol. 273:882-897(1997).
CC -1- FUNCTION: RECEPTOR FOR INTERFERON GAMMA. TWO RECEPTORS BIND ONE
CC -1- INTERFERON-GAMMA DIMER.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- PTM: PHOSPHORYLATED AT SER/THR RESIDUES.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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DR EMBL: J03143; AAA52731.1; -
DR PIR: A31555; A31555.
DR PDB: 1JRH; 25-MAR-98.
DR MIM: 107470; -
DR MIM: 209950; -
KW Receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation;
KW Immunoglobulin domain; 3D-structure.
FT SIGNAL 1 17
FT CHAIN 18 489
FT DOMAIN 18 245
FT TRANSMEM 246 266
FT DOMAIN 267 489
FT DISULFID 77 85
FT DISULFID 122 167
FT DISULFID 195 200
FT DISULFID 214 235
FT CARBOHYD 34 34
FT CARBOHYD 79 79
FT CARBOHYD 86 86
FT CARBOHYD 179 179
FT CARBOHYD 240 240
FT SEQUENCE 489 AA; 54404 MW; DCF9E574DBF47400 CRC64;

Query Match 9.88; Score 117.5; DB 1; Length 489;
Best Local Similarity 22.68; Pred. No. 0.0045;
Matches 52; Conservative 44; Mismatches 99; Indels 35; Gaps 8;

OY 3 VLLGATLVVAVGPAVLSAA-AGGRNLSPOKVEVDIDNFIKRWNSDSVGNV-T 60
DB 1 MALLFLPLVWGVGVSRAEMGTADLGPSSVPTPNVITIESYNNAPIYWEY--QIMQVPV 58
OY 61 FSPFYQKTDGMDNWKLSGCQNTSTKCNFSLLKNLYEEIKLRRA---EKENTSSYEV 117


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DB 59 FTVEVKNYGVKNSWIDACINISHYCNISDHVGFPSNLWYKARVQKE--SAYAKS 116
OY 118 DSFTPRKAOIGPPEVHLAEKAIYIH-----SPGK-----DSYVM 156
DB 117 EEFVAVCRDCKIPPKIDIKERQIMIDIFHPSVFYNGDEVDYDPEYTCYIRYNYV 176
OY 157 ALDGFSTYSLIWKNSGVEERENIYSRHKYIKLSPPTCYCLKAKAL 206
DB 177 RANGSGIOYKILYOK-----EDDCDEIQGLAIPIVSSLSQYCVSAEGVL 221

RESULT 8
INGR_MOUSE STANDARD: PRT: 477 AA.
ID INGR_MOUSE P15261:
AC 01-APR-1990 (Rel. 14, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR.
GN IFNGR1 OR IFNGR.
OS Mus musculus (Mouse).
OC Euteleia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90083245.
RA Munro S., Maniatis T.;
RT "Expression cloning of the murine interferon gamma receptor cDNA.";
RT Proc. Natl. Acad. Sci. U.S.A. 86:9248-9252(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90046824.
RA Gray P.W., Leong J., Fennie E.H., Farrar M.A., Pingel J.T.,
RA Fernandez-Luna J., Schreiber R.D.;
RT "Cloning and expression of the cDNA for the murine interferon gamma
RT receptor.";
RT Proc. Natl. Acad. Sci. U.S.A. 86:8497-8501(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90093370.
RA Hemmi S., Peghinet P., Metzler M., Merlin G., Dembic Z., Aguet M.;
RT "Cloning of murine interferon gamma receptor cDNA: expression in
RT human cells mediates high-affinity binding but is not sufficient to
RT confer sensitivity to murine interferon gamma.";
RT Proc. Natl. Acad. Sci. U.S.A. 86:9901-9905(1989).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90036866.
RA Kumar C.S., Muthukumar G., Frost L.J., Noe M., Ahn Y.H.,
RA Mariano T.M., Pestka S.;
RT "Molecular characterization of the murine interferon gamma receptor
RT cDNA.";
RT J. Biol. Chem. 264:17939-17946(1989).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90154099.
RA Cofeno F., Moore S.K., Tanaka S., Yunkl N., Landolfo S.,
RA Appella E.;
RT "Affinity purification, peptide analysis, and cDNA sequence of the
RT mouse interferon gamma receptor.";
RT J. Biol. Chem. 265:4064-4071(1990).
RN [6]
RP SEQUENCE OF 1-28 FROM N.A.
RX MEDLINE: 95197006.
RA Raval P., Obici S., Russell S.W., Murphy W.J.;
RT "Characterization of the 5' flanking region and gene encoding the
RT mouse interferon gamma receptor.";
RT Gene 154:219-223(1995).
CC -1- FUNCTION: RECEPTOR FOR INTERFERON GAMMA. TWO RECEPTORS BIND ONE
CC INTERFERON-GAMMA DIMER.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- PTM: PHOSPHORYLATED AT SER/THR RESIDUES.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

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CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M28995; AAA37895.1; ALT_INIT.
CC EMBL: M26711; AAA37896.1; -.
CC EMBL: M28233; AAA37898.1; -.
CC EMBL: M25764; AAA39177.1; -.
CC EMBL: J05265; AAA39178.1; -.
CC EMBL: U05960; AAA80980.1; -.
CC PIR: A34368; A34368.
CC PIR: A34423; A34423.
CC PIR: A34508; A34508.
CC PIR: A35468; A35468.
CC PIR: A36224; A36224.
CC HSSP: P15260; IYRH.
CC MGD: MGI:107655; IFNGR.
CC Receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation;
CC Immunoglobulin domain.
CC SIGNAL 1 22
CC CHAIN 23 477 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.
CC DOMAIN 23 253 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 254 277 POTENTIAL.
CC DOMAIN 278 477 CYTOPLASMIC (POTENTIAL).
CC DISULFID 83 91 BY SIMILARITY.
CC DISULFID 128 174 BY SIMILARITY.
CC DISULFID 203 208 BY SIMILARITY.
CC DISULFID 222 243 BY SIMILARITY.
CC CARBOHYD 61 61 POTENTIAL.
CC CARBOHYD 85 85 POTENTIAL.
CC CARBOHYD 186 186 POTENTIAL.
CC CARBOHYD 204 204 POTENTIAL.
CC CARBOHYD 211 211 POTENTIAL.
CC CONFLICT 95 95 G->E (IN REF. 2 AND 3).
CC SEQUENCE 477 AA; 32271 MW; A1FC6E9BA0B20A CRC64;

Query Match 8.6%; Score 102.5; DB: 1; Length 477;
Best Local Similarity 22.9%; Pred. No. 0.094;
Matches 54; Conservative 38; Mismatches 87; Indels 57; Gaps 14;

OY 8 ATTVLAVGPMVLSAAGGRNKS--PQVEVDIIDNFIKWNRSDESQVNTFSFD 64
DB 7 AGRMILLV--LMSAKVSGALSTEDPEPPVPVPTNVLIKSYNL-----NPVVCWE 58
OY 65 YQ-----KTGDMNIIKISGCONITSTCNSSSLNLYEELK-----LRIR 105
DB 59 YQNSQRPDIFTVOYKYVSGSW--TDSCNTISDHCC-----NIYGOIMPDVSAARVK 109
OY 106 AE-KENTSSWEVDSEFTFPRKAOIGP--EVHLAEADKAIYHISP-----GTRDSYVMA 157
DB 110 AKVGCKEDYARSKFEFLMCKLGKRGVPGPELRKKKEKDLSTLVHPEVYVNGESQGMFG 169
OY 158 LDG--LSFTYSLIWKNSGVEERENIYSRHKYIKLSPPTCYC-LKYAKALLTS 209
DB 170 -DGSCTYFTDYTVYEHNRSG-----EILHRTKHYVEKCEKNETICELNIVSTLDS 219

RESULT 9
ID INGR_MOUSE STANDARD: PRT: 575 AA.
AC 06127:
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE INTERLEUKIN-10 RECEPTOR PRECURSOR (IL-10R).

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IL10RA OR IL10R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6 X AJ F1; TISSUE-HEMATOPOIETIC;
RX MEDLINE: 94068585.
RA Ho A.S.-Y., Liu Y., Khan T.A., Hsu D.-H., Bazan J.F., Moore K.W.;
RT "A receptor for interleukin 10 is related to interferon receptors."
RL Proc. Natl. Acad. Sci. U.S.A. 90:11267-11271(1993).
CC -1- FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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CC or send an email to license@isb-sib.ch).
DR EMBL: L12120; AAA16156.1; -
DR WGD: MGI:96538; IL10RA.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 575 INTERLEUKIN-10 RECEPTOR.
FT DOMAIN 17 241 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 242 262 POTENTIAL.
FT DOMAIN 263 575 CYTOPLASMIC (POTENTIAL).
FT DISULFID 204 225 POTENTIAL.
FT CARBOHYD 50 50 POTENTIAL.
FT CARBOHYD 66 66 POTENTIAL.
FT CARBOHYD 113 113 POTENTIAL.
FT CARBOHYD 182 182 POTENTIAL.
FT CARBOHYD 238 238 POTENTIAL.
SQ SEQUENCE 575 AA; 64248 MW; 820B9CD576F686B7 CRC64;

Query Match 8.0%; Score 95.5; DB 1; Length 575;
Best Local Similarity 20.5%; Pred. No. 0.5; Mismatches 98; Indels 61; Gaps 10;
Matches 51; Conservative 39; Mismatches 98; Indels 61; Gaps 10;
OY 13 LVAAGPWLISAAGGKNLEKSPQVEVDIIDNFILRM---NRSDSYGNVTFSEDYQKT 68
DB 9 LVTISLSLEFIAYGTETLPSYVWFARFQHIILMKRIPNOSTEYVAL---KQY 64
OY 69 GMDNRIKLSGCONITSTKCNFSSKLNVYE--IKLRIR-EKENTSSWYEVDS-FTPF 123
DB 65 GNSYNDHICRKAQALSCDITFTLDYHRSYGRARAVDNSQYSMTTETETFT-- 123
OY 124 RKAQIGPPEVHLAEADKAVIHISPTKDSY-MMALDGLSFYSLILWNSSGVERLEN 182
DB 123 -----VDEVIL-----TYDSVTLKADGILTYTHPPRTTTPAGEYEQ 162
OY 183 IYSRHKIYKLS-----PEY-----TYCLKYAAALLTSKMGVYSP 217
DB 163 VKDLRVYKISIRKFSKLNATKRVKQEFITLTPVIGYKFKVYKPLRESINNAEMSE 222
OY 218 VHCITTYE 226
DB 223 EOCILITTE 231

RESULT 10
PWP2-CAEEL STANDARD: PRT: 925 AA.
AC P91341;
RT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE PERIODIC TRYPTOPHAN PROTEIN 2 HOMOLOG.

F55F8.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematozoa; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditioidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX Gating S., Scheet P., Kemp K.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).
CC -1- SIMILARITY: BELONGS TO THE PWP2 FAMILY OF WD-REPEAT PROTEINS.
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CC or send an email to license@isb-sib.ch).
DR EMBL: U80447; AAB37807.1; -
DR WORKREP: F55F8.3; CE11192.
DR PRINTS: PR00320; GPROTEINRPT.
DR PROSITE: PS00678; WD_REPEATS; 1.
DR PFW: PF00400; WD40; 4.
KW Hypothetical protein; Repeat; WD repeat.
FT REPEAT 188 218 WD1.
FT REPEAT 358 388 WD2.
FT REPEAT 400 430 WD3.
FT REPEAT 486 514 WD4.
FT REPEAT 524 554 WD5.
FT REPEAT 599 627 WD6.
SQ SEQUENCE 925 AA; 103899 MW; 439F35881B398CD1 CRC64;

Query Match 8.0%; Score 95.5; DB 1; Length 925;
Best Local Similarity 25.7%; Pred. No. 0.91; Mismatches 70; Indels 21; Gaps 4;
Matches 38; Conservative 19; Mismatches 70; Indels 21; Gaps 4;
OY 70 MDNRIKLSGCONIT--STKCNFSSKLNVYEI--KLRIRAKENTSSWYEVDSFTPFK 125
DB 1 MDNRIKLSGCONITSTKCNFSSKLNVYEI--KLRIRAKENTSSWYEVDSFTPFK 125
OY 126 AQIGPPEVHLAEADKAVIHISPTKDSY-MMALDGLSFYSLILWNSSGVERLEN 182
DB 61 LSISSPGYHLLASBERGVHVVHLLSEFKIYTFRSNRPISGLQSPDTRVAICRENDLQ 120
OY 169 IWKNSGVEERIKENTISYRHKIYKLSPT 196
DB 121 IHEFGKSIENKYNVPFSLSRKLSDS 148

RESULT 11
IL10R_HUMAN STANDARD: PRT: 578 AA.
ID IL10R_HUMAN
AC Q1651;
RT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 15-DEC-1998 (Rel. 37, Last annotation update)
DE INTERLEUKIN-10 RECEPTOR PRECURSOR (IL-10R).
GN IL10RA OR IL10R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LYMPHOMA;
RX MEDLINE: 94165477.
RA Liu Y., Wei S.H.-Y., Ho A.S.-Y., de Waal Malefyt R., Moore K.W.;
RT "Expression cloning and characterization of a human IL-10 receptor."
RL J. Immunol. 152:1821-1829(1994).
CC -1- FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: SPLEEN, THYMUS, AND PBMC. FAINT EXPRESSION
CC IN PANCREAS, SKELETAL MUSCLE, BRAIN, HEART, AND KIDNEY. PLACENTA,
CC LUNG, AND LIVER SHOWED INTERMEDIATE LEVELS. MONOCYTES, B CELLS,
CC LARGE GRANULAR LYMPHOCYTES, AND T CELLS EXPRESS HIGH LEVELS OF IL-
CC 10R.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC
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CC
CC EMBL: U00672; AAA17896.1; -
CC DR MIM: 146933; -
CC KW Receptor; Transmembrane; Glycoprotein; signal.
CC FT SIGNAL 1 21
CC FT CHAIN 1 21
FT DOMAIN 22 578 INTERLEUKIN-10 RECEPTOR.
FT TRANSMEM 236 256 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 257 578 POTENTIAL.
FT DISULFID 202 223 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 50 50 POTENTIAL.
FT CARBOHYD 74 74 POTENTIAL.
FT CARBOHYD 110 110 POTENTIAL.
FT CARBOHYD 154 154 POTENTIAL.
FT CARBOHYD 177 177 POTENTIAL.
FT CARBOHYD 189 189 POTENTIAL.
SQ SEQUENCE 578 AA; 62903 MW; EELB29064338157C CRC64;

Query Match 7.9%; Score 95; DB 1; Length 578;
Best Local Similarity 19.7%; Pred. No. 0.56;
Matches 51; Conservative 45; Mismatches 91; Indels 72; Gaps 11;

OY 2 MVLGATTVLVAVGFWLAAAGKLNKSPQKVEVDIDNFIIRWNSDESGVWTF 61
DB 5 LVVLAA--LISRLG-----SDAHGELDPSPSVWFEEAFPHILMTIPQSESTCY 57
OY 62 SFDYKGTMDNWKILSGCONITSTKCNFSSSLKLVYEE--IKLRIR- EKENTSSW--- 115
DB 58 EVALLRGIEMSNISNCSTLS--YDLTAVTLDLYHSNGYRARVAVDGRSRSNTVTN 115
OY 115 --LEVDSTFPRKAOICPRPVHLEADKAVIHIS--PGTDSYMMALDGLSFYSLILIK 171
DB 116 TRRSVDEVT---LTVG--SVNLEIHNGFLIKIQIPRPX----- 150
OY 172 NSSGVEERIENTYSRHKIKYKLSPEPT-----YCLKVKA 205
DB 150 -MAPANDTYESIFSHREYELAIRKVPNGNFTTHKKYKHENFSLISGVEGECVQKPS 208
OY 206 LITSWKIGVSPVHCIKTT 224
DB 209 VASRSNKGMSKECISLT 227
RESULT 12
TF_BOVIN
ID TF_BOVIN STANDARD; PRT; 292 AA.
AC P30931;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III).
GN F3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE-ADRENAL GLAND;
RX MEDLINE: 92109720.
RA Takayenoki Y., Muta T., Miyata T., Iwanaga S.;
RL "cDNA and amino acid sequences of bovine tissue factor.";
RT Biochem. Biophys. Res. Commun. 181:1145-1150(1991).
CC -1- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
CC CIRCULATING FACTOR VII OR VITA. THE (TF-VIIA) COMPLEX ACTIVATES
CC FACTORS IX OR X BY SPECIFIC LIMITED PROTEOLYSIS. TF PLAYS A ROLE IN
CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
CC PROPAGATION OF THE COAGULATION PROTEASE CASCADE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC
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CC
CC EMBL: S74147; AAB20755.1; -
CC DR PIR: J01319; KFB03.
DR HSSP: P24055; IAA1.
DR PRINTS: PR00346; TISSUEFACTOR.
DR PROSITE: PS00621; TISSUE_FACTOR. 1.
DR PFM: PF01108; Tissue_fac. 1.
KW Glycoprotein; Blood coagulation; Transmembrane; signal; Lipoprotein;
KW Palmitate.
FT SIGNAL 1 35
FT CHAIN 36 292
FT DOMAIN 36 248 TISSUE FACTOR.
FT TRANSMEM 249 271 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 272 292 POTENTIAL.
FT SITE 46 48 WKS MOTIF.
FT CARBOHYD 43 43 POTENTIAL.
FT CARBOHYD 153 153 POTENTIAL.
FT CARBOHYD 181 181 POTENTIAL.
FT DISULFID 81 89 BY SIMILARITY.
FT DISULFID 215 238 BY SIMILARITY.
FT LIPID 274 274 PALMITATE (BY SIMILARITY).
SQ SEQUENCE 292 AA; 32475 MW; 5E471D92BFBE163 CRC64;

Query Match 7.7%; Score 92.5; DB 1; Length 292;
Best Local Similarity 22.7%; Pred. No. 0.39;
Matches 40; Conservative 35; Mismatches 70; Indels 31; Gaps 9;

OY 70 MDNWKILSGCONITSTKCNFS--SLKLVYEEIKLRIRAEKENTSS-----WEVDSTFP 122
DB 74 LCNW--KNKCFYTTNTECDVDEIVKNREYLAIVLSYPADTSSSTVEPPTNSPEFTP 131
OY 123 FRKAOICP-----EVHLEADKAVIHISPGKDSYMMALD---GLSFYSLII 169
DB 132 YLETNIGOPTIOSFQVGTKNLVTVODARTLR-----ANSFELSLRDVFGADLYTLTY 186
OY 170 WR-NSSGVEERIENTYSRHKIKYKLSPEPTCYCKVRAALTSWKIGVSPVHCIKTT 224
DB 187 WKASSTGKKKATTN--TNGFLIDVDKGENYCPHQAVIL--SRVAVQKSPESPIKCT 239
RESULT 13
TF_HUMAN
ID TF_HUMAN STANDARD; PRT; 295 AA.
AC P13726;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUL-1993 (Rel. 38, Last annotation update)
DE TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III)
DE (THROMBOPLASTIN) (CD142 ANTIGEN).
GN F3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 89247359.
 RA Mackman N., Morrissey J.H., Fowler B., Edgington T.S.;
 RT "Complete sequence of the human tissue factor gene, a highly
 RT regulated cellular receptor that initiates the coagulation protease
 RT cascade.";
 RL Biochemistry 28:1755-1762(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 87260946.
 RA Spicer E.K., Horton R., Bloem L., Bach R., Williams K.R., Guha A.,
 RA Krius J., Lin T.C., Nemerson Y., Konigsberg W.H.;
 RT "Isolation of cDNA clones coding for human tissue factor: primary
 RT structure of the protein and cDNA.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:5148-5152(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 87244317.
 RA Morrissey J.H., Fakhrai H., Edgington T.S.;
 RT "Molecular cloning of the cDNA for tissue factor, the cellular
 RT receptor for the initiation of the coagulation protease cascade.";
 RL Cell 50:129-135(1987).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 88050796.
 RA Scarpati E.M., Wen D., Broze G.J. Jr., Miletich J.P.,
 RA Flandermeier R.R., Siegel N.R., Sadler J.E.;
 RT "Human tissue factor: cDNA sequence and chromosome localization of
 RT the gene.";
 RL Biochemistry 26:5234-5238(1987).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 88100453.
 RA Fisher K.L., Gorman C.M., Vehar G.A., O'Brien D.P., Lawn R.M.;
 RT "Cloning and expression of human tissue factor cDNA.";
 RL Thromb. Res. 48:89-99(1987).
 RN [6]
 RP DISULFIDE BONDS, AND PALMITOYLATION.
 RX MEDLINE: 89000604.
 RA Bach R., Konigsberg W.H., Nemerson Y.;
 RT "Structure of the extracellular domain of human tissue factor:
 RT location of the factor VIIa binding site.";
 RL Biochemistry 33:10864-10870(1994).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 33-243.
 RX MEDLINE: 94368785.
 RA Muller Y.A., Utsch M.H., Kelley R.F., de Vos A.M.;
 RT "Structure of the extracellular domain of human tissue factor:
 RT location of the factor VIIa binding site.";
 RL Biochemistry 33:10864-10870(1994).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 33-243.
 RX MEDLINE: 96190957.
 RA Muller Y.A., Utsch M.H., de Vos A.M.;
 RT "The crystal structure of the extracellular domain of human tissue
 RT factor refined to 1.7-A resolution.";
 RL J. Mol. Biol. 256:144-159(1996).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 33-251 IN COMPLEX WITH FVIIA.
 RX MEDLINE: 96175641.
 RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
 RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;
 RT "The crystal structure of the complex of blood coagulation factor
 RT VIIa with soluble tissue factor.";
 RL Nature 380:41-46(1996).
 CC -1- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
 CC CIRCULATING FACTOR VII OR VIIA. THE [TF:VIIA] COMPLEX ACTIVATES
 CC FACTORS IX OR X BY SPECIFIC LIMITED PROTEOLYSIS. TF PLAYS A ROLE IN
 CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
 CC PROPAGATION OF THE COAGULATION PROTEASE CASCADE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- INDUCTION: TF EXPRESSION IS HIGHLY DEPENDENT UPON CELL TYPE. TF

CC CAN ALSO BE INDUCED BY THE INFLAMMATORY MEDIATORS INTERLEUKIN 1
 CC AND TNF, AS WELL AS BY ENDOTOXIN, TO APPEAR ON MONOCYTES AND
 CC VASCULAR ENDOTHELIAL CELLS AS A COMPONENT OF CELLULAR IMMUNE
 CC RESPONSE.
 CC -1- DATABASE: NAME=PROT; NOTE=CD guide CD142 entry;
 CC WWW-http://www.ncbi.nlm.nih.gov/prov/cd/cd142.htm".
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 CC -----
 DR EMBL: J02931; AAA61150.1; -
 DR EMBL: M16553; AAA61151.1; -
 DR EMBL: J02846; AAA61152.1; -
 DR EMBL: M27436; AAA36734.1; -
 DR EMBL: A19048; CAA01438.1; -
 DR PIR: A28320; KFRU3.
 DR PIR: A43645; A43645.
 DR PIR: A47574; A47574.
 DR PDB: 1BOY; 10-UTN-96.
 DR PDB: 2HFT; 29-UNN-96.
 DR PDB: 1DAN; 04-SEP-97.
 DR PDB: 1TFH; 25-FEB-98.
 DR PDB: 1AHM; 19-AUG-98.
 DR PDB: 1TFH; 19-AUG-98.
 DR MIM: 134390; -
 DR PRINTS: PR00346; TISSUEFACTOR.
 DR PROSITE: PS00621; TISSUE_FACTOR; 1.
 DR PFAM: PF01108; Tissue_fac; 1.
 KW Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;
 KW Palmitate; 3D-structure.
 FT SIGNAL 1 32
 FT CHAIN 33 295
 FT DOMAIN 33 251
 FT TRANSMEM 252 274
 FT DOMAIN 275 295
 FT SITE 46 48
 FT SITE 77 79
 FT SITE 190 192
 FT CARBOHYD 156 156
 FT CARBOHYD 169 169
 FT DISULFID 81 89
 FT DISULFID 218 241
 FT LIPID 277 277
 FT CONFLICT 260 260
 FT SEQUENCE 295 AA; 33067 MW; D3486C713ED8EAD0 CRC64;
 SQ
 Query Match 7.7%; Score 92; DB 1; Length 295;
 Best Local Similarity 21.1%; Pred. No. 0.44;
 Matches 52; Conservative 42; Mismatches 100; Indels 52; Gaps 13;
 QY 8 ATTIVAVGVV--LSAAGCKNLSPOKVEVDIIDNFIILNMN-RSDSVGNVTFSE 63
 DB 17 ARTILL-----GVFAQVAGASGTTNTVAAYNLTKSNFTILEMEKRPVNOVTVQIS- 72
 QY 64 DYQRTGDMNWKISGCONITSTKCNFSSLKLVYEIKLRIR-----EKENTSS-- 114
 DB 72 ----TKSGDW--KSKCYTTDTDCDLND---EIVKDYKQYLAIVFSYPAGNVSTSGAG 122
 QY 114 ---WYEDSFPPFRKAIGRP-----EVLHLEDAKAIYHISPGKDSYMAALD- 160
 DB 123 EPLTENSPEFLPYLETMLDGOPTIOSFQVGTQVAVTEDETLVR-----RNNTFLSLRD 177
 QY 160 --GLSFYSLILKMSNGVEERINIRSRHIYLSPEYTYCLVKAAAL--LFSMKIGYV 215
 DB 178 VFGDLDLYTLTYKWSSSS-GKTKTKNTNFEFLVDVNGENVCFSVQAVISRTYVNRSTD 236
 QY 216 SPVHCI 221

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DB      237 SPVECM 242

RESULT 14
CD45_HUMAN STANDARD: PRT; 1304 AA.
ID      CD45_HUMAN
AC      P08575;
DT      01-AUG-1988 (Rel. 08, Created)
DT      01-AUG-1988 (Rel. 08, Last sequence update)
DT      01-NOV-1997 (Rel. 35, Last annotation update)
DE      LEUCOCYTE COMMON ANTIGEN PRECURSOR (EC 3.1.3.48) (L-CA) (CD45 ANTIGEN)
DE      (T200).
GN      PTPRC OR CD45.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC      Euthera; Primates; Catarrhini; Hominoidea; Homo.
OC      [1]
RN      SEQUENCE FROM N.A.
RP      TISSUE-LYMPHOCYTES;
RX      MEDLINE: 88061067.
RA      Streuli M., Hall L.R., Saga Y., Schlossman S.F., Salto H.;
RT      "Differential usage of three exons generates at least five different
RT      mRNAs encoding human leukocyte common antigens.";
RL      J. Exp. Med. 166:1548-1566(1987).
RN      [2]
RP      FUNCTION.
RX      MEDLINE: 89017162.
RA      Chabonneau H., Tonks N.K., Walsh K.A., Fischer E.H.;
RT      "The leukocyte common antigen (CD45): a putative receptor-linked
RT      protein tyrosine phosphatase.";
RL      Proc. Natl. Acad. Sci. U.S.A. 85:7182-7186(1988).
RN      [3]
RP      MUTAGENESIS.
RX      MEDLINE: 90316093.
RA      Streuli M., Krueger N.X., Thal T., Tang M., Salto H.;
RT      "Distinct functional roles of the two intracellular phosphatase like
RT      domains of the receptor-linked protein tyrosine phosphatases LCA and
RT      LAR.";
RL      EMBO J. 9:2399-2407(1990).
CC      -1- FUNCTION: REQUIRED FOR T-CELLS ACTIVATION THROUGH THE ANTIGEN
CC      RECEPTOR. THE FIRST PTPASE DOMAIN HAS ENZYMACTIC ACTIVITY, WHILE
CC      THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE
CC      THE FIRST ONE.
CC      -1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O =
CC      PROTEIN TYROSINE + ORTHOPHOSPHATE.
CC      -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC      -1- ALTERNATIVE PRODUCTS: THERE ARE 8 DIFFERENT VARIANTS OF L-CA,
CC      WHICH ARISE BY ALTERNATIVE SPLICING.
CC      -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
CC      -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC      -1- DATABASE: NAME-PROW: NOTE-CD guide CD45 entry;
CC      WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd45.htm".
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: Y00638; CAA68669.1; -.
DR      HSSP: P18052; LYPO.
DR      MIM: 151460;
DR      PRINTS: PR00700; PRTPHPTASE.
DR      PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR      PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
DR      PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
DR      PFAM: PF00041; fn3; 2.
DR      PFAM: PF00102; X-Phosphatase; 2.
KW      Glycoprotein; Transmembrane; Phosphorylation; B-cell; T-cell; Repeat;
KW      Alternative splicing; Hydrolase; Signal.

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FT      SIGNAL      1      23
FT      CHAIN       24      1304
FT      DOMAIN      24      575
FT      TRANSMEM    576      597
FT      DOMAIN      598      1304
FT      DOMAIN      598      1304
FT      DOMAIN      598      1304
FT      DOMAIN      598      1304
FT      DOMAIN      598      1304
FT      DOMAIN      598      1304
FT      DOMAIN      598      1304
FT      ACT_SITE    1167      1167
FT      ACT_SITE    1167      1167
FT      MUTAGEN     851      851
FT      CARBOHYD    78      90
FT      CARBOHYD    90      90
FT      CARBOHYD    95      95
FT      CARBOHYD    184      184
FT      CARBOHYD    190      190
FT      CARBOHYD    197      197
FT      CARBOHYD    232      232
FT      CARBOHYD    260      260
FT      CARBOHYD    270      270
FT      CARBOHYD    276      276
FT      CARBOHYD    335      335
FT      CARBOHYD    378      378
FT      CARBOHYD    419      419
FT      CARBOHYD    468      468
FT      CARBOHYD    488      488
FT      CARBOHYD    529      529
SQ      SEQUENCE    1304 AA; 147253 MW; 1F357BC5632618B2 CRC64;

```

Query Match 7.6%; Score 90.5; DB 1; Length 1304;
 Best Local Similarity 20.9%; Pred. No. 3.9;
 Matches 36; Conservative 23; Mismatches 60; Indels 53; Gaps 6;

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OY      53 DESGVNTFFSDYQKTGMNKLKSGCNTSTKCNFSSKLKLYEIKLRIRAKENTS 112
DB      227 DEKYNITVDLYNKK-----ETKLFATKLNVENVEK-----GNWTC 263
OY      113 SMYEDSTPPPKKQIGPEVHLEADKAIYIHISPG----- 151
DB      264 TNNENHNLTECKNLSVSIHNSCTAPDPTLLDPVGEKFOHDCQVERADPTTCLKW 323
OY      151 KDSYMMALDGLSFTYSL-----LWKSSGVERENTISRRKIYKLSPTTY 198
DB      324 KNIEFTDQNTNITRYFCGGMNIFDK--EIKENLEPENE-YKCOSEILY 371

RESULT 15
ID      6DCS_SOYBN STANDARD: PRT; 315 AA.
AC      P26690;
DT      01-AUG-1992 (Rel. 23, Created)
DT      01-AUG-1992 (Rel. 23, Last sequence update)
DT      01-AUG-1992 (Rel. 23, Last annotation update)
DE      NAO(P/H DEPENDENT 6'-DEOXYCHALCONE SYNTHASE (EC 1.-.-.-).
OS      Glycine max (Soybean).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      eudicotyledons; Magnoliophyta; eudicotyledons;
OC      core eudicot; Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae;
OC      Glycyne.
RN      [1]
RP      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC      STRAIN-CV: HAROSY 63;
RX      MEDLINE: 91177016.
RA      Welle R., Schroeder G., Schiltz E., Grisebach H., Schroeder J.;
RT      "Induced plant responses to pathogen attack. Analysis and
RT      heterologous expression of the key enzyme in the biosynthesis of
RT      phytoalexins in soybean (Glycine max L. Merr. cv. Harosoy 63).";
RL      Eur. J. Biochem. 196:423-430(1991).
CC      -1- FUNCTION: CO-ACTS WITH CHALCONE SYNTHASE IN FORMATION OF
CC      4,2',4'-TRIHYDROXYCHALCONE, INVOLVED IN THE BIOSYNTHESIS OF
CC      GLYCOPOLIN TYPE PHYTOALEXINS.

```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 1, 2000, 04:38:14 ; Search time 69.16 Seconds
(without alignments)
229.577 Million cell updates/sec

Title: US-09-240-675-2_COPY_1_229
Perfect score: 1196
Sequence: 1 MMVVLGATTLVYVNGPMV.....WKIGVSPHCIRKIVENEL 229

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SPTREMBL.12.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	430.5	36.0	569	13 Q9YHMO	Q9YHMO gallus gall
2	219	18.3	349	11 Q61190	Q61190 mus musculu
3	203	17.0	332	11 Q63953	Q63953 mus musculu
4	179	15.0	341	13 Q9YGC8	Q9YGC8 gallus gall
5	113.5	9.5	484	4 Q14936	Q14936 homo sapien
6	97.5	8.2	6048	5 Q23020	Q23020 caenorhabd1
7	97.5	8.2	6831	5 Q23550	Q23550 caenorhabd1
8	97.5	8.2	7160	5 Q23551	Q23551 caenorhabd1
9	91.5	7.7	6875	6 Q28733	Q28733 oryctolagus
10	90.5	7.6	1143	4 Q16614	Q16614 homo sapien
11	89.5	7.5	508	13 Q9YHV9	Q9YHV9 gallus gall
12	89.5	7.5	2033	11 Q54711	Q54711 mus musculu
13	89.5	7.5	2213	6 Q95208	Q95208 oryctolagus
14	89.5	7.5	2213	11 Q88307	Q88307 mus musculu
15	89	7.4	239	4 Q15467	Q15467 homo sapien
16	88.5	7.4	1220	3 Q12465	Q12465 saccharomyc
17	87.5	7.3	504	4 Q99624	Q99624 homo sapien
18	87	7.3	874	11 P97378	P97378 mus musculu
19	87	7.3	1083	5 Q45604	Q45604 caenorhabd1
20	87	7.3	1120	3 Q08773	Q08773 saccharomyc

21	87	7.3	26926	4 Q10466	Q10466 homo sapien
22	86.5	7.2	429	3 Q06103	Q06103 saccharomyc
23	84.5	7.1	2214	4 Q92673	Q92673 homo sapien
24	83.5	7.0	430	10 Q23854	Q23854 brassica ca
25	82.5	6.9	406	1 Q58459	Q58459 methanococ
26	82.5	6.9	746	12 Q90754	Q90754 foot-and-mo
27	82	6.9	508	5 Q20930	Q20930 caenorhabd1
28	82	6.9	817	13 Q07784	Q07784 gallus gall
29	82	6.9	1093	11 Q70535	Q70535 rattus norv
30	81.5	6.8	1040	13 Q96675	Q96675 brachydanto
31	81	6.8	1009	1 Q58863	Q58863 methanococ
32	81	6.8	1375	5 Q94537	Q94537 drosophila
33	81	6.8	1493	11 P97798	P97798 mus musculu
34	81	6.8	1526	5 Q94538	Q94538 drosophila
35	81	6.8	2340	11 Q6705	Q6705 mus musculu
36	80.5	6.7	334	11 Q70367	Q70367 rattus norv
37	80.5	6.7	962	4 Q94977	Q94977 homo sapien
38	80	6.7	513	11 Q35664	Q35664 mus musculu
39	79.5	6.6	431	10 Q23861	Q23861 brassica ca
40	79.5	6.6	829	5 Q9XMD9	Q9XMD9 caenorhabd1
41	79.5	6.6	1074	2 Q9X257	Q9X257 thermotoga
42	79	6.6	247	11 Q35663	Q35663 mus musculu
43	79	6.6	248	11 Q35983	Q35983 mus musculu
44	79	6.6	442	3 Q06349	Q06349 saccharomyc
45	79	6.6	513	11 Q35238	Q35238 mus musculu

ALIGNMENTS

RESULT 1
Q9YHMO PRELIMINARY; PRT; 569 AA.
AC Q9YHMO;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE INTERFERON ALPHA/BETA RECEPTOR 1.
GN IFNARI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA REBOU J., GARDINER K., MONNERON D., UZE G., LUTPALLA G.;
RT "Comparative genomic analysis of the Interferon/Interleukin-10
receptor gene cluster";
RL Genome Res. 0:0-0(1999).
DR EMBL; AF082664; AAD13669.1; -.
KW Receptor.
SQ SEQUENCE 569 AA; 64055 MW; F99BC099 CRC32;

Query Match 36.0%; Score 430.5; DB 13; Length 569;
Best Local Similarity 43.8%; Pred. No. 7.4e-31;
Matches 99; Conservative 37; Mismatches 79; Indels 11; Gaps 6;
QY 7 GATLVVAVGPMWLSAAGKLNKSPKQEVVDIIDNFIILMRNRSDESGVTFSPDQ 66
DB 9 GRLAVALLCVLLVVSRCAGOTNLKSPDIOVAVNNFTLMWYTDGCT-NVTFSAQYQ 67
QY 67 -----KTGMNMWIKLSCONTSTKCNFSSLLKLVNVEIKLRIRAE-KENTSSWEYDSF 120
DB 68 CFDDLOLSEPEMKELSGCQNVNHTCECFSSALITVYDTHHRIAREKRAKSPSSIFEM 127
QY 121 TPRKKAQIGPEVHLAEADKAIVIHISPGTDSV--KMAIDGSLFTYSLIKNSGVEE 178
DB 128 IPRYIAQIGPEIALOSINGAIKINISPEANQVRKMK-LISYFVKYNNVIMDNSNV-E 185
QY 179 RIENIYSNRIKYKLSPEFTYCLKYKAKALLSMKIGVSPVHCITTT 224
DB 186 KVRSLIPDIVINDIAPETTYCLKVQATVPLEDKGLSPHCITKT 231

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RESULT 2
ID 061190 PRELIMINARY: PRT: 349 AA.
AC 061190:
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, last annotation update)
DE CYTOKINE RECEPTOR FAMILY 2, MEMBER 4 (CLASS II CYTOKINE RECEPTOR 4).
GN IL10RB OR CRFB4 OR CRF2-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE: 97199375.
RA GIBBS V.C., PENNICA D.;
RT "CRF2-4: Isolation of cDNA clones encoding the human and mouse
RT proteins."
RL Gene 186:97-101(1997).
DR EMBL: U53696; AAC53062.1; -
DR MGD: MGI:109380; IL10rb.
DR PFM: PFM0041; fn3; 1.
SQ SEQUENCE 349 AA: 39774 MW: 4AC1802A CRC32;

```

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Query Match 18.3%; Score 219; DB 11; Length 349;
Best Local Similarity 28.2%; Pred. No. 4.5e-12;
Matches 62; Conservative 47; Mismatches 83; Indels 28; Gaps 9;

```

```

OY 16 VCPWVLSAAGGKLNKSPKVEVDIIDNFIILRNRSDESVCNTPSFYQ--KTGMDNM 73
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 9 LGGFLVLPALG--MIPPEKVRNNSVNFKNILDMVEPAPKPTUTLTAAQESTRSQD- 66
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 74 IKLSGQNTSTKCNFSSKLNYEIKLRRAE-KENTSWYEVDSFTFRKAQIGPPE 132
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 66 -----CKRPASTQCDFS--HLKSKGYTVRAELADEHSEWNV--TFCPEVDITLIGPPE 117
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 133 VHLAEADKAIVHIIS-----PGTKDSVMALDGL--SFTSYLLWKSSGVEEIEINI 183
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 118 MOIESLAESLHLRFSAPOIENEPE-----WTLKNITDSWAVYQWKNGTNEKFGVSP 172
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 184 YSRHKIYKLSPEPTYCLKVAALLTSMKIGVSPVHCIRT 223
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 173 YDSEVLRNLEPWTTCIYQVGFLLDQNRGEMSEPICERI 212

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RESULT 3
ID 063953 PRELIMINARY: PRT: 332 AA.
AC 063953:
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, last annotation update)
DE INTERFERON GAMMA RECEPTOR 2 (INTERFERON GAMMA RECEPTOR BETA SUBUNIT).
GN IFNGR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE: 94170381.
RA HEMMI S., BOHNT R., STARK G., DI MARCO F., AGUET M.;
RT "A novel member of the murine interferon receptor family complements
RT functionality of the murine interferon gamma receptor in human
RT cells."
RL Cell 76:803-810(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-129SV/7J.
RX MEDLINE: 97118072.
RA EBENBERGER C., RHEE S., MUTHUKUMARAN G., LEMBO D., DONNELLY R.,

```

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RA PESTKA S., DEMBIC Z.;
RT "Genomic organization and promoter analysis of the gene IfngR2
RT encoding the second chain of the mouse interferon-gamma receptor."
RL Scand. J. Immunol. 44:599-606(1996).
DR EMBL: U69599; AAC52938.1; -
DR EMBL: U69594; AAC52938.1; JOINED.
DR EMBL: U69595; AAC52938.1; JOINED.
DR EMBL: U69596; AAC52938.1; JOINED.
DR EMBL: U69597; AAC52938.1; JOINED.
DR EMBL: U69598; AAC52938.1; JOINED.
DR MGD: MGI:107654; AAB30165.1; -
DR PFM: PFM0041; fn3; 1.
SQ SEQUENCE 332 AA: 37471 MW: 0BF24E9E CRC32;

```

```

Query Match 17.0%; Score 203; DB 11; Length 332;
Best Local Similarity 30.1%; Pred. No. 1.2e-10;
Matches 69; Conservative 38; Mismatches 86; Indels 36; Gaps 13;

```

```

OY 21 LSAAGG-----KNLSPKVEVDIIDNFIILRNRSDES-----YGNVTSPFYQKTGM 70
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 16 LGAAASPSDFSQLAAPLNPRLHLYNDEQILTWEPSPSSNDPRVYQVEYSF-----I 69
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 71 D-NWIKL--SCQNTSTKCNFSS--LKLNYE-EIKLRIRAKEN-TSSWYEVDSFTP 122
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 70 DGSWRLLEPNCITDITERKCDLTGGRLKLPHPFTYFLRAKRGNTSKWGLEPQH 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 123 FRKAQIGPPE-VHLAEADKAIVHIISPQKDSVMALDGLSFTSYLLWKSSGVEEIE 181
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 130 YENVTVGPKNISVTPGKSLVTHSPFD-----VFHGATFQYLHVHWKSEFTQEQVE 184
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 182 NYSRHKIY--KLSPETTCYCKVAAL-LTSMKI--GVSPVHCIRT 224
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 185 GPFKSNSTVLGNLKPVRVYCLQTEAQLILKNKRLRPHGLISVNSCHETT 233

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```

RESULT 4
ID 09YGC8 PRELIMINARY: PRT: 341 AA.
AC 09YGC8:
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, last sequence update)
DT 01-MAY-1999 (TREMblrel. 10, last annotation update)
DE INTERLEUKIN-10 RECEPTOR 2.
GN IL10R2.
OS Gallus gallus (chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RA REBOUL J., GARDINER K., MONNERON D., UZE G., LUTRALA G.;
RT "Comparative genomic analysis of the Interferon/Interleukin-10
RT receptor gene cluster."
RL Genome Res. 0:0-0(1999).
DR EMBL: AF082667; AAD13678.1; -
DR EMBL: AF082666; AAD13671.1; -
KW Receptor.
SQ SEQUENCE 341 AA: 39062 MW: 7433D364 CRC32;

```

```

Query Match 15.0%; Score 179; DB 13; Length 341;
Best Local Similarity 26.0%; Pred. No. 1.8e-08;
Matches 53; Conservative 45; Mismatches 84; Indels 22; Gaps 9;
OY 33 POKVEVDIIDNFIILRNRSDESVCNTPSFYQ----YQKGMWNKILSGQNTSTKCN 88
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 24 PNAIRISSVNFSSVLLMPDPGVRKGNLSYTVQAKSIFPKQNFNN-----VTNINLVTECD 78
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 89 FSSLNLYEEKRLIRAKENTSWYEVDSFTFRKAQIGPPEVHLAEADKAIVHIIS- 148
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 79 VSS--LSVYGAIVYLRVTEWEDHSDMAVVRFKPMADTVIGPSPVNAKSESGLTHVDFTG 136

```


[illegible]

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ID      Q23020      PRELIMINARY;          PRT;      6048 AA.
AC      Q23020; 027232;
DT      01-NOV-1996 (TREMBLrel. 01, Created)
DT      01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT      01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE      TWITCHIN.
GN      UNC-22 OR ZK617.1.
OS      Caenorhabditis elegans.
OC      Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
OC      Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-BRISTOL N2;
RX      MEDLINE; 90044042.
RA      BENJIAN G.M., KIFF J.E., NECKELMANN N., MOERMAN D.G., WATERSON R.H.;
RT      "Sequence of an unusually large protein implicated in regulation of
RL      myosin activity in C. elegans.";
RN      Nature 342:45-50(1989).
RP      [2]
RC      SEQUENCE FROM N.A.
RX      STRAIN-BRISTOL N2;
RA      MEDLINE; 93387664.
RA      BENJIAN G.M., L'HERNAULT S.W., MORRIS M.E.;
RT      "Additional sequence complexity in the muscle gene, unc-22, and its
RL      encoded protein, twitchin, of Caenorhabditis elegans.";
RN      Genetics 134:1097-1104(1993).
RP      [3]
RC      SEQUENCE FROM N.A.
RA      HARRIS B.;
RL      Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; X15423; CA933463.1; -.
DR      EMBL; Z73899; CA98081.1; ALT-INT.
DR      EMBL; Z73897; CA98081.1; JOINED.
DR      HSSP; Q63450; 1A06.
DR      PFAM; PF00041; fn3; 31.
DR      PFAM; PF00047; ig; 13.
DR      PFAM; PF00069; Pkinase; 1.
DR      PRINTS; PR00014; FNTYPEPITI.
KW      Myosin; Kinase.
SQ      SEQUENCE 6048 AA; 668449 MW; 1977C602 CRC32;

Query Match      8.2%; Score 97.5; DB 5; Length 6048;
Best Local Similarity 22.8%; Pred. No. 17;
Matches 44; Conservative 22; Mismatches 74; Indels 53; Gaps 10.

QY      30 LKSPK-----EV-DIIDNFIILRNRSDESGVNTFSPYOK--TGMDNWKILSGCONI 82
DB      1073 LDRPSKPNGLPEVSDVDFEDNLNLSKPPDDGGEFIEYEVKLTATGRWPF---CAKY 1129

QY      83 TSTKCNFSSLLNLYEIEIKLRIR-A-EKENTSSWEYVDSFTPRKAQIGPPEVHLBAEDKA 141
DB      1130 KDTAKHIDGLKKG--QTQGFPRYKAVANKGASALSTDKTKAKNPYDEGCK----- 1180

QY      142 IVYHISPEKTSQVMALDGLSTFTSYSLIW---KNSSGYEERLENIYSRKIKYIKLSPEPTY 198
DB      1180 -----GTPPVVDMDADRVRS-----LEMEPKSDGG-----APITQY 1210

QY      199 CLKYKAAALLTSMK 211
DB      1211 VIEKKGKHGRDQ 1223

RESULT
ID      Q23550      PRELIMINARY;          PRT;      6831 AA.
AC      Q23550;
DT      01-NOV-1996 (TREMBLrel. 01, Created)
DT      01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT      01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE      UNC-22 PROTEIN.
GN      UNC-22.
OS      Caenorhabditis elegans.

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OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabdilia; Rhabdilitia;
OC Rhabdilitia; Rhabdilitidae; Rhabdilitidae; Peloderinae; Caenorhabdilitis.
RN [1]
RP SEQUENCE FROM N.A.
RA WHITE S.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: 273897; CA98064.1; -.
DR EMBL: 273899; CA98064.1; JOINED.
DR HSSP: P02751; 1FNA.
DR PFAM: PF00041; fn3; 31.
DR PFAM: PF00047; 19; 17.
DR PFAM: PF00069; pkinase; 1.
DR PRINTS: PR00014; FNTYPEI11.
SQ SEQUENCE 6831 AA; 752579 MW; 0A66C338 CRC32;

Query Match      8.2%; Score 97.5; DB 5; Length 6831;
Best Local Similarity 22.8%; Pred. No. 20;
Matches 44; Conservative 22; Mismatches 74; Indels 53; Gaps 10;

OY 30 LKSPQK---VEV-DIIDNFIKRNRSDESGVNTFSPDYOK--TGMDNMKLSGCONI 82
DB 1856 LDRSPKNGPLEVSDVFDNLSMKRPDDGGEPIEYVEKLDATGAWVP---CAKV 1912
OY 83 TSTKCNFSSSLKLNVEEIKLRIRA-EKENTSSWTEVDSFTPFKAQIGPEVHLEADKA 141
DB 1913 KDTKAHIDGLKKG--QTYOFKRVKAVNKGASDALSTDKTKAKNYDEPKT----- 1963
OY 142 IVIHISPTKDSVMWALDGLSFTYSLLIW--KNSSGVEERIEIENYSRHKIYKLSPEPTY 198
DB 1963 -----GTPDVYDWDADRVS-----LEWEPPKSDG-----APITQY 1993
OY 199 CLKVKAALLTSWK 211
DB 1994 VIEKKGKGRDQWQ 2006

RESULT 8
O23551 PRELIMINARY; PRT; 7160 AA.
AC O23551;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE ZK617.1B.
GN Caenorhabdilitis elegans.
OS Eukaryota; Metazoa; Secernentea; Rhabdilia; Rhabdilitidae;
OC Rhabdilitia; Rhabdilitidae; Peloderinae; Caenorhabdilitis.
RN [1]
RP SEQUENCE FROM N.A.
RA HARRIS B.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPESEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DUREBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOMKNEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 kb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
RP SEQUENCE FROM N.A.
RA WHITE S.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

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DR EMBL: 273899; CA98082.1; -.
DR EMBL: 273897; CA98082.1; JOINED.
DR EMBL: 273897; CA98065.1; -.
DR EMBL: 273899; CA98065.1; JOINED.
DR HSSP: P02751; 1FNA.
DR PFAM: PF00041; fn3; 31.
DR PFAM: PF00047; 19; 17.
DR PFAM: PF00069; pkinase; 1.
DR PRINTS: PR00014; FNTYPEI11.
SQ SEQUENCE 7160 AA; 789211 MW; EDD567FE CRC32;

Query Match      8.2%; Score 97.5; DB 5; Length 7160;
Best Local Similarity 22.8%; Pred. No. 21;
Matches 44; Conservative 22; Mismatches 74; Indels 53; Gaps 10;

OY 30 LKSPQK---VEV-DIIDNFIKRNRSDESGVNTFSPDYOK--TGMDNMKLSGCONI 82
DB 2185 LDRSPKNGPLEVSDVFDNLSMKRPDDGGEPIEYVEKLDATGAWVP---CAKV 2241
OY 83 TSTKCNFSSSLKLNVEEIKLRIRA-EKENTSSWTEVDSFTPFKAQIGPEVHLEADKA 141
DB 2242 KDTKAHIDGLKKG--QTYOFKRVKAVNKGASDALSTDKTKAKNYDEPKT----- 2292
OY 142 IVIHISPTKDSVMWALDGLSFTYSLLIW--KNSSGVEERIEIENYSRHKIYKLSPEPTY 198
DB 2292 -----GTPDVYDWDADRVS-----LEWEPPKSDG-----APITQY 2322
OY 199 CLKVKAALLTSWK 211
DB 2323 VIEKKGKGRDQWQ 2335

RESULT 9
O28733 PRELIMINARY; PRT; 6875 AA.
AC O28733;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1998 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE TITIN (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-CE12;
RA LABEIR S.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-6805 FROM N.A.
RC STRAIN-CE12;
RX MEDLINE: 92258380.
RA LABEIR S., GAUTEL M., LAKEY A., TRINICK J.;
RT "Towards a molecular understanding of titin."
RL EMBO J. 11:1711-1716(1992).
RN [3]
RP SEQUENCE OF 4305-5320 FROM N.A.
RC TISSUE-PCOAS MUSCLE;
RX MEDLINE: 90238553.
RA LABEIR S., BARLOW D.P., GAUTEL M., GIBSON T., HOLT J., HSIEH C.T.,
RA FRANCIS U., LEONARD K., WARDLE J., WHITING A., TRINICK J.;
RT "A regular pattern of two types of 100-residue motif in the sequence
RT of titin."
RL Nature 345:273-276(1990).
DR EMBL: X64696; CA445937.1; -.
DR EMBL: X17329; CA435207.1; -.
DR HSSP: P56276; 1TLK.
DR PFAM: PF00041; fn3; 50.
DR PFAM: PF00047; 19; 3.
KW Myosin; Muscle protein.
FT NON_TER 1 6875
FT 1 6875

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SEQUENCE 6875 AA; 759127 MW; E5D3B61F CRC32;
Query Match 7.7%; Score 91.5; DB 6; Length 6875;
Best Local Similarity 21.7%; Pred. No. 71;
Matches 54; Conservative 24; Mismatches 76; Indels 95; Gaps 10;
OY 8 ATTLVAVGPPVLSAAGGNLKSPQVKEVDIIDNFLRNKDESVGNVTFSDYQK 67
DB 221 ATVNVLDRPGP-----VRNLKIP-----DVSSDRCTRIRMDPEDD----- 256
OY 68 TGMOWIKISGC--QINISTKCNFSSKLKNV-----EIKLIRAK 108
DB 256 -----GGEIONVILEKCESRMRWSTYSATVLPPTVTRNLIEGNEYIFRVAEN 306
OY 109 E-----NTSWYEDSFTEPRKAQIGPPEVHLEADKAIVI-----HISP 148
DB 307 KIGTGPPEBKRVIAKTYKDRGRDPPEVTYKSEKMTVWSPPEYDGGKSTGYLEK 366
OY 149 GTKDSVMALDGLSTFTYSLILKNSGVEERIENTYSRRKIYKLSPEPTYCLKRAALLT 208
DB 367 KEKHSVRM-----VFNKSAIPER-----RLKVNLI.PGHEYCFRVA----- 405
OY 209 SMKIGVYSP 217
DB 405 ENELGVGP 413
RESULT 10
O16614 PRELIMINARY: PRT; 1143 AA.
AC Q16614;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE 1200 LEUKOCYTE COMMON ANTIGEN (CD45, LC-A) PRECURSOR (EC 3.1.3.48)
DE (CD45, LC-A).
GN PTPRC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 87275816.
RA RALPH S.J., THOMAS M.L., MORTON C.C., TROMBRIDGE I.S.;
RT "Structural variants of human T200 glycoprotein (leukocyte-common antigen)".
RL EMBO J. 6:1251-1257(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-PLACENTA;
RX MEDLINE; 89009812.
RA HALL L.R., STREUBLI M., SCHLOSSMAN S.F., SAITO H.;
RT "Complete exon-intron organization of the human leukocyte common antigen (CD45) gene".
RL J. Immunol. 141:2781-2787(1988).
DR EMBL; M23492; AAD15273.1; JOINED.
DR EMBL; M23461; AAD15273.1; JOINED.
DR EMBL; M23462; AAD15273.1; JOINED.
DR EMBL; M23466; AAD15273.1; JOINED.
DR EMBL; M23467; AAD15273.1; JOINED.
DR EMBL; M23468; AAD15273.1; JOINED.
DR EMBL; M23469; AAD15273.1; JOINED.
DR EMBL; M23470; AAD15273.1; JOINED.
DR EMBL; M23471; AAD15273.1; JOINED.
DR EMBL; M23472; AAD15273.1; JOINED.
DR EMBL; M23473; AAD15273.1; JOINED.
DR EMBL; M23474; AAD15273.1; JOINED.
DR EMBL; M23475; AAD15273.1; JOINED.
DR EMBL; M23476; AAD15273.1; JOINED.
DR EMBL; M23477; AAD15273.1; JOINED.
DR EMBL; M23478; AAD15273.1; JOINED.
DR EMBL; M23479; AAD15273.1; JOINED.

DR EMBL; M23480; AAD15273.1; JOINED.
DR EMBL; M23481; AAD15273.1; JOINED.
DR EMBL; M23482; AAD15273.1; JOINED.
DR EMBL; M23483; AAD15273.1; JOINED.
DR EMBL; M23484; AAD15273.1; JOINED.
DR EMBL; M23485; AAD15273.1; JOINED.
DR EMBL; M23486; AAD15273.1; JOINED.
DR EMBL; M23487; AAD15273.1; JOINED.
DR EMBL; M23488; AAD15273.1; JOINED.
DR EMBL; M23489; AAD15273.1; JOINED.
DR EMBL; M23490; AAD15273.1; JOINED.
DR EMBL; M23491; AAD15273.1; JOINED.
DR EMBL; Y00062; CA86269.1; -.
DR HSSP; P18052; IYFO.
DR PROSITE; PS00383; TYR-PHOSPHATASE_1; 2.
DR PFAM; PF00041; fn3; 2.
DR PFAM; PF00102; X-PHOSPHATASE; 2.
DR PRINTS; PRO0700; PRTYPRPHASE.
KW Signal; Alternative splicing; Hydrolase.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 1143 POTENTIAL.
SQ SEQUENCE 1143 AA; 130897 MW; 97A3A561 CRC32;
Query Match 7.6%; Score 90.5; DB 4; Length 1143;
Best Local Similarity 20.9%; Pred. No. 8.2;
Matches 36; Conservative 23; Mismatches 60; Indels 53; Gaps 6;
OY 53 DESVGNVTFSDYQKTDGNDNKKLSGCONITSTKCNFSSKLKNVYEELKIRAKETS 112
DB 66 DEKANTITVDLYNKK-----ETKLETAFLNNEVECC-----GNNTC 102
OY 113 SWEYDSETPPRKAQIGPPEVHLEADKAIVIHISPT----- 151
DB 103 TNEVHNTECKNMSVSSHSCTAPDKTLIDVPPGYEKQLHDCQVEAKDTTICKM 162
OY 151 KDSVMALDGLSTFTYSL---LKNSSGVEERIENTYSRRKIYKLSPEPTY 198
DB 163 KNIETFTCDTQNTYRFQCGNMIFDNK---EIKLENLEPEHE-YKCDSEILY 210
RESULT 11
OYTHV9 PRELIMINARY: PRT; 508 AA.
AC OYTHV9;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE INTERFERON ALPHA/BETA RECEPTOR 2.
GN IFNAR2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LIVER;
RA REBOUL J., GARDINER K., MONNERON D., UZE G., LUTFALLA G.;
RT "Comparative genomic analysis of the interferon/interleukin-10 receptor gene cluster".
RL Genome Res. 0:0-0(1999).
DR EMBL; AF082665; AAD13670.1; -.
DR HSSP; P13726; IYFH.
KW Receptor.
SQ SEQUENCE 508 AA; 57049 MW; 2DC4E498 CRC32;
Query Match 7.5%; Score 89.5; DB 13; Length 508;
Best Local Similarity 23.2%; Pred. No. 3.5;
Matches 61; Conservative 35; Mismatches 96; Indels 71; Gaps 15;
OY 2 MVVLIGAT---TLVAVGPPVLSAAGGNLKSPQV--EVDIIDNF--ILRW-RS 52
DB 1 MFTLMGGPLRFYQLVFVSI--LCACYSSLSEKIPREPPDNLQMTSNFQHILSWRAHS 57

OY	53	DESVC----	NTFSSFOYKGTGMNWKLSGCCQNTSTKCNFSKLNVYEE-----IKLRIR	105
Db	58	DPVTPTTYRVLVS-----	SSHNKMIKACSCSIVTVPFCULTDFOVYSDSEIYAFVQSPYG	111
OY	106	AEKENTSSWYEDSFTPPRKAQIGPPEVHLEADKAIVIHIS-PGT----	KDSVMALDGL	161
Db	112	TEVFNSSLLH-----	FSPISEFTLGPPEFLNSCVCHINCINTIKLPTHLKKNKL-----	162
OY	162	SFTYSLLWKKSSGVGEERENITYSRK-----	IKYLSPEPTYLKY-----	203
Db	162	---LSLFDIYNKVNYEITLRTVGEEHKRSPEKVTSEPSFISVIEELYPNKNYCVSMVTAS	218	
OY	203	--KAALLTSMKIGVSPVHCIKT	223	
Db	219	LNKHSIPSAWK-----	CITTT 233	
RESULT	12			
ID	054711	PRELIMINARY:	PRT: 2033 AA.	
AC	054711:			
DT	01-JUN-1998	(TREMBLrel. 06, Created)		
DT	01-JUN-1998	(TREMBLrel. 06, Last sequence update)		
DT	01-NOV-1999	(TREMBLrel. 12, Last annotation update)		
DE	SORTILIN-RELATED RECEPTOR, LDRR CLASS A REPEATS-CONTAINING PRECURSOR (GP250) (FRAGMENT).			
GN	SORL1.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-BRAIN:			
RA	HEKMAN-BORGEYER I., HAMPE W., SCHINKE B., METHNER A., NYKAER A.,			
RA	SUSSENS U., FENGER U., HERBARTH B., SCHALLER H.C.;			
RL	Mech. Dev. 0:0-0(1997).			
DR	EMBL; AF031816; AAC16739.1; -			
DR	HSSP; P01130; 1A7J.			
DR	MCD; MGI:1203296; Sorl1.			
DR	PROSITE; PS01209; LDRR_1; 10.			
DR	PFAM; PF00041; In3; 4.			
DR	PFAM; PF00057; Idl_recept_a; 11.			
DR	PFAM; PF00058; Idl_recept_b; 5.			
KW	Glycoprotein.			
FT	NON_TER	1		
SO	SEQUENCE	2033 AA; 227305 MW; DC8108CD CRC32;		
Query Match		7.5%; Score 89.5; Db 11; Length 2033;		
Best Local Similarity		19.2%; Pred. No. 22;		
Matches	33; Conservative	33; Mismatches 77; Indels 29; Gaps		
OY	44	NFILMNRNSDESV-----	GNV-TFSFDYOKTGMWNKLSGCCQNTSTKCNFS	90
Db	1474	NLOLNLNEEEGVIIIGHNAPVHTGILREYIYEVSRSGSKMMASOAAASNSTEIK----	1530	
OY	91	SLKLWVEIEIKRIAEKENTSSWYEVDSFTTPRKAQIGPPEVHLEADKAIV-----	144	
Db	1530	NLLNLAALTVR-AAVTSRGICNMSDSKITTIKGKVIOAPINHIDSYDENSELSFTLTMD	1588	
OY	144	--IHISPGTKDSVMNALDGLSFTYSLLWKNSGVGEERENITYSRHKIKYKLS	193	
Db	1589	GDIKYN-CVYVNLFWSPFDHAKOEKKTLSRGSALSHTKYSNL-TAHTSYEIS	1638	
RESULT	13			
ID	095209	PRELIMINARY:	PRT: 2213 AA.	
AC	095209:			
DT	01-FEB-1997	(TREMBLrel. 02, Created)		
DT	01-FEB-1997	(TREMBLrel. 02, Last sequence update)		
DT	01-NOV-1999	(TREMBLrel. 12, Last annotation update)		

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DE      LR11.
OS      Oryctolagus cuniculus (Rabbit).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC      Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN      (1)
RP      SEQUENCE FROM N.A.
RC      TISSUE-LIVER:
RC      MEDLINE: 96394640.
RA      YAMAZAKI H., BUDO H., KUSUNOKI J., SEIMIYA K., KANAOKI T., MORISAKI N.,
RA      SCHNEIDER W.T., SAITO Y.;
RT      "Elements of neural adhesion molecules and a yeast vacuolar protein
RT      sorting receptor are present in a novel mammalian low density
RT      1,10protein receptor family member."
RL      J. Biol. Chem. 271:24761-24768(1996).
DR      EMBL: D86350; BAA13075.1; -.
DR      HSSP: P01130; 1AJJ.
DR      PROSITE: PS01209; LDLRA_1; 10.
DR      PFAW: PF00057; ldl_recept_a; 11.
DR      PFAW: PF00058; ldl_recept_b; 4.
DR      PFAW: PF00041; fn3; 5.
DR      PRINTS: PR00261; LDLRECEPTOR.
DR      PRINTS: PR00014; FNTYPEI11.
KW      Glycoprotein.
SQ      SEQUENCE 2213 AA; 247764 MW; B35F3995 CRC32;

Query Match          7.5%; Score 89.5; DB 6; Length 2213;
Best Local Similarity 17.1%; Pred. No. 24;
Matches 32; Conservative 36; Mismatches 76; Indels 43; Gaps

QY      32  SQAQYVDIIDDN---FLIRNRSDSEYGNV-TSFSDYQKTMGMWIKISGCONITSTKC 87
DB      1652  APOINQLSLHGESECVIVGHWSPPTHGTLIREYIYESRSGSKWTSERAASNFTEIK- 1711
QY      88  NSSSLKLVNVEIKRIRAREKENTSWYEVDSFTFPFRKQIQPPEVHLEAEDEKAYIHIS 147
DB      1711  ---NLIVNTLYIVRV-AAVTSGKIGMSDSKSIITVKGALIPPNHIDNYE----- 1760
QY      148  PETKDSYVMALDGLSFTYSL-----LIKRNSSGVEER---IENIYSRRKIYK 191
DB      1760  -----NSLSFTLTVDGNIRKNGVYVNLFWAFDTHKQEKKTMMNFGSSVSHKGN 1808
QY      192  LSPFTTY 198
DB      1809  LTAOTAY 1815

RESULT  14
088307 PRELIMINARY; PRT; 2215 AA.
AC      088307;
DT      01-NOV-1998 (TREMBlrel. 08, Created)
DT      01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT      01-NOV-1998 (TREMBlrel. 12, Last annotation update)
DE      LR11.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC      Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN      (1)
RP      SEQUENCE FROM N.A.
RC      TISSUE-LIVER:
RC      MEDLINE:
RA      KANAOKI T., BUDO H., HIRAYAMA S., TANAKA K., YAMAZAKI H., SEIMIYA K.,
RA      MORISAKI N., SCHNEIDER W.T., SAITO Y.;
RT      "Developmental regulation of LR11 expression in murine brain."
RL      DNA Cell Biol. 0:0-0(1998).
DR      EMBL: AB015790; BAA31219.1; -.
DR      HSSP: P01130; 1AJJ.
DR      PROSITE: PS01209; LDLRA_1; 10.
DR      PFAW: PF00057; ldl_recept_a; 11.
DR      PFAW: PF00058; ldl_recept_b; 5.
DR      PFAW: PF00041; fn3; 4.
DR      PRINTS: PR00261; LDLRECEPTOR.
DR      PRINTS: PR00014; FNTYPEI11.

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2000, 05:53:09 ; Search time 903.62 Seconds
(without alignments)
-1445.806 Million cell updates/sec

Title: US-09-240-675-1
Perfect score: 1343
Sequence: 1 CTCGACGAGTCTCGCGCGC.....ATACCTCTAATGAGGTACC 1343

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 882769 seqs, -486395729 residues

Total number of hits satisfying chosen parameters: 1765538

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_dal:*
2: gb_dal:*
3: gb_dal:*
4: gb_ov:*
5: gb_ov:*
6: gb_ov:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1343	100.0	1343	5	A26593	A26593 Human Inter
2	1343	100.0	1343	5	A32389	A32389 Interferon
3	1343	100.0	1343	5	A76127	A76127 Sequence 1
4	1334	99.3	1755	5	A26595	A26595 Human Inter
5	1334	99.3	1755	5	A32391	A32391 Interferon
6	1334	99.3	1755	5	A76129	A76129 Sequence 3
7	1330.8	99.1	2755	5	HMIFNRA	HMIFNRA Human Inter
8	1330.8	99.1	2755	13	G28571	G28571 Human STS S
9	1330.8	99.1	2784	5	AR030347	AR030347 Sequence 1
10	1330.8	99.1	2784	5	IR3602	IR3602 Sequence 1
11	824.2	61.4	3230	3	BOVIFNRA	BOVIFNRA Bos taurus
12	824.2	61.4	3284	3	BOVIFNRA	BOVIFNRA Bos taurus
13	821	61.1	2914	3	OVIFNRA	OVIFNRA Ovis aries
14	819.4	61.0	2559	3	OVIFNRA	OVIFNRA Ovis aries
15	540.2	40.2	3894	12	MUSIFNRA	MUSIFNRA Mus musculus
16	251.8	18.7	22937	9	AP000297	AP000297 Human IFNAR
17	251.8	18.7	32906	9	HSIFNAR	HSIFNAR Human IFNAR
18	251.8	18.7	100000	9	AP000044	AP000044 Homo sapi
19	251.8	18.7	100000	9	AP000112	AP000112 Homo sapi
20	251.8	18.7	100000	9	AP000188	AP000188 Homo sapi
21	190.2	14.2	2425	4	AF082664	AF082664 Gallus ga
22	155.6	11.6	25560	9	AP000298	AP000298 Homo sapi
23	126	9.4	360	5	IS0846	IS0846 Sequence 1
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25	98.6	7.3	18188	9	AP000296	AP000296 Homo sapi
26	79.2	5.9	907	12	U06238	U06238 Mus musculus
27	58.8	4.4	46304	4	AF082667	AF082667 Gallus ga
28	49.8	3.7	41667	7	SPBC365	SPBC365 S. pombe
29	49	3.6	168	5	IS0850	IS0850 Sequence 8
30	47.4	3.5	10176	35	AE001370	AE001370 Plasmodiu
31	45.4	3.4	17430	34	SPENDOFNR	SPENDOFNR S. frugiperd
32	45	3.4	135599	7	CP030821	CP030821 Cytophaga
33	44.8	3.4	175815	45	AC009621	AC009621 Homo sapi
34	44.8	3.3	145578	44	AC016875	AC016875 Homo sapi
35	44.4	3.3	176109	51	AC003992	AC003992 Human BAC
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37	44.2	3.3	34043	34	CEFA586	CEFA586 Caenorhabdi
38	44.2	3.3	188926	33	AL138927	AL138927 Homo sapi
39	44	3.3	173588	44	AC011041	AC011041 Homo sapi
40	43.8	3.2	167471	45	AC019247	AC019247 Homo sapi
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42	43.4	3.2	181949	52	AC006196	AC006196 Homo sapi
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44	43.2	3.2	162919	55	AC022758	AC022758 Homo sapi
45	43.2	3.2	180717	55	AC020712	AC020712 Homo sapi

ALIGNMENTS

RESULT 1
A26593 1343 bp DNA PAT 02-OCT-1995
LOCUS Human interferon alpha receptor gene.
ACCESSION A26593
VERSION A26593.1 GI:1247458
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 1343)
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AUTHORS
TITLE WATER-SOLUBLE POLYPEPTIDES HAVING HIGH AFFINITY FOR INTERFERONS
alpha AND beta
JOURNAL Patent: WO 9218626-A 17 29-OCT-1992;
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Query Match 100.0%; Score 1343; DB 5; Length 1343;
Best Local Similarity 100.0%; Pred. No. 2.8e-296;
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RESULT 2
A32389 1343 bp DNA PAT 08-JUL-1996
LOCUS Interferon receptor gene.
DEFINITION
ACCESSION A32389
VERSION A32389.1 GI:1567382
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominiidae; Homo.


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QY 1 CTGCAGGAGTCTGCGGCGCTCCAGATGATGTCCTCCCTGCGGCGGAGACCTTAG 60
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RESULT 5
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 LOCUS A32391
 DEFINITION Interferon alpha and beta receptor gene.
 VERSION A32391
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 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Primates; Catarrhini; Hominoidea; Homo.
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BASE COUNT 593 a 324 c 334 g 504 t
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 Query Match 99.3%; Score 1334; DB 5; Length 1755;
 Best Local Similarity 100.0%; Pred. No. 3.1e-294;
 Matches 1334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
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LOCUS Sequence 3 from Patent W09320187.
DEFINITION A76129.1 GI:6088265
ACCESSION A76129.1
VERSION A76129.1
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1755)
AUTHORS Benoit, P. and Meyer, F.
TITLE MONOCLONAL ANTIBODIES AGAINST THE INTERFERON RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I INTERFERON
JOURNAL Patent: WO 9320187-A 14-OCT-1993;
EUROP BIOLOGIE (FR); BENOIT PATRICK (FR)
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ORIGIN
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Matches 1334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 7
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LOCUS Human Interferon-alpha receptor (HuIFN-alpha-Rec) mRNA, complete cds.
ACCESSION J03171.1 GI:184645
VERSION J03171.1
KEYWORDS Interferon-alpha receptor.
SOURCE Human cell line DAUDI, cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE Use G., Lutfalla G. and Gresser I.
Genetic transfer of a functional human Interferon alpha receptor
into mouse cells: cloning and expression of its cDNA
Cell 60 (2), 225-234 (1990)
JOURNAL Draft entry and computer-readable sequence for [1] kindly submitted
MEDLINE by G. Use, 29-NOV-1989, for release after publication.
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BASE COUNT 867 a 553 c 578 g 757 t
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Query Match 99.1%; Score 1330.8; DB 9; Length 2755;
Best Local Similarity 99.9%; Pred. No. 1,7e-293;
Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 533 ATAGTGTATGTGGGCTTGGATGGTTAAGCTTTACATATAGTCTTCTATCTGAAAA 592
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ACCESSION G28571.1 GI:1408386
VERSION STS: STS sequence, primer; sequence tagged site.
KEYWORDS STS: STS sequence, primer; sequence tagged site.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 2755)
AUTHORS Myers,R.M.
JOURNAL Unpublished (1996)
COMMENT
Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 415/7259687
Fax: 415/7259689
Email: myers@shgc.stanford.edu

Primer A: TGACAGAAATGAACCTGTCA
Primer B: TTATAATAGTTAAGACCTTGCCG
STS size: 175
PCR Profile:
Initial Incubation: 94 degrees C for 90 seconds
Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600
Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Tag Polymerase: 0.05 units/uL
Total Vol: 10 uL
Buffer:
MgCl2: 2.5 mM
KCl: 50 mM
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pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from J03171
-- Washington University/Merck EST sequence.
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BASE COUNT 867 a 553 c 578 g 757 t
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Query Match 99.1%; Score 1330.8; DB 13; Length 2755;
 Best Local Similarity 99.9%; Pred. No. 1.7e-293;
 Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 173 CTCCTCAAAAAGTAGAGTGCATATGATGACAACTTATCCGAGGTGAACAGGA 232
OY 181 GCGATGAGTCTGCGGGAATGTGACTTTTTCATTCGATTATCAAAAACCTGGATGATA 240
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    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1073 TACTTCCTCAGTCTTTTAAATTTAGATCCCTAGTATCATTCATATCATATGCGTG 1132
OY 1081 CTCCAAAAAGTCTGGAAGACAGCGCTGTGATCCAGATTTATCCACTGTTTATGAATA 1140
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1133 CTCCAAAAAGTCTGGAAGACAGCGCTGTGATCCAGATTTATCCACTGTTTATGAATA 1192
OY 1141 TTTTGGGAAAACACTCAATGCTGAGAGAAAATATGAGAGAAAAAATGATGTTA 1200
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1193 TTTTGGGAAAACACTCAATGCTGAGAGAAAATATGAGAGAAAAAATGATGTTA 1252
OY 1201 CAGTTCCTAATTTGAAACAGTACTGTATATTTGTGAAAGCCAGACACACACATAG 1260
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DB 1253 CAGTTCCTAATTTGAAACAGTACTGTATATTTGTGAAAGCCAGACACACACATAG 1312
OY 1261 ATGAAAAGCTGAATTAAGACAGTGTGTTTATGACGCTGTATGTGAGAAAACAAACAG 1320
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DB 1313 ATGAAAAGCTGAATTAAGACAGTGTGTTTATGACGCTGTATGTGAGAAAACAAACAG 1372
OY 1321 GAAATACCTTAA 1334
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RESULT 9
 AR030347 2784 bp DNA PAT 29-SEP-1999
 LOCUS AR030347 Sequence 1 from patent US 5861258.
 DEFINITION AR030347
 ACCESSION AR030347
 VERSION AR030347.1 GI:5943561
 KEYWORDS
 SOURCE
 . Unknown.
 ORGANISM Unknown.
 REFERENCE
 1 (bases 1 to 2784)
 Mogenssen, K. Erik, Use, G., Lutfalla, G. and Gresser, I.
 TITLE Use of the alpha interferon receptor and cells which express the
 JOURNAL receptor, for identification of alpha interferon agonists
 FEATUES Patent: US 5861258-A 1 19-JAN-1999;
 1. Location/Qualifiers
 1. .2784
 /organism="unknown"
 BASE COUNT 896 a 553 c 578 g 757 t
 ORIGIN

Query Match 99.1%; Score 1330.8; DB 5; Length 2784;
 Best Local Similarity 99.9%; Pred. No. 1.7e-293;
 Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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OY 121 CTCCTCAAAAAGTAGAGTGCATATGATGACAACTTATCCGAGGTGAACAGGA 180
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DB 173 CTCCTCAAAAAGTAGAGTGCATATGATGACAACTTATCCGAGGTGAACAGGA 232
OY 181 GCGATGAGTCTGCGGGAATGTGACTTTTTCATTCGATTATCAAAAACCTGGATGATA 240
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DB 233 GCGATGAGTCTGCGGGAATGTGACTTTTTCATTCGATTATCAAAAACCTGGATGATA 292
OY 241 ATTGATATAAATTTGCTGGGTGCAGAAATATCTAGTACCAAAATGCAACTTTCTGCAC 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 293 ATTGATATAAATTTGCTGGGTGCAGAAATATCTAGTACCAAAATGCAACTTTCTGCAC 352
OY 301 TCAAGCTGAATGTTTATGAAGAAATTAATGCGTAAAGACAGAAAAAGAACACTT 360
  
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Db 353 TCAGCTGATGTTTATGAAGAAATTAATGGCTATAGAGAGAGAAAAAGAAACACTT 412
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Db 413 CTTCAGGATGATGGTGGACTCATTTACACCAATTTGCCAAAGCTCGAGTTGCTCCAG 472
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Db 473 AAGTACATTTAGACAGTGAAGATTAAGCAATAGTATACACATCTCTCGAAGCAAAAG 532
QY 481 ATAGTGTATGTTGGCTTTGATGTTTAAAGCTTTACATATAGCTTACTTATCTGAAAA 540
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Db 713 TTGGTGTCTATAGTCCAGTACATTTGATTAAGACACAGTTGAAAATGAACTACCTCAC 772
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QY 1201 CAGTTCCTAATTTGAAACACAGTGTATATTGTGTAAGGACAGACACACCATG 1260
Db 1253 CAGTTCCTAATTTGAAACACAGTGTATATTGTGTAAGGACAGACACACCATG 1312
QY 1261 ATGAAAAGTGAATAAAGAGTGTGTTAGTGAAGCTATATGTAAGAAAAACCAAG 1320
Db 1313 ATGAAAAGTGAATAAAGAGTGTGTTAGTGAAGCTATATGTAAGAAAAACCAAG 1372
QY 1321 GAAATACCTTAAA 1334
Db 1373 GAAATACCTTAAA 1386
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RESULT 10

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193602
LOCUS 193602 2784 bp -DNA
DEFINITION Sequence 1 from patent US 5731169.
ACCESSION 193602
VERSION 193602.1 GI:3938072
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unpublished.
AUTHORS (bases 1 to 2784)
Mogensen, K. Erik, Use, G., Lutfalla, G. and Gresser, I.
TITLE cDNA fragment coding the alpha interferon receptor gene and process
for the preparation of a corresponding protein
JOURNAL Patent: US 5731169-A 1 24-MAR-1998;
FEATURES
Source Location/Qualifiers
1..2784
BASE COUNT 896 a /organism="unknown" 757 t
ORIGIN
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Query Match 99.1%: Score 1330.8; DB 5; Length 2784;
Best Local Similarity 99.9%: Pred. No. 1/e-293;
Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 61 TGCTGTGCGCGTGGGCCATGGGTGTGTCGCGAGCCGAGGTGGAATAATCTAAAT 120
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Db 173 CTCCTCAAAAAGTATAGGTTCGACATCATAGATGACACTTTATCTGAGGTGAACAGA 232
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OY 721 CAGAAATATAGAGTCACTGTCACAAATCAGAACTATCTTCTTAATGGATTATACAT 780
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Db 1193 TTTTGGAAAACTTCTTAATGCTGAGAGAAAAATTTATCGAGAAAAAATCGAGTTTA 1252
OY 1201 CAGTTCCTATTTGAAACCACTGACTGTATATGTTGTGAAAGCCAGACACACCATG 1260
Db 1253 CAGTTCCTATTTGAAACCACTGACTGTATATGTTGTGAAAGCCAGACACACCATG 1312
OY 1261 ATGAAAAGCTGAATTAAGCAGTGTGTTTGTAGTACGCTGTATGTGAAAAACAAACG 1320
Db 1313 ATGAAAAGCTGAATTAAGCAGTGTGTTTGTAGTACGCTGTATGTGAAAAACAAACG 1372
OY 1321 GAAATACCTCTTAA 1334
Db 1373 GAAATACCTCTTAA 1386

RESULT 11
BTFNAR
LOCUS BTFNAR 3230 bp mRNA MAM 20-JAN-1993
DEFINITION B. taurus IFNAR mRNA for Interferon receptor type I.
ACCESSION X68443
VERSION X68443.1 GI:431
KEYWORDS cytokine receptor; Interferon receptor.
SOURCE Bos taurus.
ORGANISM Bos taurus.
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Artiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE
1 (bases 1 to 3230)
AUTHORS Lutfalla, G.
TITLE Direct Submission
JOURNAL Submitted (14-SEP-1992) G. Lutfalla, CNRS Lab of Viral
Oncology-IRSC, 7 Rue Guy Moquet Bp 8, 94801 Villejuif Cedex, FRANCE
2 (bases 1 to 3230)
AUTHORS Mouchel-Vieilh, E., Lutfalla, G., Mogenssen, K.E. and Uze, G.
TITLE Specific antiviral activities of the human alpha interferons are
determined at the level of receptor (IFNAR) structure
JOURNAL FEBS Lett. 313 (3), 255-259 (1992)
MEDLINE
93076908
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Location/Qualifiers
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2171..3230
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BASE COUNT 951 a 643 c 751 g 885 t
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Best Local Similarity 79.3%; Freq. No. 5.9e-118;
Matches 1057; Conservative 0; Mismatches 258; Indels 18; Gaps 6;
OY 14 CGCGGCTCCCGATGATGATGCTGCTCTGCGGCGAGACCTAGTGCCTGCGCCT 73
Db 109 CGCGGCTCCCGAGATGATGCTGCTCTGCGGCGAGACCTAGTGCCTGCGCCTG 168
OY 74 GGGCCCATGGGTGTGTGCGGACCGCAGAGTGAAGAAAAATCTAAATCTCTCAAAAAGT 133
Db 169 GAG---ATGGGTGTGCGCGCGCGCTCAAGGGAAGCAATCTGA---GCTGAAGAAATGT 222
OY 134 AAGATCGACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 193
Db 223 CGAGATCCACATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 282
OY 194 CGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 253
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OY 254 GTCTGGGTGTCAGAAATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 310
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OY 368 GTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 427
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Db 523 TTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 582
OY 485 TGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 544

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Db 583 TATCATGTGGGCTATGATCGTTCAAGCTTAGATAGCGTGTATCTGAAAAATC 642
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Oy 605 ACCAGACTACTTATTTGCTTAAAGTTAAGCAGCAGTACTAGTCAATGAAAAATGG 664
Db 703 ACCAGACTACTTATTTGCTTAAAGTTAAGCAGCAGTACTAGTCAATGAAAAATGG 762
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Db 1423 AATACCTCTTAA 1435

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RESULT 12
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DEFINITION Bos taurus alpha-Interferon receptor (IFNAR) mRNA, complete cds.
ACCESSION L06320
VERSION L06320.1 GI:163187
KEYWORDS alpha-Interferon receptor.
SOURCE Bos taurus lung cDNA to mRNA.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Bovidae; Bos.
Bovine; Bos.
REFERENCE 1 (bases 1 to 3284)
AUTHORS Lim,J.K. and Langer,J.A.

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TITLE Cloning and characterization of a bovine alpha interferon receptor
JOURNAL Biochim. Biophys. Acta 1173 (3), 314-319 (1993)
MEDLINE 93305725
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Query Match 61.4%; Score 824.2; DB 3; Length 3284;
Best Local Similarity 79.3%; Pred. No. 5.9e-178;
Matches 1057; Conservative 0; Mismatches 258; Indels 18; Gaps 6;
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Oy 74 GGGCCCATGGGATGCTGCGGAGCGGAGTGGAAAAATGTAATCTCTCAAAAGT 133
Db 228 GAG---ATGGTGTCTGCGCCGCGCCGCTCAGGGACCAATCTGAA---GCTGAAAATGT 281
Oy 134 AGAGTGCATCATATGATGACAACTTATCTGAGGTGGAACAGAGCGATGACTGT 193
Db 282 CGAGATCCATCATATGATGACAAATTTTCTGAAAGTGAACAGACAGAGTACTGT 341
Oy 194 CGGGAATGACTTTTTCATTCGATTAATCAAAAACTGGGATGATTAATGATTAAT 253
Db 342 CAGAGATGACTTTTTCAGCAGATTAATCAATATAGAACGATTAAGTAACTGAAAT 401
Oy 254 GTCGTGGTGCAGAAATTAATGACCAATGCAACTTTCTTCACTCAAGCT---GAA 310
Db 402 GTCTGGGTCTCAATATTAATGATGACCAATGCAACTTTCTTCACTGAGCTGAAAA 461
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Db 582 TTTAGAGCTGAAGATTAAGGCAATGATGATGATCTCTCTCCCTGGAACAAAGATAG 641
Oy 485 TGTATGTGGGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 544

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Job time: 17841 sec

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Db 447 ATCCGTTTATTCATTTCTACACAGCTCAGATGAGCCCCCAGAAAGTACGTTAGAAAGCTG 506
OY 439 AAGATTAAGCAATAGTATGATACACATCTCTCTGGAACAAAGATAGTATGTGGGCTT 498
Db 507 AAGATTAAGCCATAGTATGATACATCTCTCTCCGAGACAGAGGAAACATGTGGGAC 566
OY 499 TGGATGGTTAAGCTTTACATATAGCTTATCTGGAAGAACTCTTGAGGTAGAG 558
Db 567 TGGAGAAACCTTCTTCACTTACACCATGCAATCTGGCAGAGCTTCCAGTGACAAA 626
OY 559 AAAGATTTGAAATTTATTTTCCAGACATTAATTTATTAAGTCTCACGAGACTACTT 618
Db 627 AAACATTTACTCTACGTATTTATGTAAGAAAGTACAGACTCTTGCCAGAGACTACTT 686
OY 619 ATGTCTAAAGTTAAAGCAGCAGTACTACGTATGATGAAATGTGTATAGTCCAG 678
Db 687 ACTGTTAAGATTAAAGCAATACATCCGTCACTTAAGAAACAGACATTTACAGACTG 746
OY 679 TACATTTGTTAAAGACACAGTTGAAATGAACCTACTCCACGAAATATAGAAGTCA 738
Db 747 TGCAGTGTAAAGCAGACAGTGGCAAAATGAATGCTGTGCCAGAAATCTCAAGTGG 806
OY 739 GTGCCAAATCAGAACTATGTTCTTAATGGGATTA---TACATATGCAAACTAGACT 795
Db 807 ATGCCAAGGCAAGAGCTATGTCTGAAATGGAGTACATTTGCGTGTGACAGTGTCT 866
OY 796 TTCAAGTTCAGTGCTCCAGGCTTTTAAAGGAATCCTGGAACCATTTGTATTAAT 855
Db 867 TCAGGGCAGAGTGGCTTCTGCTATTTCAAAAAGCAGTTCTGGAAGCCATTCAGATTAAT 926
OY 856 GGAACCAATACTGCTGCTGAAATATGCAAACTACCCAGTGTGTCTTCTCTCAAAAG 915
Db 927 GGAACCAATACCACCTGTGCAAAATGTCCAGACGTGCTGTCTTCTCAAGATA 986
OY 916 TTTCCAAAAGGAATTTACCTTCTCCGCTACAAAGCATCTGATGGAATTAACACATCTT 975
Db 987 CTGTCTACAGAGAAAGCTTCTTCTCAGTACAAAGCTCAGAGGAAATCACACATCTT 1046
OY 976 TTTGGTCTGAGAGATTAAGTTGATATGAAATACAGCTTCTTCTCTCCAGTCT 1035
Db 1047 TTTGGTCTGAGAGATTAAGTTGATATGAAATACACATCTTCTCTCCAGTCT 1106
OY 1036 TTAACATTTAGTCCCTTAGTATTCATTCATATCTATTCGTTGCTCCAAAAGACTGTG 1095
Db 1107 TTTACTCTACCCGCTAGCTGACCTCTGTCTTATGTG----- 1148
OY 1096 GAAACAGCCCTGTGATCCAGAGATTAATCCAGTATTTAGAAATTTTGGGAAACA 1155
Db 1148 --AAGTGTGAGGACACATGTGATGACTCATTTAGCAATCATCTTTGGGAAACA 1205
OY 1156 CTTCAATGCTGAGAGAAAAATTTATGAGAAAAAACTGATGTACAGTTCTTAATTGA 1215
Db 1206 CTTCCATATCTAAGATAGCATGAGAGAGAGGCCCCAGAGTTCACTCAAGAACTGC 1265
OY 1216 AACCACTGACTGATTTGTGTGAAGCCAGACACACATGATGTAAGGCTGAATA 1275
Db 1266 AGCCGCTGACTGTGTCTGTGTCAGGCGAGAGTGTCTTCAAG---GCCCTGTGAATA 1322
OY 1276 AAAGCAGTGTTTTACTGACGCTGTATGTGAGAAAAAACAACAGGAAATACCTCTA 1332
Db 1323 AGACGAGCAACTCAGTGAAGAGCTGTGTGAGAAAAACAGTCCAGAGATTTTCCA 1379

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2000, 05:54:19 ; Search time 64.86 Seconds
(without alignments)
5180.511 Million cell updates/sec

Title: US-09-240-675-1

Perfect score: 1343
Sequence: 1 CTGCAGGATCTGCGCGGC.....ATACCTTAATGAGTACC 1343

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 311585 seqs, 125096042 residues

Total number of hits satisfying chosen parameters: 623170

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : N_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1343	100.0	1343	014239	Encodes soluble in
2	1343	100.0	1343	030532	Sequence encoding
3	1343	100.0	1343	049625	Human interferon r
4	1338.2	99.6	1343	086457	IFN-R extracellular
5	1334	99.3	1755	014240	Encodes complete I
6	1334	99.3	1755	030533	Sequence encoding
7	1334	99.3	1755	049624	Human interferon r
8	1332.4	99.2	1755	086458	Human IFN receptor
9	1330.8	99.1	2784	011701	Human alpha-interf
10	126	9.4	360	173519	Transmembrane Int
11	49	3.6	168	173521	Interferon alpha-r
12	40.6	3.0	6119	011377	Genes encoding T.
13	40.2	3.0	1953	143223	Antiscarab pest to
14	40.2	3.0	2425	005679	bPGS1208 gene. Ne
15	38.6	2.9	1953	038654	bt isolate 43f cod
16	38.6	2.9	1977	081495	Bacillus thuringie
17	38.6	2.9	2190	027945	Sequence of CryIII
18	38	2.8	7900	X13068	Enterococcus faeca
19	37.8	2.8	1607	175167	Staphylococcus aur
20	37.8	2.8	110000	V21209_09	Continuation (10 o
21	37.4	2.8	4228	X20277	Continuation (3 of
22	37	2.8	1511	028302	Borrelia burgdorfe
23	37	2.8	1511	028302	AMEPV tk DNA. New
24	37	2.8	1511	066798	AMEPV thymidine-X1
25	36.8	2.7	615	X30838	AMEPV entomopoxvir
26	36.8	2.7	20199	V52139	Streptococcus pneu
27	36.2	2.7	1951	094449	Bacterial transfer
28	36.2	2.7	1951	094449	Transferin receptor
29	36.2	2.7	1951	V21443	H. Influenzae sira
30	36.2	2.7	4663	X20273	Borrelia burgdorfe
31	35.6	2.7	2636	V01871	Human brain specific
32	35.6	2.7	110000	V21209_02	Continuation (3 of
33	35.4	2.6	1291	014659	Part of bti260 gen
34	35.4	2.6	1972	014098	B. thuringiensis cr

35	35.4	2.6	3543	1	014669	Dipteran active to
36	35.4	2.6	3543	1	081178	B.t. toxin PS71M3
37	35.4	2.6	3940	1	N93054	Delta-endotoxin cr
38	35.4	2.6	4571	1	N93059	Delta-endotoxin cr
39	35.4	2.6	4934	1	N81490	Insecticidal (Dipt
40	35.4	2.6	5391	1	V71729	Upstream sequence
41	35.4	2.6	5407	1	V71738	Upstream sequence
42	35.2	2.6	11464	1	V48228	Interleukin 18 con
43	35.2	2.6	28994	1	V15826	Genomic DNA for In
44	34.8	2.6	1271	1	046869	Growth factor gene
45	34.8	2.6	11225	1	N91695	Sequence of fow1p0

ALIGNMENTS

RESULT 1	
ID 014239	Standard: DNA; 1343 BP.
AC 014239;	
DT 16-JAN-1992 (first entry)	
DE Encodes soluble interferon-alpha/beta receptor.	
KW IFN; autoimmune disease; graft rejection; histocompatibility; ss.	
OS Homo sapiens.	
EH Key	Location/Qualifiers
FT cds	27..1337
FT	/*tag-a
FT	/product- soluble receptor
FR 657881-A.	
PD 09-AUG-1991.	
PF 05-FEB-1990; 001298.	
PR 05-FEB-1990; FR-001298.	
PA (FUBI-) LAB EURO BIOTECHNO.	
PI Eild P. Gresser I, Lutfalla G, Meyer F, Mogenssen KE;	
PI Toyey MG. Use G;	
DR WPI: 91-319778/44.	
DR P-PSDB: R14487.	
PT New water-soluble polypeptide(s) with affinity for IFN-alpha and	
PT beta - used to treat e.g. lupus erythematosus, Behcet's disease,	
PT aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.	
PS Claim 10; Page 45; 52pp; French.	
CC The protein encoded by this sequence corresponds to the soluble,	
CC extracellular portion of the interferon-alpha and/or beta receptor.	
CC The transmembrane and cytoplasmic domains of the native receptor	
CC have been deleted to obtain a soluble, circulating form of the	
CC receptor. Potentially immunogenic epitopes have thus been eliminated.	
CC See also Q14240.	
CC Sequence 1343 BP; 449 A; 254 C; 264 G; 376 T;	
Query Match	100.0%; Score 1343; DB 1; Length 1343;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 CTGCAGGATCTGCGCGGCTCCAGATGATGTCCTCTGCGGCGGCGACGACCTAG 60	
DB 1 CTGCAGGATCTGCGCGGCTCCAGATGATGTCCTCTGCGGCGGCGACGACCTAG 60	
QY 61 TGCCTGCGCGGCGGCGGCTCCAGATGATGTCCTCTGCGGCGGCGACGACCTAG 60	
DB 61 TGCCTGCGCGGCGGCGGCTCCAGATGATGTCCTCTGCGGCGGCGACGACCTAG 60	
QY 121 CTCTCAAAAAGTAGAGGTGACATCATATGACATGACATTTATTCCTGAGTGAACAGA 180	
DB 121 CTCTCAAAAAGTAGAGGTGACATCATATGACATGACATTTATTCCTGAGTGAACAGA 180	
QY 181 GCGATGAGTCTGCGGGAATGATGATCTTTTCATTCATTTCAAAAAACGCGATGATA 240	
DB 181 GCGATGAGTCTGCGGGAATGATGATCTTTTCATTCATTTCAAAAAACGCGATGATA 240	
QY 241 ATTGGATTAATGCTGCGGCTGACAGATATTTACTAGTACCAATGCACTTTCTTCCAC 300	
DB 241 ATTGGATTAATGCTGCGGCTGACAGATATTTACTAGTACCAATGCACTTTCTTCCAC 300	


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QY 301 TCAAGCTGAATGTTTATGAGAATTAATTCGCTATTAAGAGCAGAAAAAGAAACACTT 360
DB 301 TCAAGCTGAATGTTTATGAGAATTAATTCGCTATTAAGAGCAGAAAAAGAAACACTT 360
QY 361 CTTCATGATGATGAGGTGACTATTACACCATTTGCAAAAGCTCAGATTGCTCCAG 420
DB 361 CTTCATGATGATGAGGTGACTATTACACCATTTGCAAAAGCTCAGATTGCTCCAG 420
QY 421 AAGTACATTAGAGCTGAAGCAATAGCAATAGTATACACCTCTCTCGAACAAG 480
DB 421 AAGTACATTAGAGCTGAAGCAATAGCAATAGTATACACCTCTCTCGAACAAG 480
QY 481 ATAGCTATAGTGGCTTTGGAGTGTAAAGCTTACATATAGCTTACTATATGAAAA 540
DB 481 ATAGCTATAGTGGCTTTGGAGTGTAAAGCTTACATATAGCTTACTATATGAAAA 540
QY 541 ACTCTCAGCTGATAGAGAAAGATTGAAATATTTATTCACACATATAAATTATTAAC 600
DB 541 ACTCTCAGCTGATAGAGAAAGATTGAAATATTTATTCACACATATAAATTATTAAC 600
QY 601 TCTCACCAGAGTACTATTATGCTAAAGTTAAAGCAGACTAGCTAGCTATGAAAA 660
DB 601 TCTCACCAGAGTACTATTATGCTAAAGTTAAAGCAGACTAGCTAGCTATGAAAA 660
QY 661 TTGGTCTATAGTCCAGTACATTTGATAAGACACAGTTGAAATGAACTACTCCAC 720
DB 661 TTGGTCTATAGTCCAGTACATTTGATAAGACACAGTTGAAATGAACTACTCCAC 720
QY 721 CAGAAAAATAGAGTACTGCTCCAAAATCAGAACTATGTTCTTAAATGGGATTAACAT 780
DB 721 CAGAAAAATAGAGTACTGCTCCAAAATCAGAACTATGTTCTTAAATGGGATTAACAT 780
QY 781 ATGCAAAACATGACCTTCAAGTTCAGTGGCTCAGCGCTTTTAAAGAAATCCCGAA 840
DB 781 ATGCAAAACATGACCTTCAAGTTCAGTGGCTCAGCGCTTTTAAAGAAATCCCGAA 840
QY 841 ACCATTGTATAATGGAACAAATACCTGACTGTGAAATGTCAAACTACCCAGTGTG 900
DB 841 ACCATTGTATAATGGAACAAATACCTGACTGTGAAATGTCAAACTACCCAGTGTG 900
QY 901 TCTTTCTCAAAACGTTTCCAAAAGAAATTAACCTTCCCGCTGCAAGCATCTGATG 960
DB 901 TCTTTCTCAAAACGTTTCCAAAAGAAATTAACCTTCCCGCTGCAAGCATCTGATG 960
QY 961 GAAATACACATCTTTTGGTGTGAAGATAAGTTGATGTAATCAAGCTTTC 1020
DB 961 GAAATACACATCTTTTGGTGTGAAGATAAGTTGATGTAATCAAGCTTTC 1020
QY 1021 TACTCTCCAGTCTTTAACATTAGATCCCTTAGTATTCATTCATATATATGCGTG 1080
DB 1021 TACTCTCCAGTCTTTAACATTAGATCCCTTAGTATTCATTCATATATATGCGTG 1080
QY 1081 CTGCAAAACAGTGTGGAACAGCCGTGTGATCCAGAGTTATCCAGATGATTAAGAAATTA 1140
DB 1081 CTGCAAAACAGTGTGGAACAGCCGTGTGATCCAGAGTTATCCAGATGATTAAGAAATTA 1140
QY 1141 TTTTGGGAAAAACACTTCAATGCTGAGAGAAAAATTAAGAAAAAACTGATGTA 1200
DB 1141 TTTTGGGAAAAACACTTCAATGCTGAGAGAAAAATTAAGAAAAAACTGATGTA 1200
QY 1201 CAGTTCCTAATTTGAAACCACTGATATATGTTGTAAGAGCAGACACACATGG 1260
DB 1201 CAGTTCCTAATTTGAAACCACTGATATATGTTGTAAGAGCAGACACACATGG 1260
QY 1261 ATGAAAAAGCTGATTAAGAGAGTGTGTTAGTACGCTGATATGAGAAAAACAAACAG 1320
DB 1261 ATGAAAAAGCTGATTAAGAGAGTGTGTTAGTACGCTGATATGAGAAAAACAAACAG 1320
QY 1321 GAAATACCTTAATGAGTACC 1343
DB 1321 GAAATACCTTAATGAGTACC 1343

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RESULT 2
ID 030532
AC Q30532: standard; DNA: 1343 BP.
DT 31-MAR-1993 (first entry)
DE Sequence encoding a soluble form of the interferon (IFN) receptor
KM with a high affinity for IFN-alpha and -beta.
OS Interferon receptor; alpha-interferon; beta-interferon; ss.
FH Synthetic.
FT Key Location/Qualifiers
FT cds 27..1337
FT /tag= a
MO0218626-A.
PD 29-OCT-1992.
PR 17-APR-1991; F00318.
PR 17-APR-1991; MO-F00318.
PA (EBI-) LAB EURO BIOTECHNOLOGIE.
PI EId P, Gresser I, Lutfalla G, Meyer F, Mogensen KE.
PI Tovey M, Uze G.
DR WPI: 92-382110/46.
DR P-PSDB: R28495.
PT Water soluble polypeptide(s) strongly bind interferon(s) alpha
PT and beta - useful as immunosuppressants, for treating auto-immune
PT diseases and transplant rejection
PS Claim 10; Fig 1; 58pp; English.
CC DNA encoding the water-soluble polypeptide with a high affinity for
CC IFN-alpha and -beta is isolated by PCR, using appropriate
CC oligonucleotides as primers and cloned cDNA as template. For example,
CC bacteriophage lambda ZAP, containing the entire coding sequence of
CC the IFN-alpha and -beta receptor (Q30533), was incubated with Oligos
CC Q30534 and Q30535. R28496 represents the complete receptor. R28495
CC IFN in the same way as antibodies so are immunosuppressants e.g. for
CC treating autoimmune diseases and graft rejection. They lack the
CC toxic side-effects of known immunosuppressants such as steroids.
SQ Sequence 1343 BP; 449 A; 254 C; 264 G; 376 T;

Query Match 100.0%; Score 1343; DB 1; Length 1343;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCAAGGATCTGCGCGGCTCCAGATGATGCTGCTCTGCGCGAGACCTTAG 60
DB 1 CTGCAAGGATCTGCGCGGCTCCAGATGATGCTGCTCTGCGCGAGACCTTAG 60
QY 61 TCTCTGTCGCGCTGGGCCCATGGGTGTGTCGCGAGCCGAGGTGAAAAATCTAAAT 120
DB 61 TCTCTGTCGCGCTGGGCCCATGGGTGTGTCGCGAGCCGAGGTGAAAAATCTAAAT 120
QY 121 CTGCTCAAAAATAGAGGTCGACATATAGATGAACAATTTATCTGAGGTGGAACAGA 180
DB 121 CTGCTCAAAAATAGAGGTCGACATATAGATGAACAATTTATCTGAGGTGGAACAGA 180
QY 181 GCGATGAGTCTGTCGGAATGACTTTTCTTCAATGATTATCAAAAACTGGGATGATA 240
DB 181 GCGATGAGTCTGTCGGAATGACTTTTCTTCAATGATTATCAAAAACTGGGATGATA 240
QY 241 ATTGATTAATTTGCTGGGTGTCAGAAATTTACTAGTACCAATGCAACTTTTCTTAC 300
DB 241 ATTGATTAATTTGCTGGGTGTCAGAAATTTACTAGTACCAATGCAACTTTTCTTAC 300
QY 301 TGAAGTGAATTTATGAGAAATTAATGCGTATAGAGCAGAAAAAGAAACACTT 360
DB 301 TGAAGTGAATTTATGAGAAATTAATGCGTATAGAGCAGAAAAAGAAACACTT 360
QY 361 CTTCATGATGATGAGGTGACTATTACACCATTTGCAAAAGCTCAGATTGCTCCAG 420
DB 361 CTTCATGATGATGAGGTGACTATTACACCATTTGCAAAAGCTCAGATTGCTCCAG 420
QY 421 AAGTACATTAGAGCTGAAGCAATAGCAATAGTATACACCTCTCTCGAACAAG 480
DB 421 AAGTACATTAGAGCTGAAGCAATAGCAATAGTATACACCTCTCTCGAACAAG 480

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Db 421 AAGTACATTTAGACGTAAGATTAAGCAATAGTATACATCTCTCGAACAAG 480
 Qy 481 ATAGTATATGCGCTTGGATGGTTAGCTTACATATAGCTTACTATCTGAAA 540
 Db 481 ATAGTATATGCGCTTGGATGGTTAGCTTACATATAGCTTACTATCTGAAA 540
 Qy 541 ACTCTTCAGGTTAGAGCAAGATTAATATTATTCAGACATAAATTTTAAAC 600
 Db 541 ACTCTTCAGGTTAGAGCAAGATTAATATTATTCAGACATAAATTTTAAAC 600
 Qy 601 TCTCAGCAGAGCTACTATGTCTAAAGTAAAGCAGACTACTTCGTCATGAAA 660
 Db 601 TCTCAGCAGAGCTACTATGTCTAAAGTAAAGCAGACTACTTCGTCATGAAA 660
 Qy 661 TTGCTGTATAGTCCAGTACATTTATTAAGACACAGTTGAAATGAACTACCTCAC 720
 Db 661 TTGCTGTATAGTCCAGTACATTTATTAAGACACAGTTGAAATGAACTACCTCAC 720
 Qy 721 CAGAAATATAGAGTCACTGTCACAAATCAGACATAGTTCTTAAATGGATTATACAT 780
 Db 721 CAGAAATATAGAGTCACTGTCACAAATCAGACATAGTTCTTAAATGGATTATACAT 780
 Qy 781 ATGCAACATGACCTTTCAAGTTCAGTGGCTCCAGCCCTTTTAAAGGAATCCTGGA 840
 Db 781 ATGCAACATGACCTTTCAAGTTCAGTGGCTCCAGCCCTTTTAAAGGAATCCTGGA 840
 Qy 841 ACCATTGTATTAATGAACAAATACCGATGATGAAATGTCAAAATCCACAGTGTG 900
 Db 841 ACCATTGTATTAATGAACAAATACCGATGATGAAATGTCAAAATCCACAGTGTG 900
 Qy 901 TCTTTCCTCAAAAGCTTTTCCAAAAGAAATTTACCTTCCGCGTACAGCATGTATG 960
 Db 901 TCTTTCCTCAAAAGCTTTTCCAAAAGAAATTTACCTTCCGCGTACAGCATGTATG 960
 Qy 961 GAAATACACATCTTTGGTGTGAAGATTAAGTATGATCTGAAATACAGCTTCC 1020
 Db 961 GAAATACACATCTTTGGTGTGAAGATTAAGTATGATCTGAAATACAGCTTCC 1020
 Qy 1021 TACTTCCTCAAGCTTTTAACATTAGATCCCTAGTATCATCATATCTATCTGATG 1080
 Db 1021 TACTTCCTCAAGCTTTTAACATTAGATCCCTAGTATCATCATATCTATCTGATG 1080
 Qy 1081 CTCCAAAACAGTCTGAAAACAGCCTGTGATCAGGATATCCAGTATTTGAAATTA 1140
 Db 1081 CTCCAAAACAGTCTGAAAACAGCCTGTGATCAGGATATCCAGTATTTGAAATTA 1140
 Qy 1141 TTTTGGGAAACACTTCAATGCTGAGAGAAAATTTCCAGAAAATAATGATGTTA 1200
 Db 1141 TTTTGGGAAACACTTCAATGCTGAGAGAAAATTTCCAGAAAATAATGATGTTA 1200
 Qy 1201 CAGTTCCTAATTTGAACACAGTACTGTATTTGTGTAAGCCAGAGCACACCATGG 1260
 Db 1201 CAGTTCCTAATTTGAACACAGTACTGTATTTGTGTAAGCCAGAGCACACCATGG 1260
 Qy 1261 ATGAAAGCTGAATAAAGCAGTGTGTTAGTACGCTGTATGAGAAAACCAACAG 1320
 Db 1261 ATGAAAGCTGAATAAAGCAGTGTGTTAGTACGCTGTATGAGAAAACCAACAG 1320
 Qy 1321 GAAATACCTCTAATGAGGTACC 1343
 Db 1321 GAAATACCTCTAATGAGGTACC 1343

RESULT 3

ID 049625
 AC 049625 standard; DNA: 1343 BP.

DT 20-APR-1994 (first entry)
 DE Human interferon receptor extracellular domain coding sequence.
 KW IFN-R; extracellular domain; monoclonal antibody; viral infection;
 cell proliferation; allograft rejection; systemic lupus erythematosus;
 psoriasis; multiple sclerosis; Behcet's Disease; aplastic anaemia;
 immunodeficiency; measles virus; Interferon-alpha-beta; ss.

OS Homo sapiens.
 FH Key Location/Qualifiers
 FT 27..1337
 FT cds
 FT /tag- a
 FT /note- "encodes extra cellular domain of IFN-R"
 PN EP-563487-A.
 PD 06-OCT-1993.
 PE 31-MAR-1992; 400902.
 PR 31-MAR-1992; EP-400902.
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
 PI Benoit P, Maguire D, Meyer F, Plavec I, Tovey MG.
 DR WPI: 93-312951/40.
 DR P-PSDB: R42635 (part).
 PT Monoclonal antibody to human interferon type-I receptor - having
 PT neutralising activity against human type I interferon, used for
 PT therapy and diagnosis
 PS Disclosure: Fig 2: 21pp: English.
 CC Monoclonal antibodies produced against soluble forms of the human
 CC interferon alpha-beta receptor based on the full-length human IFN-R
 CC sequence are claimed. (See 049624 for sequence coding for
 CC full-length IFN-R). The antibodies are useful for treatment and
 CC prophylaxis of disorders involving cell proliferation and/or viral
 CC infection.
 SO Sequence 1343 BP; 449 A; 254 C; 264 G; 376 T;
 Query Match 100.0%; Score 1343; DB 1; Length 1343;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CTCGAGGATCTGCGGGGCTCCAGATGATGTCGTCTCTGGGCGCAGACCTAG 60
 Db 1 CTCGAGGATCTGCGGGGCTCCAGATGATGTCGTCTCTGGGCGCAGACCTAG 60
 Qy 61 TGCCTGTCGCGGTCGGCCATGAGGTTGTCGCGAGCGGAGGAAAATCTAAAT 120
 Db 61 TGCCTGTCGCGGTCGGCCATGAGGTTGTCGCGAGCGGAGGAAAATCTAAAT 120
 Qy 121 CTCCTCAAAAGTAGAGTGCACATCATAGATGACAACTTATCTGTAGTGAACAGA 180
 Db 121 CTCCTCAAAAGTAGAGTGCACATCATAGATGACAACTTATCTGTAGTGAACAGA 180
 Qy 181 GCGATGACTGTGCGGAGTGAATGACTTTTTCATTCGATTCACAAAATCTGGATGATA 240
 Db 181 GCGATGACTGTGCGGAGTGAATGACTTTTTCATTCGATTCACAAAATCTGGATGATA 240
 Qy 241 ATTGGATTAATTTCTCGGCTGTCAGAAATATTAAGTACCAATGCAACTTCTCTCAC 300
 Db 241 ATTGGATTAATTTCTCGGCTGTCAGAAATATTAAGTACCAATGCAACTTCTCTCAC 300
 Qy 301 TCAAGCTGAATGTTATGAAGAAATTAATGCTATAGAGCAGAAAACAACTT 360
 Db 301 TCAAGCTGAATGTTATGAAGAAATTAATGCTATAGAGCAGAAAACAACTT 360
 Qy 361 CTTCATGATGAGTGTGACTCATTTACACCATTTCCGAAAGTCAAGTTGGTCTCCAG 420
 Db 361 CTTCATGATGAGTGTGACTCATTTACACCATTTCCGAAAGTCAAGTTGGTCTCCAG 420
 Qy 421 AAGTACATTTGAAGCTGAAGATTAAGCAATAGATACATCTCTCCGGAACAAAG 480
 Db 421 AAGTACATTTGAAGCTGAAGATTAAGCAATAGATACATCTCTCCGGAACAAAG 480
 Qy 481 ATAGTATATGCGCTTGGATGGTTAGCTTACATATAGCTTACTATCTGAAA 540
 Db 481 ATAGTATATGCGCTTGGATGGTTAGCTTACATATAGCTTACTATCTGAAA 540
 Qy 541 ACTCTTCAGGTTAGAGCAAGATTAATATTATTCAGACATAAATTTTAAAC 600
 Db 541 ACTCTTCAGGTTAGAGCAAGATTAATATTATTCAGACATAAATTTTAAAC 600
 Qy 601 TCTCAGCAGAGCTACTATGTCTAAAGTAAAGCAGACTACTTCGTCATGAAA 660
 Db 601 TCTCAGCAGAGCTACTATGTCTAAAGTAAAGCAGACTACTTCGTCATGAAA 660

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Oy 661 TTGGTCTATAGTCCAGTACATGTATAAGACCACAGTTGAAATGAACTACCTCCAC 720
Db 661 TTGGTCTATAGTCCAGTACATGTATAAGACCACAGTTGAAATGAACTACCTCCAC 720
Oy 721 CAGAAATATAGAAAGTCAAGTCCAAATGAACTATGTTCTTAATGGATTAATACAT 780
Db 721 CAGAAATATAGAAAGTCAAGTCCAAATGAACTATGTTCTTAATGGATTAATACAT 780
Oy 781 ATGCAAAATGACCTTTCAAGTCCAGTCCAGCCCTTTTAAAAAGAAATCCGAA 840
Db 781 ATGCAAAATGACCTTTCAAGTCCAGTCCAGCCCTTTTAAAAAGAAATCCGAA 840
Oy 841 ACCATTGTATTAATGGAACCAATACCTAGTGTAAATGTCAAAATCAACCAAGTGTG 900
Db 841 ACCATTGTATTAATGGAACCAATACCTAGTGTAAATGTCAAAATCAACCAAGTGTG 900
Oy 901 TCTTCTCAAAAGCTTTTCCAAAGAAATTAACCTTCTCCGCTCAAGACATCTGATG 960
Db 901 TCTTCTCAAAAGCTTTTCCAAAGAAATTAACCTTCTCCGCTCAAGACATCTGATG 960
Oy 961 GAAATACACATCTTTTGGTCTGAGAGATTAAGTTGATCTGAAATCAAGCTTTC 1020
Db 961 GAAATACACATCTTTTGGTCTGAGAGATTAAGTTGATCTGAAATCAAGCTTTC 1020
Oy 1021 TACTCTCCAGTCTTAACTATAGATCCCTAGTGTATGATCCATATCTATATGCTG 1080
Db 1021 TACTCTCCAGTCTTAACTATAGATCCCTAGTGTATGATCCATATCTATATGCTG 1080
Oy 1081 CTCGAAACAGTCTGGAACAGCCCTGTGATCCAGATTAATCACTGATTAATGAATTA 1140
Db 1081 CTCGAAACAGTCTGGAACAGCCCTGTGATCCAGATTAATCACTGATTAATGAATTA 1140
Oy 1141 TTTTGGGAAAAACCTTCAATGCTGAGAGAAAAATTAATCGAAAAAACTGATGTTA 1200
Db 1141 TTTTGGGAAAAACCTTCAATGCTGAGAGAAAAATTAATCGAAAAAACTGATGTTA 1200
Oy 1201 CAGTCTCAATTTGAAACCACTGATATGTTGTGAAAGCCAGACACACATG 1260
Db 1201 CAGTCTCAATTTGAAACCACTGATATGTTGTGAAAGCCAGACACACATG 1260
Oy 1261 ATGAAAGCTGAATTAAGAGAGTGTTTTATGTAAGCTGTATGAGAAAAACCAACAG 1320
Db 1261 ATGAAAGCTGAATTAAGAGAGTGTTTTATGTAAGCTGTATGAGAAAAACCAACAG 1320
Oy 1321 GAAATACCTTAATGAGTACC 1343
Db 1321 GAAATACCTTAATGAGTACC 1343

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RESULT

4

O86457

ID

O86457

AC

16-OCT-1995

DT

IFN-R extracellular domain

DE

IFN-R: Interferon receptor; Interferon-alpha; Interferon-beta;

KM

Monoclonal antibody; immunomodulator; AIDS; ss.

OS

Homo sapiens.

FH

Key

Location/Qualifiers

FT

cds

27..1337

/*tag- a

MO9507716-A.

PD

23-MAR-1995

PF

16-SEP-1994

PR

17-SEP-1993

PI

Benlari EJ, Tovey MG;

DR

P-PSDB: R71723

PT

Compsn. of monoclonal antibodies against Interferon receptor

PS

disclosure; Fig. 2A-2B; 105bp; English.

CC DNA encoding the extracellular domain of the human IFN class I
 CC receptor is given in O86457. Monoclonal antibodies were raised
 CC against the recombinant soluble form of the encoded protein (R1723)
 CC expressed in either E. coli or COS cell hosts.
 SQ Sequence 1343 BP; 449 A; 257 C; 261 G; 376 T;

Query Match 99.6%; Score 1338.2; DB 1; Length 1343;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1340; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Oy 1 CTGCAAGGATCTCGCGGCGCTCCAGATGATGTGCTCTCGGCGGAGACCTAG 60
Db 1 CTGCAAGGATCTCGCGGCGCTCCAGATGATGTGCTCTCGGCGGAGACCTAG 60
Oy 61 TCTGCTCGCGCTGGGCCCATGGGTGTGTCCGACGCCGACAGTGAATCTAAAT 120
Db 61 TCTGCTCGCGCTGGGCCCATGGGTGTGTCCGACGCCGACAGTGAATCTAAAT 120
Oy 121 CTCCTCAAAATAGAGTCCGACATCATATGATGACACCTTTATCTGAGGTGGAACAGA 180
Db 121 CTCCTCAAAATAGAGTCCGACATCATATGATGACACCTTTATCTGAGGTGGAACAGA 180
Oy 181 GCGATGAGTCTGCGGGAATGACTTTTTCATGATTAACAAAACTGGAGTGA 240
Db 181 GCGATGAGTCTGCGGGAATGACTTTTTCATGATTAACAAAACTGGAGTGA 240
Oy 241 ATGGATTAATTTGTCTGGGTCTCAGAAATATTAATCAACAACTTTCTTAC 300
Db 241 ATGGATTAATTTGTCTGGGTCTCAGAAATATTAATCAACAACTTTCTTAC 300
Oy 301 TCAAGCTGAATTTTATGAAAGAAATTAATGCGTATAGAGACAAAAACCACTT 360
Db 301 TCAAGCTGAATTTTATGAAAGAAATTAATGCGTATAGAGACAAAAACCACTT 360
Oy 361 CTTCATGATGATGAGTGTGACTCATTTACACATTTCCGAAAGCTCAGATTGGTCTCCAG 420
Db 361 CTTCATGATGATGAGTGTGACTCATTTACACATTTCCGAAAGCTCAGATTGGTCTCCAG 420
Oy 421 AAGTACATTTAGAACTGAGATTAAGCAATGATGATACATCTCTCTGGAAACAAAG 480
Db 421 AAGTACATTTAGAACTGAGATTAAGCAATGATGATACATCTCTCTGGAAACAAAG 480
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Db 481 ATAGTGTATGAGGCTTGTGATGATTAAGCTTACTTAATGCTTACTTAATCTGAAAA 540
Oy 541 ACTCTTCAGGTAGAAAGAAAGATTAATTTATCCAGACATTAATTTTAAAC 600
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Oy 601 TCTCACAGAGACACTATTTGTCTAAAGTTAAAGACACACTACTTACGTATGAAAA 660
Db 601 TCTCACAGAGACACTATTTGTCTAAAGTTAAAGACACACTACTTACGTATGAAAA 660
Oy 661 TTGGTGTCTATGTCAGTACATTTATTAAGACACAGTTGAAATTAATCTACTCCAC 720
Db 661 TTGGTGTCTATGTCAGTACATTTATTAAGACACAGTTGAAATTAATCTACTCCAC 720
Oy 721 CAGAAATATAGAAAGTCAAGTCCAAATGAACTATGTTCTTAATGGATTAATACAT 780
Db 721 CAGAAATATAGAAAGTCAAGTCCAAATGAACTATGTTCTTAATGGATTAATACAT 780
Oy 781 ATGCAAAATGACCTTTCAAGTCCAGTCCAGCCCTTTTAAAAAGAAATCCGAA 840
Db 781 ATGCAAAATGACCTTTCAAGTCCAGTCCAGCCCTTTTAAAAAGAAATCCGAA 840
Oy 841 ACCATTGTATTAATGGAACCAATACCTAGTGTAAATGTCAAAATCAACCAAGTGTG 900
Db 841 ACCATTGTATTAATGGAACCAATACCTAGTGTAAATGTCAAAATCAACCAAGTGTG 900
Oy 901 TCTTCTCAAAAGCTTTTCCAAAGAAATTAACCTTCTCCGCTCAAGACATCTGATG 960
Db 901 TCTTCTCAAAAGCTTTTCCAAAGAAATTAACCTTCTCCGCTCAAGACATCTGATG 960

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Db 901 TCTTCTCCTCAAAAGCTTTTCCAAAAGAAATTTACCTTCTCCGGCTACAGCATCTGATG 960
Qy 961 GAAATACACATCTTTTGGTCTGAAGATTAAGTTGATCTACTAATAATACAGCTTCC 1020
Db 961 GAAATACACATCTTTTGGTCTGAAGATTAAGTTGATCTACTAATAATACAGCTTCC 1020
Qy 1021 TACTTCTCCTCAAGCTTTTAACTAATCCTTGTAGTATTCATTCATCTATATCGGTG 1080
Db 1021 TACTTCTCCTCAAGCTTTTAACTAATCCTTGTAGTATTCATTCATCTATATCGGTG 1080
Qy 1081 CTCCTCAAGCTCTGGAAGACAGCTGTGATCCAGATTAATCAGATTTATGAAATTA 1140
Db 1081 CTCCTCAAGCTCTGGAAGACAGCTGTGATCCAGATTAATCAGATTTATGAAATTA 1140
Qy 1141 TTTTGGGAAAACACTTCAAAATGCTGAGAGAAAATTAATGAGAAAATGATGTTA 1200
Db 1141 TTTTGGGAAAACACTTCAAAATGCTGAGAGAAAATTAATGAGAAAATGATGTTA 1200
Qy 1201 CAGTTCCTTAATTTGAACCACTGACTGATATTTGTGAAAGCCAGAGACACACATGG 1260
Db 1201 CAGTTCCTTAATTTGAACCACTGACTGATATTTGTGAAAGCCAGAGACACACATGG 1260
Qy 1261 ATGAAACCTGATAATGAAAGCACTGTTTGTAGTACGCTGTATGAGAGAAAACCAAG 1320
Db 1261 ATGAAACCTGATAATGAAAGCACTGTTTGTAGTACGCTGTATGAGAGAAAACCAAG 1320
Qy 1321 GAAATACCTCTTAATGAGTACC 1343
Db 1321 GAAATACCTCTTAATGAGTACC 1343
RESULT 5
ID Q14240
Q14240 Q14240 standard; DNA: 1755 BP.
AC Q14240:
DE 16-JAN-1992 (first entry)
EN Encodes complete Interferon- α /pna/beta receptor.
KW IFN; autoimmune disease; graft rejection; histocompatibility; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 27..1760
FT /tag= a
FN FR2657881-A.
PD 09-AUG-1991.
PR 05-FEB-1990; 001298.
PA (EUBI-) LAB EURO BIOTECHNO.
PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE.
PI Royce MG, Uze G.
DR WP1: 91-31978/44.
DR P-PSDB: R14488.
PT New water-soluble polypeptide(s) with affinity for IFN- α and
PT beta - used to treat e.g. lupus erythematosus, Behcet's disease,
PT aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.
PS Discloure: Page 47; 32pp; French.
CC The protein encoded by this sequence corresponds to the complete
CC Interferon- α and/or beta receptor. The invention covers
CC derivatives of the receptor obtained by deleting the transmembrane
CC and cytoplasmic domains of the native receptor or by substitution.
CC See also Q14239.
SQ Sequence 1755 BP; 593 A; 324 C; 334 G; 504 T;

Query Match 99.3%; Score 1334; DB 1; Length 1755;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCAAGGATCTGCGGGCTCCAGATGATGCTCTCTCTGCGCGGAGACCTTAG 60
Db 1 CTGCAAGGATCTGCGGGCTCCAGATGATGCTCTCTCTGCGCGGAGACCTTAG 60
Qy 61 TGCTGTCGCGCCCTGGCCCATGGGTGTCTCCGACGCCAGTGGAAAAATCTAAAT 120
Db 61 TGCTGTCGCGCCCTGGCCCATGGGTGTCTCCGACGCCAGTGGAAAAATCTAAAT 120

Db 61 TGCTGTCGCGCCCTGGCCCATGGGTGTCTCCGACGCCAGTGGAAAAATCTAAAT 120
Qy 121 CTCCTCAAAAAGTAGAGTGCATCATAGATGACAATTTATCTGAGTGAACAGA 180
Db 121 CTCCTCAAAAAGTAGAGTGCATCATAGATGACAATTTATCTGAGTGAACAGA 180
Qy 181 GCGATGAGTCTGCGGGAATGACTTTTCATTCGATATATCAAAAAATCGATGATA 240
Db 181 GCGATGAGTCTGCGGGAATGACTTTTCATTCGATATATCAAAAAATCGATGATA 240
Qy 241 ATTGGATTAATTTCTGGGCTGAGAAATATATAGTACCAATGCACTTTCTTCAC 300
Db 241 ATTGGATTAATTTCTGGGCTGAGAAATATATAGTACCAATGCACTTTCTTCAC 300
Qy 301 TCAAGCTAATGTTATGAAATTAATGCGTATAGAGCAAGAAAACACTT 360
Db 301 TCAAGCTAATGTTATGAAATTAATGCGTATAGAGCAAGAAAACACTT 360
Qy 361 CTTCATGCTATGAGGTGACTCATTTACACCATTTGCGAAAGCTCAGATTGCTCCAG 420
Db 361 CTTCATGCTATGAGGTGACTCATTTACACCATTTGCGAAAGCTCAGATTGCTCCAG 420
Qy 421 AAGTACATTTGAAGCTGAAATAGGCAATAGATACATCTCTCTGGAACAAAG 480
Db 421 AAGTACATTTGAAGCTGAAATAGGCAATAGATACATCTCTCTGGAACAAAG 480
Qy 481 ATAGTATATGAGGCTTGGATGTTAAGCTTATACATATAGCTTACTATGAAAA 540
Db 481 ATAGTATATGAGGCTTGGATGTTAAGCTTATACATATAGCTTACTATGAAAA 540
Qy 541 ACTCTCAGTGTGAAAGAAAGATGAAATATTTATTCAGACATTAATTTATAAC 600
Db 541 ACTCTCAGTGTGAAAGAAAGATGAAATATTTATTCAGACATTAATTTATAAC 600
Qy 601 TCTACCGAGACTACTATTTGTCTAAAAGCTTAAGCGACTACTACGCAAGGAAA 660
Db 601 TCTACCGAGACTACTATTTGTCTAAAAGCTTAAGCGACTACTACGCAAGGAAA 660
Qy 661 TTGGTGTATAGTCCAGTACATTTGTAAGACACAGTGAAGAAATGAACTACCTCAC 720
Db 661 TTGGTGTATAGTCCAGTACATTTGTAAGACACAGTGAAGAAATGAACTACCTCAC 720
Qy 721 CAGAAATATAGAGTCCAGTCCAAATCAGAACTATGTTCTTAATGGATTAACAT 780
Db 721 CAGAAATATAGAGTCCAGTCCAAATCAGAACTATGTTCTTAATGGATTAACAT 780
Qy 781 ATGCAAAATACCTTTCAATTCAGTGCCTCCAGCGCTTTTAAAAAGAAATCCTGAA 840
Db 781 ATGCAAAATACCTTTCAATTCAGTGCCTCCAGCGCTTTTAAAAAGAAATCCTGAA 840
Qy 841 ACCATTTGTATTAATGAGAAACAAATACCTGACTGAAATATGTCAAAACCTCCAGTGTG 900
Db 841 ACCATTTGTATTAATGAGAAACAAATACCTGACTGAAATATGTCAAAACCTCCAGTGTG 900
Qy 901 TCTTCTCAAAAAGCTTTTCCAAAAGAAATTAACCTTCTCCGGTACAACTGTATG 960
Db 901 TCTTCTCAAAAAGCTTTTCCAAAAGAAATTAACCTTCTCCGGTACAACTGTATG 960
Qy 961 GAAATACACATCTTTTGGCTGAGAGAAATTTGATGATGAAATACAACTTTCC 1020
Db 961 GAAATACACATCTTTTGGCTGAGAGAAATTTGATGATGAAATACAACTTTCC 1020
Qy 1021 TACTTCTCCTCAAGCTTTTAACTAATCCTTGTAGTATTCATTCATCTATATCGGTG 1080
Db 1021 TACTTCTCCTCAAGCTTTTAACTAATCCTTGTAGTATTCATTCATCTATATCGGTG 1080
Qy 1081 CTCCTCAAGCTCTGGAAGACAGCTGTGATCCAGATTAATCAGATTTATGAAATTA 1140
Db 1081 CTCCTCAAGCTCTGGAAGACAGCTGTGATCCAGATTAATCAGATTTATGAAATTA 1140
Qy 1141 TTTTGGGAAAACACTTCAAAATGCTGAGAGAAAATTAATGAGAAAATGATGTTA 1200
Db 1141 TTTTGGGAAAACACTTCAAAATGCTGAGAGAAAATTAATGAGAAAATGATGTTA 1200

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OY 1201 CAGTTCCTAATTGAAACCACTGCTATATTGTGTGAAGCCAGACACACCATG 1260
DB 1201 CAGTTCCTAATTGAAACCACTGCTATATTGTGTGAAGCCAGACACACCATG 1260
OY 1261 ATGAAAAGCTGAATAAAGCAGTGTGTTAGTGACGCTATGTGAAAAACAAACAG 1320
DB 1261 ATGAAAAGCTGAATAAAGCAGTGTGTTAGTGACGCTATGTGAAAAACAAACAG 1320
OY 1321 GAAATACCTCTAAA 1334
DB 1321 GAAATACCTCTAAA 1334

RESULT 6
O30533
ID O30533 standard; DNA: 1755 BP.
AC O30533;
DR 31-MAR-1993 (first entry)
DE Sequence encoding a soluble form of the interferon (IFN) receptor
DE with a high affinity for IFN-alpha and -beta.
KW Interferon receptor; alpha-interferon; beta-interferon; SS.
OS Synthetic.
FH key Location/Qualifiers
FT cds 27..1700
FT key /*tag= a
PN MO9218626-A.
PD 29-OCT-1992.
PF 17-APR-1991; F00318.
PR 17-APR-1991; WO-F00318.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,
PI Toyer M, Ise G.
DR WPI: 92-382110/46.
DR P-PDB: R28496.
PT Water soluble polypeptide(s) strongly bind interferon(s) alpha
PT and beta - useful as immunosuppressants, for treating auto-immune
PT diseases and transplant rejection
PS Claim 10: Fig 2: 58pp: English.
CC DNA encoding the water-soluble polypeptide with a high affinity for
CC IFN-alpha and -beta is isolated by PCR, using appropriate
CC oligonucleotides as primers and cloned cDNA as template. For example,
CC bacteriophage lambda ZAP, containing the entire coding sequence of
CC the IFN-alpha and -beta receptor (O30533), was incubated with oligos
CC O30534 and O30535. R28496 represents the complete receptor. R28495
CC lacks the transmembrane and cytoplasmic domains. Both forms bind
CC IFN in the same way as antibodies, so are immunosuppressants e.g. for
CC treating autoimmune diseases and graft rejection. They lack the
CC toxic side-effects of known immunosuppressants such as steroids.
SQ Sequence 1755 BP; 593 A; 325 C; 333 G; 504 T;

Query Match 99.3%; Score 1334; DB 1; Length 1755;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 241 ATTGATTAATTTGTCTGGGTGTCAGAAATATTACTAGCAAAATGCACTTTCTTCAC 300
OY 301 TCAAGCTGAATGTTTATGAGAAATTAATTCGCTATAGAGCAGAAAAAAGCACTT 360
DB 301 TCAAGCTGAATGTTTATGAGAAATTAATTCGCTATAGAGCAGAAAAAAGCACTT 360
OY 361 CTGATGATGAGGTGACCTATTACCATTTCCAAAGCCAGATGTCCTCCAG 420
DB 361 CTGATGATGAGGTGACCTATTACCATTTCCAAAGCCAGATGTCCTCCAG 420
OY 421 AAGTACATTTAGAAAGCTGAAATAGGCAATAGATACACATCTCTCGGAACAAAG 480
DB 421 AAGTACATTTAGAAAGCTGAAATAGGCAATAGATACACATCTCTCGGAACAAAG 480
OY 481 ATAGTGTATGTGGGCTTTGGATGGCTTTAGCTTTACATATAGCTTATCTGAAAA 540
DB 481 ATAGTGTATGTGGGCTTTGGATGGCTTTAGCTTTACATATAGCTTATCTGAAAA 540
OY 541 ACTCTTCAGGTGTGAAGAAGATGAAATATTATTCAGACATPAAATTTATTAAC 600
DB 541 ACTCTTCAGGTGTGAAGAAGATGAAATATTATTCAGACATPAAATTTATTAAC 600
OY 601 TCTCACAGAGACTACTATTGTCTPAAAGTTAAAGCAGCACTACTTACGTCATGAAAA 660
DB 601 TCTCACAGAGACTACTATTGTCTPAAAGTTAAAGCAGCACTACTTACGTCATGAAAA 660
OY 661 TTGGTGTATATAGTCCAGTACATTTGATTAAGACACAGTTGAAATAGAACTACCTCCAC 720
DB 661 TTGGTGTATATAGTCCAGTACATTTGATTAAGACACAGTTGAAATAGAACTACCTCCAC 720
OY 721 CAGAAATATATGAAGTCAAGTCCAAATACGAATCTATGCTTAATGGATTAATCAT 780
DB 721 CAGAAATATATGAAGTCAAGTCCAAATACGAATCTATGCTTAATGGATTAATCAT 780
OY 781 ATGCAACATGACCTTTCAAGTCAAGTCCCAAGCCTTTTAAAAAGAAATCTGAAA 840
DB 781 ATGCAACATGACCTTTCAAGTCAAGTCCCAAGCCTTTTAAAAAGAAATCTGAAA 840
OY 841 ACCATTTTATTAATGAAACAAATACCTGACTGTGAATATGTAACCACTCCAGTGTG 900
DB 841 ACCATTTTATTAATGAAACAAATACCTGACTGTGAATATGTAACCACTCCAGTGTG 900
OY 901 TCTTCCCAAGAGCTTTCCAAAGAAATTTACCTCTCCGGGTCAACACATCTGTG 960
DB 901 TCTTCCCAAGAGCTTTCCAAAGAAATTTACCTCTCCGGGTCAACACATCTGTG 960
OY 961 GAAATTAACACATCTTTTGTGCTGAAGAGATPAAAGTTGATACGAAATACAACTTTC 1020
DB 961 GAAATTAACACATCTTTTGTGCTGAAGAGATPAAAGTTGATACGAAATACAACTTTC 1020
OY 1021 TACTTCCCTCAGCTTTTAACATTAGATCCCTTAGATGATCTCATATCTATCGGTG 1080
DB 1021 TACTTCCCTCAGCTTTTAACATTAGATCCCTTAGATGATCTCATATCTATCGGTG 1080
OY 1081 CTCGAAACAGCTGGAACACAGCCTGTGATCCAGATTAATCCACTGTTATATAATTA 1140
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OY 1141 TTTTGGGAAAAACACTTCAATGCTGAGAGAAAAATTAAGAGAAAAAACTGATGTTA 1200
DB 1141 TTTTGGGAAAAACACTTCAATGCTGAGAGAAAAATTAAGAGAAAAAACTGATGTTA 1200
OY 1201 CAGTTCCTAATTGAAACCACTGCTATATTGTGTGAAGCCAGACACACCATG 1260
DB 1201 CAGTTCCTAATTGAAACCACTGCTATATTGTGTGAAGCCAGACACACCATG 1260
OY 1261 ATGAAAAGCTGAATAAAGCAGTGTGTTAGTGACGCTATGTGAAAAACAAACAG 1320
DB 1261 ATGAAAAGCTGAATAAAGCAGTGTGTTAGTGACGCTATGTGAAAAACAAACAG 1320
OY 1321 GAAATACCTCTAAA 1334
DB 1321 GAAATACCTCTAAA 1334

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KM monoclonal antibody; immunomodulator; AIDS; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT cds 27..1700
 FT /tag- a
 PN W09507716-A.
 PD 23-MAR-1995.
 PF 16-SEP-1994.
 PR 17-SEP-1993; EP-402279.
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
 PI Beniziri EJ, Tovey MG;
 DR WPI: 95-131187/17.
 DR P-PDB: R75356.
 PT Compn. of monoclonal antibodies against interferon receptor
 PT useful as immunomodulator, eg. for treating AIDS
 PS Disclosure: Fig.3A-28; 105pp; English.
 CC DNA encoding the extracellular domain of the human IFN class I
 CC receptor is given in 086457; the full IFN receptor gene
 CC is given in 086458. Immunomodulator monoclonal antibodies were
 CC raised against the recombinant soluble form of the extracellular
 CC domain (R71723) expressed in E. coli or COS cell hosts.
 SO Sequence 1755 BP; 592 A; 324 C; 334 G; 505 T;

Query Match 99.2%; Score 1332.4; DB 1; Length 1755;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTCGAGGATCTGCGCGGCTCCCAAGATGATGTCCTCTCGGCGCGAGCCCTAG 60
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 Db 1 CTCGAGGATCTGCGCGGCTCCCAAGATGATGTCCTCTCGGCGCGAGCCCTAG 60

QY 61 TGGTCGCGCGGCGGCGGCTGTCGCGCGAGCCGAGGATGGAATAAATCTAAAT 120
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 Db 61 TGGTCGCGCGGCGGCGGCTGTCGCGCGAGCCGAGGATGGAATAAATCTAAAT 120

QY 121 CTCCTCAAAAAGTAGAGTGCACATCATAGATGACAACCTTATCTGAGTGGACAGA 180
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 Db 121 CTCCTCAAAAAGTAGAGTGCACATCATAGATGACAACCTTATCTGAGTGGACAGA 180

QY 181 GCGATGAGTGTGCGGGAATGTGACTTTTCATTTCATTATCAAAAACTGGATGATA 240
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 Db 181 GCGATGAGTGTGCGGGAATGTGACTTTTCATTTCATTATCAAAAACTGGATGATA 240

QY 241 ATGGATAAATGTGCGGCTGACAAATATCTAGTACCAATCAATTTCTTCAC 300
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 Db 241 ATGGATAAATGTGCGGCTGACAAATATCTAGTACCAATCAATTTCTTCAC 300

QY 301 TCAAGCTGAATGTTATGAAGAAATTAATGCGTATAGAGCAGAAAAAGAACACTT 360
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 Db 301 TCAAGCTGAATGTTATGAAGAAATTAATGCGTATAGAGCAGAAAAAGAACACTT 360

QY 361 CTTCATGATGATGAGTGGTACTCATTTACACCAATTTGGCAAGTCAAGTTCCTCCAG 420
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 Db 361 CTTCATGATGATGAGTGGTACTCATTTACACCAATTTGGCAAGTCAAGTTCCTCCAG 420

QY 421 AAGTACATTAGAGGATGAAGATAGAGCAATAGTATACACTCTCCGGAACAAAAG 480
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 Db 421 AAGTACATTAGAGGATGAAGATAGAGCAATAGTATACACTCTCCGGAACAAAAG 480

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 Db 481 ATAGTGTATAGTGGGCTTTGGATGTTAAGCTTACATATAGCTTATCTATCTGAAAA 540

QY 541 ACCTTCAGGTGATGAAGAAAGATGAAATTTATTTCAACACATTAATTTATTAAC 600
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 Db 541 ACCTTCAGGTGATGAAGAAAGATGAAATTTATTTCAACACATTAATTTATTAAC 600

QY 601 TCTCACCAGAGACTACTTATGCTAAAGATTAAGAGAGCACTACTAGCTATGAAAA 660
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 Db 601 TCTCACCAGAGACTACTTATGCTAAAGATTAAGAGAGCACTACTAGCTATGAAAA 660

QY 661 TTGGTGTCTATAGTCCAGTACATTTGATAAAGACACAGTTGAAAAATGAATCTACTCCAC 720

Db 661 TTGGTGTCTATAGTCCAGTACATTTGATAAAGACACAGTTGAAAAATGAATCTACTCCAC 720
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QY 721 CAGAAAAATATAGAACTAGTGTCCAAAAATCAGAACTATGTTCTTAAATGGATTATACAT 780
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Db 721 CAGAAAAATATAGAACTAGTGTCCAAAAATCAGAACTATGTTCTTAAATGGATTATACAT 780

QY 781 ATGCAAAATATGACCTTTCAAGTTGAGTGGCTCCAGCCTTTTAAAAAGAAATCTGAA 840
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Db 781 ATGCAAAATATGACCTTTCAAGTTGAGTGGCTCCAGCCTTTTAAAAAGAAATCTGAA 840

QY 841 ACCATTTGATTAATATGAAACAAATATCAGTGTGAAATATGCAAACTACCAAGTGTG 900
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Db 841 ACCATTTGATTAATATGAAACAAATATCAGTGTGAAATATGCAAACTACCAAGTGTG 900

QY 901 TCTTTCTCAAAACGTTTCCAAAAAGAAATTTACCTTCTCCGCTACACATCTGATG 960
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Db 901 TCTTTCTCAAAACGTTTCCAAAAAGAAATTTACCTTCTCCGCTACACATCTGATG 960

QY 961 GAAATTAACACATCTTTTGGTGTGAGAGATTAAGTTGATAGTGAATACAGCTTCC 1020
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Db 961 GAAATTAACACATCTTTTGGTGTGAGAGATTAAGTTGATAGTGAATACAGCTTCC 1020

QY 1021 TACTTCTCCAGTCTTTTACATTTAGATCCCTTAGTATTCATTCATATATCGGTG 1080
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Db 1021 TACTTCTCCAGTCTTTTACATTTAGATCCCTTAGTATTCATTCATATATCGGTG 1080

QY 1081 CTCCAAAAACAGTGTGAAACAGCGCTGTGATCCAGAGATTATTCACATTTATGAATTA 1140
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Db 1081 CTCCAAAAACAGTGTGAAACAGCGCTGTGATCCAGAGATTATTCACATTTATGAATTA 1140

QY 1141 TTTTGGAAAAACACTTCAATAGCTGAGAGAAAAATATGAGAAAAAACTGATGTTA 1200
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Db 1141 TTTTGGAAAAACACTTCAATAGCTGAGAGAAAAATATGAGAAAAAACTGATGTTA 1200

QY 1201 CAGTTCCTAATTTGAACACAGTGTATATGTTGTGAAAAAGCCAGACACACATGAG 1260
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Db 1201 CAGTTCCTAATTTGAACACAGTGTATATGTTGTGAAAAAGCCAGACACACATGAG 1260

QY 1261 ATGAAAAAGCTGAATTAAGACAGTGTTTTAGTACGCTGTATGTGAAAAACAAACAG 1320
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Db 1261 ATGAAAAAGCTGAATTAAGACAGTGTTTTAGTACGCTGTATGTGAAAAACAAACAG 1320

QY 1321 GAAATACCTCTAAA 1334
 |||||

Db 1321 GAAATACCTCTAAA 1334

RESULT 9
 011701.
 ID 011701 standard; DNA: 2784 BP.
 AC 011701.
 DT 18-JUL-1991 (first entry)
 DE Human alpha-interferon receptor protein encoding sequence.
 KW Human alpha IFN; IFN agonists; antiviral; anti tumour agent;
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT cds 79..1752
 FT /tag- a
 FT /product- human alpha IFN
 FT signal_peptide 79..159
 FT /tag- b
 FT /product- signal peptide 226..234
 FT /tag- c
 FT /label- glycosylation site 250..258
 FT misc_rna 250..258
 FT /tag- d
 FT /label- glycosylation site 319..327
 FT /tag- e
 FT /label- glycosylation site

Query Match	Best Local Similarity	Match Sequence 1332: Conservative	Score 99.1%	Score 99.9%	Pred. No. 0	Mismatches 0	Indels 2	Gaps 0
1	CTGCAGGATCTGCGGGCCCTCCAGATATGATGTCCTCTCTGCGGCGGACGACCCCTAG	111						
53	CTGGTGGGATCTGCGGGCCCTCCAGATATGATGTCCTCTCTGCGGCGGACGACCCCTAG	112						
61	TGCTGTCGCGCCGTGGGCCCATATGATGTCCTCTCTGCGGCGGACGACCCCTAG	120						
113	TGCTGTCGCGCCGTGGGCCCATATGATGTCCTCTCTGCGGCGGACGACCCCTAG	172						
121	CTCTCTCAAAAAGTATAGAGTGCATCATATGATGACAACTTATCTCTGAGGTGAAACAGCA	180						
173	CTCTCTCAAAAAGTATAGAGTGCATCATATGATGACAACTTATCTCTGAGGTGAAACAGCA	232						

Oy	181	GCATGAGCTGCTGCGGGAATGCACTTTTTCATTTGATATATCAAAAACTGGATGSGATA	240
Oy	233	GGGATGAGCTGCTGCGGGAATGCACTTTTTCATTTGATATATCAAAAACTGGATGSGATA	292
Oy	241	ATTGATATAATTGCTCGGGGTGCACAATAATTACTAGTACCAAAATGCAACTTTTCTTCAAC	300
Db	293	ATTGGATATAATTGTCTGGGGTGTCAATAATTACTAGTATACCAAAATGCAACTTTTCTTCAAC	352
Oy	301	TCAAAGTGAATGTTTATGAAGAAATTTAAATTGGCGTATTAAGACAGAAAAAGAAACACTT	360
Db	353	TCAAGCTGAATGTTTATGAAGAAATTTAAATTGGCGTATTAAGACAGAAAAAGAAACACTT	412
Oy	361	CTTAAGGTATAGGCTGGAATCATTTACACAAATTCGGAACCTGAGATTTGGTCTCCAG	420
Db	413	CTTATGGTATAGGCTGGAATCATTTACACAAATTCGGAACCTGAGATTTGGTCTCCAG	472
Oy	421	AAGTACATTTAGAAAGCTGAAGATTAAGCAATAGTGAATCACATCTCTCTGGACAAAG	480
Db	473	AAGTACATTTAGAAAGCTGAAGATTAAGCAATAGTGAATCACATCTCTCTGGACAAAG	532
Oy	481	ATAGTGTATAGTGGGCTTTGGATGTTTAAAGCTTTACATATAGCTTACTTATCTGGAAAA	540
Db	533	ATAGTGTATAGTGGGCTTTGGATGTTTAAAGCTTTACATATAGCTTACTTATCTGGAAAA	592
Oy	541	ACTGTCAGGCTGTAAGAAAGGATTTGAAATTTTATCCAGACATAAAAATTTTAAAC	600
Db	593	ACTGTCAGGCTGTAAGAAAGGATTTGAAATTTTATCCAGACATAAAAATTTTAAAC	652
Oy	601	TCTCACCAGAGACTACTTATTTGTCTAAAGTTTAAAGCAGACTACTTACGTATGAAAA	660
Db	653	TCTCACCAGAGACTACTTATTTGTCTAAAGTTTAAAGCAGACTACTTACGTATGAAAA	712
Oy	661	TTGTCGTCTATAGCCAGTGCATGTGTATAAGCCAGCTGTAATAATGAACACTCCAC	720
Db	713	TTGTCGTCTATAGCCAGTGCATGTGTATAAGCCAGCTGTAATAATGAACACTCCAC	772
Oy	721	CAGAAAATATAGAAGTCAGTGCCTCAAAATCAGAACTATGTTCTTAAATGGATTATACAT	780
Db	773	CAGAAAATATAGAAGTCAGTGCCTCAAAATCAGAACTATGTTCTTAAATGGATTATACAT	832
Oy	781	ATGCAAAACATGACCTTTCAAGTTCATGCGCTCCAGCCCTTTTAAAAAGAAATCCTGGAA	840
Db	833	ATGCAAAACATGACCTTTCAAGTTCATGCGCTCCAGCCCTTTTAAAAAGAAATCCTGGAA	892
Oy	841	ACCATTTGTATTAATGGAACCAATACCTGACTGTGAATATGTCAAAACTACCCAGTGTG	900
Db	893	ACCATTTGTATTAATGGAACCAATACCTGACTGTGAATATGTCAAAACTACCCAGTGTG	952
Oy	901	TCTTTCTCAAAAGCTTTCCAAAAAGAAATTTACCTTCCGCGTACAAAGCATTTGATG	960
Db	953	TCTTTCTCAAAAGCTTTCCAAAAAGAAATTTACCTTCCGCGTACAAAGCATTTGATG	1012
Oy	961	GAAATACACATCTTTTGTGTCGAAGAGATAAGTTGATATCTGAATAATACAGTTTCC	1020
Db	1013	GAAATACACATCTTTTGTGTCGAAGAGATAAGTTGATATCTGAATAATACAGTTTCC	1072
Oy	1021	TACTTCTCAGTCTTTTACATTAGATCCCTTAGTATGATTCATTCATATCTATATCGGTG	1080
Db	1073	TACTTCTCAGTCTTTTACATTAGATCCCTTAGTATGATTCATTCATATCTATATCGGTG	1132
Oy	1081	CTCCAAANAGCTGCGGAACAGCCGCTGATCAGGATTAATCAGTAAATTAAGAAATTA	1140
Db	1133	CTCCAAANAGCTGCGGAACAGCCGCTGATCAGGATTAATCAGTAAATTAAGAAATTA	1192
Oy	1141	TTTTTTGGAAAAACACTTCAAAATGCTGAGAGAAAAATTTATCAGAAAAAAAATGATGTTTA	1200
Db	1193	TTTTTTGGAAAAACACTTCAAAATGCTGAGAGAAAAATTTATCAGAAAAAAAATGATGTTTA	1252
Oy	1201	CAGTCTCTAATTTGAAAACAGTACTGTTATTTGTGTAAAGCCAGAGACACACACATGCG	1260
Db	1253	CAGTCTCTAATTTGAAAACAGTACTGTTATTTGTGTAAAGCCAGAGACACACACATGCG	1312

QY 1261 ATGAAAAGCTGATTAAGAGTGTCTTGTAGTACGCTGATGTGAGAAAACAAACAG 1320
 |||||||
 Db 1313 ATGAAAAGCTGATTAAGAGTGTCTTGTAGTACGCTGATGTGAGAAAACAAACAG 1372
 |||||||
 QY 1321 GAAATACCTCTTAA 1334
 |||||||
 Db 1373 GAAATACCTCTTAA 1386

RESULT 10

T73519
 ID T73519 standard; cDNA: 360 BP.
 AC T73519;
 DT 23-SEP-1997 (first entry)
 DE Transmembrane Interferon alpha-receptor cDNA fragment.
 KW Interferon alpha-receptor; IFNAR; ss.
 OS Homo sapiens.
 FH Key
 FT exon
 FT Location/Qualifiers
 FT 112..113
 FT /tag= a
 FT /note= "exon IX-exon X junction"
 FT 238..259
 FT /tag= b
 FT /note= "exon X-exon XI junction"
 FT 10..30
 FT /tag= c
 FT /note= "primer 1270-1290"
 FT 71..82
 FT /tag= d
 FT /note= "primer 1331..1342"
 FT 238..255
 FT /tag= e
 FT /note= "primer 1498..1515"
 FT 262..282
 FT /tag= f
 FT /note= "primer 1522..1542"
 FT 341..360
 FT /tag= g
 FT /note= "primer 1601..1619"

PN AU9475977-A.
 PD 11-MAY-1995.
 PE 20-OCT-1994; 075977.
 PR 24-OCT-1993; IL-107378.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PA (ABRA/) ABRAMOVICH C.
 PI Abramovich C, Ratovitski E, Revel M;
 WP1: 95-200634/27.
 PT New mammalian soluble interferon alpha-receptor forms - used for
 PT inhibiting, modulating or modifying the activities of interferon(s)
 PS Disclosure: Fig 6: 46pp; English.
 CC A cDNA sequence (T73519) corresponds to nucleotides 1360-1620 of
 CC a cDNA clone for human interferon alpha receptor (IFNAR, see also
 CC W21804), covering the region that codes for the transmembrane
 CC region of IFNAR. Differential splicing of IFNAR gene transcripts
 CC (see also T73520 and T73521) produces novel soluble, non-membrane
 CC bound forms of IFNAR (see also W21805 and W21806) that can be used
 CC to inhibit, modulate or modify the activities of interferons alpha
 CC and beta in cells, tissues and organisms, or for diagnostic
 CC purposes.
 SO Sequence 360 BP: 117 A: 64 C: 62 G: 117 T;

Query Match 9.4%; Score 126; DB 1; Length 360;
 Best Local Similarity 100.0%; Pred. No. 1.9e-24;
 Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1209 AATTGAAACCACTGATATATGTTGTAAGCCAGACACACATGATGAAAG 1268
 |||||||
 Db 1 AATTGAAACCACTGATATATGTTGTAAGCCAGACACACATGATGAAAG 60
 |||||||
 QY 1269 CTGAATTAAGCAGTGTCTTGTAGTACGCTGTGTGAGAAAACAAACAGAAATACC 1328
 |||||||
 Db 61 CTGAATTAAGCAGTGTCTTGTAGTACGCTGTGTGAGAAAACAAACAGAAATACC 120

QY 1329 TCTTAA 1334
 |||||||
 Db 121 TCTTAA 126

RESULT 11

T73521
 ID T73521 standard; cDNA: 168 BP.
 AC T73521;
 DT 23-SEP-1997 (first entry)
 DE Interferon alpha-receptor splice-deleted form 2 cDNA.
 KW Interferon alpha-receptor; IFNAR; ss.
 OS Homo sapiens.
 FH Key
 FT exon
 FT AU9475977-A.
 PD 11-MAY-1995.
 PE 20-OCT-1994; 075977.
 PR 24-OCT-1993; IL-107378.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PA (ABRA/) ABRAMOVICH C.
 PI Abramovich C, Ratovitski E, Revel M;
 WP1: 95-200634/27.
 PT New mammalian soluble interferon alpha-receptor forms - used for
 PT inhibiting, modulating or modifying the activities of interferon(s)
 PS Example 3: Fig 6: 46pp; English.
 CC A cDNA sequence (T73521) corresponds to a portion of splice-deleted
 CC IFN alpha-receptor (IFNAR) form 2 gene transcript, covering a
 CC region which, in comparison with transmembrane IFNAR cDNA (see
 CC also T73519), has 2 in-phase deletions of nucleotides 1318-1341 in
 CC exon IX and of nucleotides 1360-1518, i.e. the end of exon IX and
 CC all of exon X. IFNAR spliced-deleted form 2 (W21806) is predicted
 CC to have a shortened extracellular domain, no transmembrane domain
 CC and a truncated intracellular domain. The cDNA clone was detected
 CC after PCR amplification of human U266 myeloma RNA. Recombinant,
 CC soluble non-membrane bound IFNAR spliced-deleted form 1 can be
 CC expressed in host cells and used to inhibit, modulate or modify the
 CC activities of interferons alpha and beta, or for diagnostic
 CC purposes.
 SO Sequence 168 BP: 58 A: 31 C: 32 G: 47 T;

Query Match 3.6%; Score 49; DB 1; Length 168;
 Best Local Similarity 100.0%; Pred. No. 0.0004;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1218 CCACGTGATATATGTTGTAAGCCAGACACACACATGATGAAA 1266
 |||||||
 Db 1 CCACGTGATATATGTTGTAAGCCAGACACACACATGATGAAA 49
 |||||||

RESULT 12

Q11377
 ID Q11377 standard; DNA: 6119 BP.
 AC Q11377;
 DT 02-JUL-1991 (first entry)
 DE Genes encoding T. hyo 39 kD family 1 antigens 1-4.
 KW Swine dysentery; vaccine; ss.
 OS Treponema hyodysenteriae serotype B204.
 FH Key
 FT cds
 FT Location/Qualifiers
 FT 750..1910
 FT /tag= a
 FT /label= gene 1
 FT /note= "39 kd antigen 1"
 FT 2067..3227
 FT /tag= b
 FT /label= gene 2
 FT /note= "39 kd antigen 2"
 FT 3381..4550
 FT /tag= c
 FT /label= gene 3
 FT /note= "39 kd antigen 3"
 FT 4707..5859
 FT /tag= d

Query Match 9.4%; Score 126; DB 1; Length 360;
 Best Local Similarity 100.0%; Pred. No. 1.9e-24;
 Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FT /label- gene 4
 FT /note- *39 kd antigen 4*
 PN MO9104036-A.
 PD 04-APR-1991.
 PF 11-SEP-1990: U05129.
 PR 13-SEP-1989: US-406535.
 PA (MLTE-) ML Technology Ventures.
 PI Gabe J. Dragon E. McCann M.
 DR WPI: 91-117317/16.
 P-PSDB: R11484, R11485, R11486, R11487.
 PT Treponema hyodysenteriae antigens - having molecular wt. of 39 kd
 PT and their DNA codes, and use for preparing vaccine.
 PS Claim 18; Page 49; 84pp: English.
 CC The DNA includes family 1 contg. genes 1-4 encoding 39 kd antigens
 CC of T. hyo. The sequence was obtd. from clones isolated from a T.
 CC hyo genomic library in lambda gtl. The antigens can be expressed
 CC and used to prepare vaccines to protect against swine dysentery.
 CC See also 011378-011409.
 SQ Sequence 6119 BP; 2111 A; 683 C; 990 G; 2323 T;

Query Match 3.0%; Score 40.6; DB 1; Length 6119;
 Best Local Similarity 50.3%; Pred. No. 0.33;
 Matches 100; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

OY 537 AAAAAGCTCTTCAGGTGTAGAGAAAGATGAAATATTTATTCAGACATTAATTTAT 596
 DB 5217 ACATATTATACAGATACATGCTTTTAAATGAATATTAATTAATGAATGACAA 5276
 OY 597 AAACCTCCAGACAGACTATTATGCTAAAGTTAAAGACAGACTACTACGTCATG 656
 DB 5277 TTAGATATATTAATTAATGCTCCGATGTTGTTAAATATGAAGAGAACTTTTCAAG 5336
 OY 657 AAAATGCTGTCTATAGTCCAGTACATGTAATTAAGACAGACTGAATGAATGACCT 716
 DB 5337 TCATTGGTTTGAACAAGATTCATTTTTGAATACACTGTTGGAATGTAACCTATT 5396
 OY 717 CCACAGAAATATAGAG 735
 DB 5397 AATCCTTTATTAAGTAG 5415

RESULT 13
 T43223
 ID T43223 standard; DNA; 1953 BP.
 AC T43223:
 DT 28-JAN-1997 (first entry)
 DE Antiscarab pest toxin 43f coding sequence.
 KW Toxin 50C(b); scarab pest; toxin; insect; scarabaeidae; pest control;
 KW larval stage insect; grain; tuberos crop; white grub; chafer grub;
 KW cyclocephala; popillia; 43f gene; ds.
 OS Bacillus thuringiensis strain tolworthi.
 PN US5554534-A.
 PD 10-SEP-1996.
 PF 30-SEP-1994; 315468.
 PR 16-DEC-1991; US-808316.
 PR 30-JAN-1992; US-828430.
 PR 01-FEB-1993; US-014941.
 PR 30-SEP-1994; US-315468.
 PA (MICO) MTCOGEN CORP.
 PI Foncecrada L, Michaels TE, Narva KE;
 DR WPI: 96-424659/42.
 P-PSDB: W06419.
 PT New nucleic acid encoding B. thuringiensis toxin active against
 PT scarab(s) - also related toxin and transformed microbes, effective
 PT against adult pests and their larvae
 PS Example 3; Column 37-42; 24pp: English.
 CC T43221-T43223 represent the coding sequences for toxins that are active
 CC against scarab pests. This sequence was isolated from the Bacillus
 CC thuringiensis strain tolworthi. Insects in the family Scarabaeidae
 CC constitute a serious pest control problem, especially when destructive
 CC larval stage insects infest high value turf found in golf courses,
 CC playing fields and lawns. The larvae of many species also attack grains,

CC tuberos crops, and ornamentals. The larvae are known as white grubs, or
 CC chafer grubs, and can be found in decaying organic matter, or in the soil
 CC where they consume plant roots. In Europe and the U.S. populations of
 CC these larvae and adults have developed resistance to chemical
 CC insecticides such as the organochlorines and DDT. The toxins encoded by
 CC these sequences, and intact cells that are capable of expressing the
 CC proteins, can be used to control many pests of the family scarabaeidae,
 CC such as species of Cyclocephala, and Popillia. The toxins are active
 CC against larvae (present in soil) and against adults.
 SQ Sequence 1953 BP; 679 A; 323 C; 344 G; 607 T;

Query Match 3.0%; Score 40.2; DB 1; Length 1953;
 Best Local Similarity 45.2%; Pred. No. 0.25;
 Matches 147; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

OY 314 TTATGAGAAATTAATTCGCTATAGAGCAAGAAAGAAAGAAAGCTTCATGATGTA 373
 DB 1089 TTATGTAGAAAGCTAGACCTATAGATGCTTAAGATACATCACTCCCATTTATGG 1148
 OY 374 GGTGACTCATTTACACCATTTCCGAAAGCTCAGATTGCTCCAGAAATGATTTAGA 433
 DB 1149 AGATTAATCTTTGAACTATACAAAGCTAAGCTTTATGACAAAAGTTATCGAAC 1208
 OY 434 AGCTGAAGATAGGCAATAGTATGATACACATCTCTCCGAAAGAAAGATAGTTATG 493
 DB 1209 TATAGCTAATACAGACATAGCGGCTTTCCGATGCGAAGATATTTTGGTTAGCA 1268
 OY 484 GCGTTGATAGTTTAACTTACATATAGCTTACTTATCGAAAACTTTCAGGCT 553
 DB 1269 AGTTGATTTTGTCAATATGATGATCAAAAAATGAACATAGTACAAATATGATTC 1328
 OY 554 AGAAGAAAGATTGAAATTTATTTCCAGACATTAATTTAACTCCAGACAGAC 613
 DB 1329 AAAAAGATCAATGCTCTTTTAGTGCGACAGATTCATGACCAATACACAGAAC 1388
 OY 614 TACTTATTTCTAAAGTTAAAGCA 638
 DB 1389 AACAGATGACCACTTGAAAAAGCA 1413

RESULT 14
 O05679
 ID O05679 standard; DNA; 2425 BP.
 AC O05679:
 DT 03-JAN-1991 (first entry)
 DE btPGS1208 gene.
 KW Toxin; crystal; insecticide; ss.
 OS Bacillus thuringiensis strain PGS1208.
 FH Key Location/Qualifiers
 FT cds 342..2297
 FT /*tag= a
 FT /product=74 kd btPGS1208 protoxin
 FT mat_peptide 513..2294
 FT /*tag= b
 FT /product=67 kd btPGS1208 toxin
 EP-382990-A.
 PD 22-AUG-1990.
 PR 15-FEB-1989; 400428.
 PR 15-FEB-1989; EP-400428.
 PA (PLAN-) PLANT GENETIC SYST.
 PI Peferoen M, Lambert B, Joos H;
 DR WPI: 90-25362/34.
 P-PSDB: R06460.
 PT New Bacillus thuringiensis strains - producing toxin active
 PT against Coleoptera
 PS Claim 3; Fig 1; 30pp: English.
 CC The btPGS1208 strain was isolated from grain dust and was deposited
 CC at the DSM (19/1/1989) under Acc. No. 5131. The protoxin crystals
 CC produced on expression of the gene can be digested with trypsin to
 CC produce the mature protein. Plants contg. the gene are resistant
 CC to Coleoptera pests while the crystals are useful as insecticides.
 CC The gene can also be truncated and used to produce chimeric genes

CC together with the btp651245 gene (005680).
SQ Sequence 2425 BP; 872 A; 366 C; 429 G; 758 T;

Query Match 3.0%; Score 40.2; DB 1; Length 2425;
Best Local Similarity 45.2%; Pred. No. 0.28;
Matches 147; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

QY 314 TTATGAAGAAATTAATGGCTATAGACAGAAAAAAGAAACCTTCTCATGATGA 373
DB 1430 TTATGTAAGAACTAGACCTAGATAGATGATGATGATGATGATGATGATG 1489
QY 374 GGTGACATCTTACACCTATTCGCAAGCTCAGATGGCTCCGCAAGTACATTTAGA 433
DB 1490 AGATTAATCTATGTAACCTTACAAAAGCTAAGCTTTGATGACAAAAGTTATGAC 1549
QY 434 AGCTGAAGATAGGCAATAGTATGATGATGATGATGATGATGATGATGATG 493
DB 1550 TATAGCTAATACAGACATACGCGCTTTCGATGCGCAAGATATATTTGGTTAGAA 1609
QY 494 GCGTTGGATGCTTTAAGCTTTACATTTACCTTACTTATGCAAAAACCTTCAGGTG 553
DB 1610 AGTTGATTTTATGCAATGATGATGATGATGATGATGATGATGATGATG 1669
QY 554 AGAAGAAAGATGAAATATTTATTCAGACATAAATTTATTAATCTCACCAGAC 613
DB 1670 AAAAAGATACAAATGCGCTATTTAGTGACAGATCTATGACCAATATACACAGAAC 1729
QY 614 TACTTATTTGCTAAAGTTAAAGCA 638
DB 1730 AACAGATGAACCACTGAAAAAGCA 1754

RESULT 15

ID Q38654 standard; DNA; 1953 BP.
AC Q38654;
DT 15-JUL-1993 (first entry)
DE Bt isolate 43F coding sequence.
KW Lepidopteran-active; toxin; T1; R1; plant; cell; Bt; ss.
OS Bacillus thuringiensis.
PN W09304587-A.
PD 18-MAR-1993.
PF 11-SEP-1992; 007697.
PR 12-SEP-1991; US-758020.
PR 09-SEP-1992; US-941650.
PA (MYCO) MICOGEN CORP.
PI Bradfish GA, Oyeda KA;
DR WPI; 93-100566/12.
P-PSDB: R33769.
PT Controlling lepidopteran pests - using compsn. of Bacillus
PT thuringiensis strains or plants or microorganisms transformed
PT with their toxin genes
PS Claim 13; Page 25-27; 38pp; English.
CC The sequences given in Q38653-55 encode lepidopteran-active toxins.
CC These sequences were used within a T1 or R1 plasmid, to transform
CC plant cells. Whole plants can then be regenerated from the
CC transformed cells. The toxin may also be produced by cloning
CC Bacillus thuringiensis (Bt). It may then be applied directly to
CC the plant locus.
SQ Sequence 1953 BP; 679 A; 320 C; 347 G; 607 T;

Query Match 2.9%; Score 38.6; DB 1; Length 1953;
Best Local Similarity 44.9%; Pred. No. 0.68;
Matches 146; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

QY 314 TTATGAAGAAATTAATGGCTATAGACAGAAAAAAGAAACCTTCTCATGATGA 373
DB 1089 TTATGTAAGAACTAGACCTATATAGATGATGATGATGATGATGATGATG 1148
QY 374 GGTGACATCTTACACCTTACAAAAGCTAAGCTTTGATGACAAAAGTTATGAC 433

DB 1149 AGATAATCTATTGAAGCTATACAAAAGCTAAGCTTTGATGACAAAAAGTTATGAC 1208
QY 434 AGCTGAAGATAGGCAATAGATGATGATGATGATGATGATGATGATGATG 493
DB 1209 TATAGCTAATACAGACATAGCGGCTTTCGATGCGCAAGATATATTTGGTTAGCA 1268
QY 494 GCGTTGGATGCTTTAAGCTTTACATATAGCTTACTTATGCAAAAACCTTCAGGTG 553
DB 1269 AGTTGATTTTATGCAATGATGATGATGATGATGATGATGATGATGATG 1328
QY 554 AGAAGAAAGATGAAATATTTATTCAGACATGAAATTTATTAATCTCACCAGAC 613
DB 1329 AAAAAGATACAAATGCGCTATTTAGTGACAGATCTTATGCAAAATTAACACAGAAC 1388
QY 614 TACTTATTTGCTAAAGTTAAAGCA 638
DB 1389 AACAGATGAACCACTGAAAAAGCA 1413

Search completed: June 1, 2000, 11:12:25
Job time: 19086 sec

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2000, 05:53:48 : Search time 49.94 seconds
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3495.593 Million cell updates/sec

Title: US-09-240-675-1
Perfect score: 1343
Sequence: 1 CTGCAGGATCTCGCGCGC.....ATACCTTAATGAGGTACC 1343

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 230463 seqs, 64992525 residues

Total number of hits satisfying chosen parameters: 460926

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/ina/5C.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/5D.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/6.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PTCUS.COMB.seq:*
7: /cgn2_6/ptodata/1/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1343	100.0	1343	4	US-08-307-588-1
2	1334	99.3	1755	4	US-08-307-588-3
3	1330.8	99.1	2784	2	US-08-471-454-1
4	1330.8	99.1	2784	3	US-08-466-974-1
5	1330.8	99.1	2784	3	US-08-471-453-1
6	126	9.4	360	1	US-08-328-256-1
7	49	3.6	168	1	US-08-328-256-8
8	40.2	3.0	1953	1	US-08-313-468-5
9	39.4	2.9	1659	4	US-08-943-087-47
10	38.6	2.9	2430	6	PCT-US92-00040-1
11	37	2.8	1511	1	US-07-991-867B-8
12	37	2.8	1511	2	US-08-107-755A-8
13	37	2.8	1511	4	US-08-544-332-8
14	36.2	2.7	1951	2	US-08-487-890A-112
15	36.2	2.7	1951	4	US-08-478-435-112
16	36.2	2.7	1951	4	US-08-337-483-112
17	36.2	2.7	1951	4	US-08-478-373-112
18	36.2	2.7	1951	5	US-08-474-671-112
19	36.2	2.7	1951	5	US-08-483-577A-112
20	35.6	2.7	1575	4	US-08-853-659A-10
21	35.6	2.7	2636	3	US-08-820-170A-21
22	35.6	2.7	15512	4	US-08-853-659A-5
23	35.6	2.7	15512	4	US-08-853-659A-8
24	35.6	2.7	15512	4	US-08-853-659A-63
25	35.6	2.7	15512	4	US-08-853-659A-66
26	35.6	2.7	24701	4	US-08-853-659A-2
27	35.6	2.7	24701	4	US-08-853-659A-3

28	35.6	2.7	24701	4	US-08-853-659A-60	Sequence 60, Appl
29	35.6	2.7	24701	4	US-08-853-659A-61	Sequence 61, Appl
30	35.4	2.6	1291	1	US-07-952-755-2	Sequence 2, Appl
31	35.4	2.6	1291	1	US-08-443-679-2	Sequence 2, Appl
32	35.4	2.6	1482	5	US-08-996-441B-69	Sequence 69, Appl
33	35.4	2.6	1956	5	US-08-996-441B-51	Sequence 51, Appl
34	35.4	2.6	1956	5	US-08-996-441B-55	Sequence 55, Appl
35	35.4	2.6	1956	5	US-08-996-441B-57	Sequence 57, Appl
36	35.4	2.6	1959	5	US-08-996-441B-1	Sequence 1, Appl
37	35.4	2.6	1959	5	US-08-996-441B-3	Sequence 3, Appl
38	35.4	2.6	1959	5	US-08-996-441B-5	Sequence 5, Appl
39	35.4	2.6	1959	5	US-08-996-441B-7	Sequence 7, Appl
40	35.4	2.6	1959	5	US-08-996-441B-9	Sequence 9, Appl
41	35.4	2.6	1959	5	US-08-996-441B-11	Sequence 11, Appl
42	35.4	2.6	1959	5	US-08-996-441B-13	Sequence 13, Appl
43	35.4	2.6	1959	5	US-08-996-441B-15	Sequence 15, Appl
44	35.4	2.6	1959	5	US-08-996-441B-17	Sequence 17, Appl
45	35.4	2.6	1959	5	US-08-996-441B-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-307-588-1
Sequence 1, Application US/08307588
Patent No. 5919453
GENERAL INFORMATION:
APPLICANT: BENNETT, Patrick
APPLICANT: MEYER, Francois
APPLICANT: MAGUIRE, Deborah
APPLICANT: PLAVECK, Ivan
APPLICANT: TOVEY, Michael G.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00770
FILING DATE: 30-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92400902.0
FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: SAKE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 17283/117/GUPL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1343 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS

LOCATION: 27..1334
US-08-307-588-1

Query Match 100.0%; Score 1343; DB 4; Length 1343;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CTCGAGGAGATCTGCGGGGCTCCCAAGTATGTCGTCCTCTGCGGCGCAGACCTAG 60
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DB 1 CTCGAGGAGATCTGCGGGGCTCCCAAGTATGTCGTCCTCTGCGGCGCAGACCTAG 60
QY 61 TCGTCGCGCGCTGCGGCCCATGCGTGTTCGCGAGCGCGAGGAGGAAAAATCTAAAT 120
   |||
DB 61 TCGTCGCGCGCTGCGGCCCATGCGTGTTCGCGAGCGCGAGGAGGAAAAATCTAAAT 120
QY 121 CTCCTCAAAAAGTAGAGGTGACATCATGACAACTTATCTGAGGTGAGAACGA 180
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DB 121 CTCCTCAAAAAGTAGAGGTGACATCATGACAACTTATCTGAGGTGAGAACGA 180
QY 181 GCGATGAGTCTGCGGGAATGCTATTTTCATTCGATTCGATTCGAAAAAAGTGGATG 240
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DB 181 GCGATGAGTCTGCGGGAATGCTATTTTCATTCGATTCGATTCGAAAAAAGTGGATG 240
QY 241 ATTGATTAATAATGTCTGGGTGTCAGAAATTAATTAATTAATTAATTAATTAAT 300
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DB 241 ATTGATTAATAATGTCTGGGTGTCAGAAATTAATTAATTAATTAATTAATTAAT 300
QY 301 TCAAGCTGAATGTTTATGAAGAAATTAATGCGTATTAAGACGAGAAAAACACTT 360
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DB 301 TCAAGCTGAATGTTTATGAAGAAATTAATGCGTATTAAGACGAGAAAAACACTT 360
QY 361 CTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
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DB 361 CTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
QY 421 AAGTACATTTAGAAAGTGAAGATTAAGCAATAGATACATCTCTCTGAAACAAAG 480
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DB 421 AAGTACATTTAGAAAGTGAAGATTAAGCAATAGATACATCTCTCTGAAACAAAG 480
QY 481 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
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DB 481 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
QY 541 ACATTCAGGTGAGAAAGATGAAAGATTTTATTCAGACATTAATTAATTAATTAAC 600
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DB 541 ACATTCAGGTGAGAAAGATGAAAGATTTTATTCAGACATTAATTAATTAATTAAC 600
QY 601 TCTCACCAGAGACTACTTATGCTAAAGTAAAGCAGCACTACTACTGATGAGAAA 660
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DB 601 TCTCACCAGAGACTACTTATGCTAAAGTAAAGCAGCACTACTACTGATGAGAAA 660
QY 661 TTGGTGTCTATGATCCAGTCAATTTGTAAGACACAGTTGAAATGAACCTCCAC 720
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DB 661 TTGGTGTCTATGATCCAGTCAATTTGTAAGACACAGTTGAAATGAACCTCCAC 720
QY 721 CAGAAAAATATAGAAAGTCAAGTGTCCAAATATGTTCTTAAATGGATATATACAT 780
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DB 721 CAGAAAAATATAGAAAGTCAAGTGTCCAAATATGTTCTTAAATGGATATATACAT 780
QY 781 ATGCAAAACATGACCTTTCAAGTTCAGTGTCCAGGCTTTTAAAAAGAAATCTGGAA 840
   |||
DB 781 ATGCAAAACATGACCTTTCAAGTTCAGTGTCCAGGCTTTTAAAAAGAAATCTGGAA 840
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DB 841 ACCATTTGTTAATATGAAGAAATACCTACTGTGAAATGTCAAAATACCAAGTGTG 900
QY 901 TCTTCTCAAAAGCTTTTCAAAAGAAATTAACCTTCGCGGTACAAAGCATGATGAG 960
   |||
DB 901 TCTTCTCAAAAGCTTTTCAAAAGAAATTAACCTTCGCGGTACAAAGCATGATGAG 960
QY 961 GAAATACACATCTTTTGTGCTGAAGAGATTAAGTTGATGAAATCAAGCTTTCC 1020
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DB 961 GAAATACACATCTTTTGTGCTGAAGAGATTAAGTTGATGAAATCAAGCTTTCC 1020
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QY 1021 TACTTCTCAGTCTTTAATCATTAATCCCTAGTATGATTCATTCATATCATGCTG 1080
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DB 1021 TACTTCTCAGTCTTTAATCATTAATCCCTAGTATGATTCATTCATATCATGCTG 1080
QY 1081 CTCCAAAACAGTCTGAAACACGCTGTGATCCAGGATTAATCATGATTTATGAATTA 1140
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DB 1081 CTCCAAAACAGTCTGAAACACGCTGTGATCCAGGATTAATCATGATTTATGAATTA 1140
QY 1141 TTTTGGGAAAACTTAAATGCTGAGAGAAAAATTAATGAGAAAAAATGATGTTA 1200
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DB 1141 TTTTGGGAAAACTTAAATGCTGAGAGAAAAATTAATGAGAAAAAATGATGTTA 1200
QY 1201 CAGTTCCTAATTTGAACACACTGATGATATGTTGTGTAAGCCAGAGCACACCATG 1260
   |||
DB 1201 CAGTTCCTAATTTGAACACACTGATGATATGTTGTGTAAGCCAGAGCACACCATG 1260
QY 1261 ATGAAAAGCTGAATAAAGCACTGTTTATGAGAGCTGTATGTGAGAAACAAACAG 1320
   |||
DB 1261 ATGAAAAGCTGAATAAAGCACTGTTTATGAGAGCTGTATGTGAGAAACAAACAG 1320
QY 1321 GAAATACCTTAATGAGGTACC 1343
   |||
DB 1321 GAAATACCTTAATGAGGTACC 1343

RESULT 2
US-08-307-588-3
; Sequence 3, Application US/08307588
; Patent No. 5919453
; GENERAL INFORMATION:
; APPLICANT: BENOIT, Patrick
; APPLICANT: MEYER, Francois
; APPLICANT: MAGUIRE, Deborah
; APPLICANT: PLAVIE, Ivan
; APPLICANT: TOVEY, Michael G.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
; NUMBER OF SEQUENCES: 4
; INTERFERON
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/307,588
; FILING DATE: 05-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00770
; FILING DATE: 30-MAR-1993
; APPLICATION DATA:
; APPLICATION NUMBER: EP 92400902.0
; FILING DATE: 31-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 17283/117/GUPL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1755 base pairs
; TYPE: nucleic acid
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STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 27..1697
 US-08-307-588-3

Query Match 99.3%; Score 1334; DB 4; Length 1755;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACGAGATCTCGGGGGTCCAGATGATGTCCTCTCGGGGCGACGACCTAG 60
 Db 1 CTGACGAGATCTCGGGGGTCCAGATGATGTCCTCTCGGGGCGACGACCTAG 60
 QY 61 TGTCTGTCGGCGGCGCATGGGTGTGTCGCGACGCGCAGGTGAAAAATCTAAAT 120
 Db 61 TGTCTGTCGGCGGCGCATGGGTGTGTCGCGACGCGCAGGTGAAAAATCTAAAT 120
 QY 121 CTCCTCAAAAAGTAGAGGTGACATCATAGACAACTTATCTGAGGTGGAACGGA 180
 Db 121 CTCCTCAAAAAGTAGAGGTGACATCATAGACAACTTATCTGAGGTGGAACGGA 180
 QY 181 GCGATGAGTCTGCGGGAATGACCTTTTCATTGATATCAAAAAACGGGATGATA 240
 Db 181 GCGATGAGTCTGCGGGAATGACCTTTTCATTGATATCAAAAAACGGGATGATA 240
 QY 241 ATTGATATAATTTGCTGGGTGTCAGAAATATCTAGTACCAAACTTTCTTCCAC 300
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 QY 301 TCAAGCGATGTTTATGAAGAAATTAATGCGTATTAAGCAGAAAAAACCTT 360
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 QY 361 CTCACAGTATGAGGTGACATCTTACACATTTGCGAAAGCTCAGATGGTCTCCAG 420
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 Db 481 ATAGTGTATGCGCTTGGATGCTTAAAGCTTAACTATAGCTTACTATCTGAAAA 540
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 Db 541 ACTCTCAGGTGTAAGAAAGATTAATTAATTTATCCAGACATTAATTTATTAAC 600
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 Db 601 TCTCACCAGAGACTACTTATTTCTATAAAGTTAAAGCAGACTACTTACATGAAAA 660
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 Db 661 TTGCTGTATAGTCCAGTACATGATTAAGACCAAGTGAAGAACTACCTCCAC 720
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 Db 721 CAGAAAAATATGAAGTCACTGTCCTAAATCAGAACTATGTTCTTAATGGATTATCAT 780
 QY 781 ATGCAAAATGACCTTTCAAGTGTAGGCTCCAGCGCTTTTAAAAAGAACTCTGAA 840
 Db 781 ATGCAAAATGACCTTTCAAGTGTAGGCTCCAGCGCTTTTAAAAAGAACTCTGAA 840
 QY 841 ACCATTGTATTAATGAACAAATACTGCTGAAAAATGTCAAAACTAACCCAGTGTG 900
 Db 841 ACCATTGTATTAATGAACAAATACTGCTGAAAAATGTCAAAACTAACCCAGTGTG 900

QY 901 TCTTCTCAAAACGTTTCCAAAAAGAAATTTACTCTCCGCGTACAGATCTGATG 960
 Db 901 TCTTCTCAAAACGTTTCCAAAAAGAAATTTACTCTCTCCGCGTACAGATCTGATG 960
 QY 961 GAAATTAACACATCTTTTGGTCTGAAGAGATTAAGTTGATATCTGAAAAACGCTTCC 1020
 Db 961 GAAATTAACACATCTTTTGGTCTGAAGAGATTAAGTTGATATCTGAAAAACGCTTCC 1020
 QY 1021 TACTTCTCAGTCTTTAATAGATCCCTTAGTATGATCATTCATATCTATATGCGTG 1080
 Db 1021 TACTTCTCAGTCTTTAATAGATCCCTTAGTATGATCATTCATATCTATATGCGTG 1080
 QY 1081 CTCCAAAACAGTCTGGAACACAGCGCTGATGATCAGAGATTATCAGATTATGAATTA 1140
 Db 1081 CTCCAAAACAGTCTGGAACACAGCGCTGATGATCAGAGATTATCAGATTATGAATTA 1140
 QY 1141 TTTTGGGAAAAACACTTAAATGCTGAGAGAAAAATTTGAGAAAAAACTGATGTTA 1200
 Db 1141 TTTTGGGAAAAACACTTAAATGCTGAGAGAAAAATTTGAGAAAAAACTGATGTTA 1200
 QY 1201 CAGTCTAATTTGAAACACAGTACTGATATTTGTTGTAAGCAGACACACCATGG 1260
 Db 1201 CAGTCTAATTTGAAACACAGTACTGATATTTGTTGTAAGCAGACACACCATGG 1260
 QY 1261 ATGAAAGCTGAATAAAGCAGTGTATTAGTACGCGCTATGTCGAAAAACACAG 1320
 Db 1261 ATGAAAGCTGAATAAAGCAGTGTATTAGTACGCGCTATGTCGAAAAACACAG 1320
 QY 1321 GAAATACCTCTAAA 1334
 Db 1321 GAAATACCTCTAAA 1334

RESULT 3

US-08-471-454-1
 ; Sequence 1, Application US/08471454
 ; Patent No. 5731169

GENERAL INFORMATION:

APPLICANT: MOGENSEN, Knud E.
 APPLICANT: UZE, Gilles
 APPLICANT: LOTFALLA, Georges
 TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
 TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
 TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHYE P. C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/471,454
 FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 07/900,642
 FILING DATE: 15-JUN-1992

APPLICATION NUMBER: FR 89/13770
 FILING DATE: 20-OCT-1989

ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.
 REGISTRATION NUMBER: 32,205
 REFERENCE/DOCKET NUMBER: 960-7

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000

```

:
: TELEFAX: (703) 816-4100
: TELEX: 200797 NIXN UR
: INFORMATION FOR SSO ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2784 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
US-08-471-454-1

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Query Match		99.1%	Score 1330.8	DB 2	Length 2784	
Best Local Similarity		99.9%	Pred. No. 0			
Matches 1332		Conservative	0	Mismatches	2	Indels
					0	Gaps
OY	1	CTGCAGGATCTGCGCGGCTCCACAGATGATGTCCTCTCTGGCGCGAGACCTTAG	60			
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OY	61	TGCTGTGGCGCGTGGGGCCCATGGGGTGTTCGGCAGCCGAGTGGAAAAATCTAAAT	120			
Db	113	TGCTGTGGCGCGTGGGGCCCATGGGGTGTTCGGCAGCCGAGTGGAAAAATCTAAAT	172			
OY	121	CTCCCAAAAAATAGAGGTGCACAATCATAGATGACAACTTTATCCGAGGTGAACAGA	180			
Db	173	CTCCCAAAAAATAGAGGTGCACAATCATAGATGACAACTTTATCCGAGGTGAACAGA	232			
OY	181	GGGATGATCTGTCCGGGAATGTGACTTTTCATTCGATATACAAAACTGGGATGATA	240			
Db	233	GGGATGATCTGTCCGGGAATGTGACTTTTCATTCGATATACAAAACTGGGATGATA	292			
OY	241	ATTGATATAAATTTGCTGGGTGTACGAATATATACATGACCAATGCACTTTCTTCAC	300			
Db	293	ATTGATATAAATTTGCTGGGTGTACGAATATATACATGACCAATGCACTTTCTTCAC	352			
OY	301	TCAAGCTGAATGTTTATGAGAAATTTAAATTGGCTATTAAGACAGAAAAAACAACCTT	360			
Db	353	TCAAGCTGAATGTTTATGAGAAATTTAAATTGGCTATTAAGACAGAAAAAACAACCTT	412			
OY	361	CTTCAATGATAGAGGTGATCATATTACACCAATTTGCGAAAGCTGATTTGGTCCCTCAG	420			
Db	413	CTTCAATGATAGAGGTGATCATATTACACCAATTTGCGAAAGCTGATTTGGTCCCTCAG	472			
OY	421	AAGTACATTTAGAAAGCTGAAGATTAAGGCAATAGTGATACACATCTCTCTGGAAACAAAG	480			
Db	473	AAGTACATTTAGAAAGCTGAAGATTAAGGCAATAGTGATACACATCTCTCTGGAAACAAAG	532			
OY	481	ATAGGTTATGCGGCTTTGGATGGTTTAAAGCTTACATATAGCTTACTTATCTGGAAA	540			
Db	533	ATAGGTTATGCGGCTTTGGATGGTTTAAAGCTTACATATAGCTTACTTATCTGGAAA	592			
OY	541	ACTCTTCAGGTTAGAGAAAGAGATTTGAATAATTTATCCAGACATTAATAATTATAAAC	600			
Db	593	ACTCTTCAGGTTAGAGAAAGAGATTTGAATAATTTATCCAGACATTAATAATTATAAAC	652			
OY	601	TCTCACACAGAGCTACTTATTGTCTTAAAGCTTAAGCAGCACTACTTACGTATGGAAAA	660			
Db	653	TCTCACACAGAGCTACTTATTGTCTTAAAGCTTAAGCAGCACTACTTACGTATGGAAAA	712			
OY	661	TTGGGTGCTATAGTCCAGACATTTGATTAAGACACACAGTGGAAAAATGAACCTCCACAC	720			
Db	713	TTGGGTGCTATAGTCCAGACATTTGATTAAGACACACAGTGGAAAAATGAACCTCCACAC	772			
OY	721	CAGAAATATAGAACTCACTGTCCAAATACAGAACTATGTTCTTTAAATGGATATATACAT	780			
Db	773	CAGAAATATAGAACTCACTGTCCAAATACAGAACTATGTTCTTTAAATGGATATATACAT	832			
OY	781	ATGCAAAACATGACCTTTCAAGTTCAAGTTCAGGCTCCACGCTTTTAAAAAAGAAATCCCTGGAA	840			
Db	833	ATGCAAAACATGACCTTTCAAGTTCAAGTTCAGGCTCCACGCTTTTAAAAAAGAAATCCCTGGAA	892			
OY	841	ACCAATTTGATTAATGAGAAACAAATACCTGACTGTGAAAAATGTCAAAACCTACCCAGTGTG	900			

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Db      893  ACATTTGTATTAATGGAACAAATACCTGACTGCGAAATGTCAAACTACCCAGTGTG   952
QY      901  TCCTTCTCAAAACGTTTTCGAAAAAGAAATTACTTCTCCGCGTACACAGCATCTGATG   960
Db      953  TCTTTCTCAAAACGTTTTCGAAAAAGAAATTACTTCTCCGCGTACACAGCATCTGATG   1012
QY      961  GAAATTAACACATCTTTTGGCTGGAAGATGAATAAGTTGATPACTGAATPACAAAGCTTTC   1020
Db      1013  GAAATTAACACATCTTTTGGCTGGAAGATGAATAAGTTGATPACTGAATPACAAAGCTTTC   1072
QY      1021  TACTTCTCCAGTCTTTTAACATTAGATCCCTTAGTATGATTCATTCATATCATATCGGTG   1080
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Db      1133  CTCGAAACAGCTGCGAAACAGCCCGTGATCCAGATTATCCAGTATTTATGAATA   1192
QY      1141  TTTTGGGAAACACTTCAATAGTCTGAGAGAAAAATTATCGAAAAAACTGATGTTA   1200
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QY      1321  GAAATACCTGTAAA   1334
Db      1373  GAAATACCTGTAAA   1386

RESULT      4
US-08-466-974-1
; Sequence 1, Application US/08466974
; Patent No. 5861258
; GENERAL INFORMATION:
; APPLICANT: MOGENSEN, Knud E.
; APPLICANT: UZE, Gilles
; APPLICANT: LUTFALIA, Georges
; APPLICANT: GRESSER, Ion
; TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
; TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
; TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P. C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,974
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/900,642
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: FR 89/13770
; FILING DATE: 20-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205

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REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2784 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-466-974-1

Query Match 99.1% Score 1330.8 DB 3 Length 2784
Best Local Similarity 99.9% Pred. No. 0:
Matches 1332: Conservative 0: Mismatches 2: Indels 0: Gaps 0:

OY 1 CTCGAGGAGATCGCGGGCTCCAGATGATGTCCTCTCTGCGCCGACGACCTAG 60
DB 53 CTGGTGGATCGCGGGCTCCAGATGATGTCCTCTCTGCGCCGACGACCTAG 112
OY 61 TGCCTGTCGCGCGCCATGCGGTGTTCGCGACGCGGAGTGGAAAAATCTAAAT 120
DB 113 TGCCTGTCGCGCGCCATGCGGTGTTCGCGACGCGGAGTGGAAAAATCTAAAT 172
OY 121 CTCCTCAAAAAGTAGAGTGCACATCATAGATGACAACTTATCGTGGAGTGAACAGA 180
DB 173 CTCCTCAAAAAGTAGAGTGCACATCATAGATGACAACTTATCGTGGAGTGAACAGA 232
OY 181 GCGATGAGTGTGCGGAGTGCATTTTCATTCGATTACAAAACTGGAGTGA 240
DB 233 GCGATGAGTGTGCGGAGTGCATTTTCATTCGATTACAAAACTGGAGTGA 292
OY 241 ATTGATTAATTTGTCGGGTGTCAAGTATTCTAGTACCAATTCGACCTTTCTTAC 300
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OY 361 CTTCATGATGAGTGTGACTCATTTTACACATTCGCAAGCTCAGATGCTCTCCAG 420
DB 413 CTTCATGATGAGTGTGACTCATTTTACACATTCGCAAGCTCAGATGCTCTCCAG 472
OY 421 AAGTACATTTAGAACTGAAGATGAAGCAATAGTATACACATCTCTCTGACAAAAG 480
DB 473 AAGTACATTTAGAACTGAAGATGAAGCAATAGTATACACATCTCTCTGACAAAAG 532
OY 481 ATAGTATATGCGGCTTGGATGTTAAGTTCATATAGCTTACTTATCTGAAAA 540
DB 533 ATAGTATATGCGGCTTGGATGTTAAGTTCATATAGCTTACTTATCTGAAAA 592
OY 541 ACTCTCAGTGTAGAAAGAAAGATTAATTTATTCAGACATTAATTTATTAAC 600
DB 593 ACTCTCAGTGTAGAAAGAAAGATTAATTTATTCAGACATTAATTTATTAAC 652
OY 601 TCTACACGAGACTACTTATTTCTAAAGTTAAAGCAGCTACTTACGTCATGAAAA 660
DB 653 TCTACACGAGACTACTTATTTCTAAAGTTAAAGCAGCTACTTACGTCATGAAAA 712
OY 661 TTGGTGTATAGTCACATTAATTTATTAAGACACAGTGAAGAAATAGACTCCAC 720
DB 713 TTGGTGTATAGTCACATTAATTTATTAAGACACAGTGAAGAAATAGACTCCAC 772
OY 721 CAGAAAAATATAGAGTCAAGTCCAAATTCAGAACTATGTTCTTAATGGATTTACAT 780
DB 773 CAGAAAAATATAGAGTCAAGTCCAAATTCAGAACTATGTTCTTAATGGATTTACAT 832
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DB 833 ATGCAACATGACCTTTCAAGTTCAGTGTCCACGCTTTTAAAAAGGAATCTTGAA 892
OY 841 ACCATTTGATTAATGAAGCAATATACCTGATGTAAGTGTCAAACTACCAAGTGTG 900
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OY 901 TCTTCTCAAAAGCTTTTCCAAAAGGAATTTACCTTCTCCGGGTCAAGCATGTATG 960
DB 953 TCTTCTCAAAAGCTTTTCCAAAAGGAATTTACCTTCTCCGGGTCAAGCATGTATG 1012
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DB 1253 CAGTCTCAATTTTGAACCACTGATGATGATGATGATGATGATGATGATGATG 1312
OY 1261 ATGAAAAGCTGAATTAAGACAGTGTGTTTATGATGATGATGATGATGATGATG 1320
DB 1313 ATGAAAAGCTGAATTAAGACAGTGTGTTTATGATGATGATGATGATGATGATG 1372
OY 1321 GAAATACCTCTAAA 1334
DB 1373 GAAATACCTCTAAA 1386

RESULT 5
US-08-471-453-1
Sequence 1, Application US/08471453
Patent No. 5886153
GENERAL INFORMATION:
APPLICANT: MOGENSEN, Knud E.
APPLICANT: UZE, Gilles
APPLICANT: LUPFALLA, Georges
TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
PREPARATION OF THE CORRESPONDING PROTEIN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERBYE P. C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471.453
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989

ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.
 REGISTRATION NUMBER: 32,205
 REFERENCE/DOCKET NUMBER: 960-7
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000
 TELEFAX: (703) 816-4100
 TELEX: 200797 NIXN UR
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2784 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-471-453-1

Query Match 99.1%; Score 1330.8; DB 3; Length 2784;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 CTGCAGGATCTGGCGGCTCCAGATATGCTGCTCTGCGGCGGAGACCCCTAG 60
 53 CTGGTGGATCTGGCGGCTCCAGATATGCTGCTCTGCGGCGGAGACCCCTAG 112
 61 TCGTCTCCCGTGGGCGGCTCCAGATATGCTGCTCTGCGGCGGAGACCCCTAG 120
 113 TCGTCTCCCGTGGGCGGCTCCAGATATGCTGCTCTGCGGCGGAGACCCCTAG 172
 121 CTCTCTCAAAAGTAGAGTGCACATCATGATGACAACTTTATCCTGAGTGGAAACAGA 180
 173 CTCTCTCAAAAGTAGAGTGCACATCATGATGACAACTTTATCCTGAGTGGAAACAGA 232
 181 GCGATAGCTGTGCGGAAATGATCTTTTCATTCGATTATCAAAAAAAGCTGGATGATA 240
 233 GCGATAGCTGTGCGGAAATGATCTTTTCATTCGATTATCAAAAAAAGCTGGATGATA 292
 241 ATTGATTAATGCTGGGTGCAGAAATATCTAGTACCAAAATGCACTTTCTTCAC 300
 293 ATTGATTAATGCTGGGTGCAGAAATATCTAGTACCAAAATGCACTTTCTTCAC 352
 301 TCAAGCTGATGTTTATGAAGAAATTAATTCGATTAAGAGCAGAAAAAGCACTT 360
 353 TCAAGCTGATGTTTATGAAGAAATTAATTCGATTAAGAGCAGAAAAAGCACTT 412
 361 CTTCATGATGATGAGTTGACTATTACACCATTCGCAAAAGCTCAGATTGCTCCAG 420
 413 CTTCATGATGATGAGTTGACTATTACACCATTCGCAAAAGCTCAGATTGCTCCAG 472
 421 AGTACATTAGAGCTGAAGATTAAGCAATAGTATACACATCTCTCGAACAAG 480
 473 AGTACATTAGAGCTGAAGATTAAGCAATAGTATACACATCTCTCGAACAAG 532
 481 AATGTTATGTTGGCTTTGATGTTTAAAGCTTTACATATAGCTTACTATCTGAAAA 540
 533 AATGTTATGTTGGCTTTGATGTTTAAAGCTTTACATATAGCTTACTATCTGAAAA 592
 541 ACTCTCAGCTGTAGAAGAAAGATTAATTTATTCACACATTAATTAATTAAC 600
 593 ACTCTCAGCTGTAGAAGAAAGATTAATTTATTCACACATTAATTAATTAAC 652
 601 TCTCACCAGAGACTATTATTTGCTAAAGTTAAAGCAGACACTTACTGATGAAAA 660
 653 TCTCACCAGAGACTATTATTTGCTAAAGTTAAAGCAGACACTTACTGATGAAAA 712
 661 TTGGTGTCTATAGTCCAGTATGTTTAAAGCAGACACTTACTGATGAAAA 720
 713 TTGGTGTCTATAGTCCAGTATGTTTAAAGCAGACACTTACTGATGAAAA 772
 721 CAGAAAAATATAGAGTCACTGTCCAAAAATCAGAACTATGTTCTTAATGGGATTATACAT 780
 773 CAGAAAAATATAGAGTCACTGTCCAAAAATCAGAACTATGTTCTTAATGGGATTATACAT 832

781 ATGCAAAATGACCTTTCAAGTTCAGTGGCTCCACGCTTTTAAAAAGAACTCTGCA 840
 833 ATGCAAAATGACCTTTCAAGTTCAGTGGCTCCACGCTTTTAAAAAGAACTCTGCA 892
 841 ACCATTGATTAATGAAACAAATACCTGAGTGAAGTCAAACTCCAGTGTG 900
 893 ACCATTGATTAATGAAACAAATACCTGAGTGAAGTCAAACTCCAGTGTG 952
 901 TCTTCTCAAAACGTTTCCAAAAAGAAATTTACCTTCGCGGTACAGATCTGATG 960
 953 TCTTCTCAAAACGTTTCCAAAAAGAAATTTACCTTCGCGGTACAGATCTGATG 1012
 961 GAAATTAACACATCTTTTGGTCTGAAGATTAATGTTGATTAATTAACAGCTTCC 1020
 1013 GAAATTAACACATCTTTTGGTCTGAAGATTAATGTTGATTAATTAACAGCTTCC 1072
 1021 TACTCTCCAGCTCTTTAACTTATAGTCCCTTATGATTCATTCATATATGATG 1080
 1073 TACTCTCCAGCTCTTTAACTTATAGTCCCTTATGATTCATTCATATATGATG 1132
 1081 CTCAAAAACAGTCTGAAAAACAGCCTGTGATCCAGATTAATCCATGATTAATGA 1140
 1133 CTCAAAAACAGTCTGAAAAACAGCCTGTGATCCAGATTAATCCATGATTAATGA 1192
 1141 TTTTGGGAAAAACCTTCAATGCTGAGAGAAAAATTAATGAGAAAAAACTGATGTTA 1200
 1193 TTTTGGGAAAAACCTTCAATGCTGAGAGAAAAATTAATGAGAAAAAACTGATGTTA 1252
 1201 CAGTCTCAATTTGAACACAGTGAATATGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1260
 1253 CAGTCTCAATTTGAACACAGTGAATATGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1312
 1261 ATGAAAACTGAATTAAGACAGTGTGTTTATGAGCGTGTATGTGAAAAAACCAG 1320
 1313 ATGAAAACTGAATTAAGACAGTGTGTTTATGAGCGTGTATGTGAAAAAACCAG 1372
 1321 GAAATACCTTAAA 1334
 1373 GAAATACCTTAAA 1386

RESULT 6
 US-08-328-256-1
 Sequence 1, Application US/08328256
 Patent No. 5643749
 GENERAL INFORMATION:
 APPLICANT: REVEL, Michel
 APPLICANT: ABRAMOVICH, Caroljna
 APPLICANT: RATOVIJSKI, Edward
 TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWDY AND NEIMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentln Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/328,256
 FILING DATE: 24-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: IL 107378
 FILING DATE: 24-OCT-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: BROWDY, Roger L.

REGISTRATION NUMBER: REVEL-13
REFERENCE/DOCKET NUMBER: 25,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-328-256-1

Query Match 9.4%; Score 126; DB 1; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.7e-26;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1209 AATTGAAACCACTGACTGTATATTTGTGAAAGCCAGACACCATGATGAAAG 1268
DB 1 AATTGAAACCACTGACTGTATATTTGTGAAAGCCAGACACCATGATGAAAG 60
OY 1269 CTGAATTAAGCAGTGTGTTTGTGACCGCTGTATGTGAGAAAACAAACAGGAATACC 1328
DB 61 CTGAATTAAGCAGTGTGTTTGTGACCGCTGTATGTGAGAAAACAAACAGGAATACC 120
OY 1329 TCTAAA 1334
DB 121 TCTAAA 126

RESULT 7
US-08-328-256-8
Sequence 8, Application US/08328256
Patent No. 5643749
GENERAL INFORMATION:
APPLICANT: REVEL, Michel
APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVIYSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: REVEL-13
REFERENCE/DOCKET NUMBER: 25,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..168
US-08-328-256-8

Query Match 3.6%; Score 49; DB 1; Length 168;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1218 CCACTGACTGTATATTTGTGAAAGCCAGACACCATGATGAAA 1266
DB 1 CCACTGACTGTATATTTGTGAAAGCCAGACACCATGATGAAA 49

RESULT 8
US-08-315-468-5
Sequence 5, Application US/08315468
Patent No. 5554534
GENERAL INFORMATION:
APPLICANT: Michaels, Tracy Ellis
APPLICANT: Foncerra, Luis
APPLICANT: Narva, Kenneth E.
TITLE OF INVENTION: Process for Controlling Scarab Pests
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/315,468
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/014,941
FILING DATE: 01 FEB 1993
APPLICATION NUMBER: 07/828,430
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/808,316
FILING DATE: 16-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA73.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1953 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
STRAIN: tolworthi

INDIVIDUAL ISOLATE: 43F
IMMEDIATE SOURCE:
CLONE: E. coli XL1-Blue (pML198-4), NRRL B-18291
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1953
US-08-315-468-5

Query Match 3.0%; Score 40.2; DB 1; Length 1953;
Best Local Similarity 45.2%; Pred. No. 0.054;
Matches 147; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

QY 314 TTATGAAAGAAATTAATTCGTTATAGACAGAAAAACACTCTTCATGATGA 373
DB 1089 TTATGAGAAATGACCTAGTATAGATCTATGATACACATCTCCCATTTATG 1148
QY 374 GGTGACATTTACACATTTGCAAGCTCAGATTGCTCCAGAGTACATTAGA 433
DB 1149 AGATTAATCTATGAGACCTATACAAAAGCTTATGAGCAAAAAGTTATGAG 1208
QY 434 AGCTGAAGTAAAGCAATAGTATACATCTCTCGAACAAGATAGTTATGTG 493
DB 1209 TATAGCTAATACAGACATAGCGCTTTCCGATGGCAAGATATATTTGGTTACGAA 1268
QY 494 GCGTTGATGCTTTAGCTTACATATAGCTTATCTGGAAGACCTCCAGGTGT 553
DB 1269 AGTTGATTTAGCAATATGATGATCAAAAAATGAAACTAGTACAAACATATATTG 1328
QY 554 AGAAGAAAGATTAATAATTTATTCAGACATTAATAATTTATTAATCTACACAGAG 613
DB 1329 AAAAAGATCAATGGCTATTTAGTGCACAGATTTCTATGACCAATTTACACAGAAAC 1388
QY 614 TACTTATTTCTTAAAGTTAAAGCA 638
DB 1389 AACAGATGAACCACTTGAAGAAAGCA 1413

RESULT 9

US-08-943-087-47
Sequence 47, Application US/08943087
Patent No. 5945511
GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Kho, Choon J.
APPLICANT: Jelmeberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: 08/803,305
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743

REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 1659 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..1659
OTHER INFORMATION:
US-08-943-087-47

Query Match 2.9%; Score 39.4; DB 4; Length 1659;
Best Local Similarity 49.8%; Pred. No. 0.084;
Matches 128; Conservative 0; Mismatches 126; Indels 3; Gaps 1;

QY 198 AATGTGACTTTTTCATTCGATTATCAAAAACTGGATGATTAATGGATAAATGTCT 257
DB 196 AAGTACTTATACCTGTCAGATTTTATATGGCAGAAAGATGGCTGAATAGTCA 255
QY 258 GGGTCTCAGATTAATAGTACCAATGCAACTTTTCTTACTCAGCTAATGTTAT 317
DB 256 GAGTGTCAAAATATCAATGCAACCTATGTATCTCTGTGAGACTTCTGATTATAG 315
QY 318 GAGAAATTAATTCGATTAAGCAGCAAAAAAGAACTCTTC--ATGGATAG 374
DB 316 CATCAGTATTTATGCCAAGCTTAAGCCATTGGGGGACAAAGTGTCCAACTGGGCTAG 375
QY 375 GTTGACTATTATACACATTTGCAAACTGAGATTTGCTCCAGAAATGATTAGAA 434
DB 376 AGTGGCGGTTTATCTCTTCTAGAGCAGCATTTGGCGGACAAAGTGTCCAACTGGGCTAG 435
QY 435 GCTGAAGATTAAGCAAT 451
DB 436 ACGGATGAGAAGTCCAT 452

RESULT 10

PCT-US92-00040-1
Sequence 1, Application PC/TUS920040
GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Rupert, Mark J.
APPLICANT: Slaney, Annette C.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CYI11C(D) TOXIN
TITLE OF INVENTION: GENE AND PROTEIN TOXIC TO COLEOPTERAN INSECTS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00040
FILING DATE: 19920103
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/649,562

```

1      FILING DATE: 31-JAN-1991
2      ATTORNEY/AGENT NAME:
3      NAME: Egolf, Christopher
4      REGISTRATION NUMBER: 27613
5      REFERENCE/DOCKET NUMBER: 7205-29 PI
6      TELECOMMUNICATION INFORMATION:
7      TELEPHONE: 215-757-1590
8      INFORMATION FOR SEQ. ID NO.: 1:
9      SEQUENCE CHARACTERISTICS:
10     LENGTH: 2430 base pairs
11     TYPE: NUCLEIC ACID
12     STRANDEDNESS: double
13     TOPOLOGY: circular
14     MOLECULE TYPE: DNA (genomic)
15     FEATURE:
16     NAME/KEY: CDS
17     LOCATION: 144..2099
18     CDT-US92-00040-1

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Query Match	2.9%	Score 38.6	DB 6	Length 2430
Best Local Similarly	44.9%	Pred. No. 0.17		
Matches 146	Conservative 0	Mismatches 179	Indels 0	Gaps 0

Oy	314	TTATGGAAGAAATTAATTTGGTTATGAGACAGAAAAAGAAACACTTGTATGCTGTGTA	373
Db	1232	TTATGTGGAAGAACTAGACACTAGTATAGAGACTCTAGTAAGCAATTAAGTCTCCACTTTTATGG	1291
Oy	374	GGTTGACTCTTTACACCACTTTGCGCAACGCTCAGATTTGGTCTCCAGAAGTACATTAGA	433
Db	1392	AGATTAATCTCTACGAACCTGTACAAAAAGTTAAGCTTTGTGACAAAAAGTTTATCGAAC	1351
Oy	434	AGCTGAAGATTAAGCAATAGTATGATACACATCTCTCCGCAACAAAGAATAGTATGATG	493
Db	1352	TATAGCTAATACAGACGTACGGGCTTGCGCGAATGSCAAGATATATTTTGGTGTACGAA	1411
Oy	494	GGCTTTGGATGGTTTAAAGCTTTACATATAGCTTACTTATCTGAAAAAACTCTTCAGGTGT	553
Db	1412	AGTTGATTTTATAGTCAAATATGATGATCAAAAAATGAACTAATACCAAAACATATGATTC	1471
Oy	554	AGAGAAGAGGATTTGAAATATTTATTTCAGACATATAAATTTTAAACTCTCACCGAGAC	613
Db	1472	AAAAAGAAACAATGGCCATGTAGTGTGACAGATTTCTATTGACCAATTACCCACGAAC	1531
Oy	614	TACTTATTTGTCTAAAGTTAAAGCA	638
Db	1532	AACGATGAACCACTTGAAAAACCA	1556

1
US-07-991-8678-8/C
Sequence 8, Application US/07991867B
Patent No. 5476781
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/991,867B

```

1      FILING DATE: 12-DEC-1992
2      CLASSIFICATION: 435
3      PRIOR APPLICATION DATA:
4      APPLICATION NUMBER: WO 92/14818
5      FILING DATE: 12-FEB-1992
6      PRIOR APPLICATION DATA:
7      APPLICATION NUMBER: US 07/827,685
8      FILING DATE: 30-JAN-1992
9      PRIOR APPLICATION DATA:
10     APPLICATION NUMBER: US 07/657,584
11     FILING DATE: 19-FEB-1991
12     ATTORNEY/AGENT INFORMATION:
13     NAME: Saliwanhik, David R.
14     REGISTRATION NUMBER: 31,794
15     REFERENCE/DOCKET NUMBER: UF114.C3
16     TELECOMMUNICATION INFORMATION:
17     TELEPHONE: 904-375-8100
18     TELEFAX: 904-372-5800
19     INFORMATION FOR SEQ ID NO: 8:
20     SEQUENCE CHARACTERISTICS:
21     LENGTH: 1511 base pairs
22     TYPE: nucleic acid
23     STRANDEDNESS: double
24     TOPOLOGY: unknown
25     MOLECULE TYPE: DNA (genomic)
26     ORGANISM: Amsacta moorei entemopoxvirus
27     FEATURE:
28     NAME/KEY: CDS
29     LOCATION: complement (18..218)
30     FEATURE:
31     NAME/KEY: CDS
32     LOCATION: complement (234..782)
33     FEATURE:
34     NAME/KEY: CDS
35     LOCATION: 852..1511
36     US-07-991-867B-8

```

Query Match	2.8%	Score 37	DB 1	Length 1511
Best Local Similarity	45.1%	Pred. No.	0.36	
Matches 124	Conservative	0	Mismatches 145	Indels 0
			Gaps	0

Qy	962	AAATACACATCTTTTGGCTGACAGAAATGTTGATACGAAATCAAGCTTCT	1021
Qy	963	TTTATTTATATGATCATCTCTCTAAATTAACTAATTTTTTAAATATTTAATTAAC	936
Qy	1022	ACTTCCTCCAGTCTTTACATTTAGATCCCTTACTGATTCATTCCAATTCATATCGTGC	1081
Db	935	ATATATCTGTATTTATTTATTTTATTTTAAATATATATATTTTAAATATTTATTAAT	876
Qy	1082	TCCAAAACAGCTCGAAGAACACGCCCTGATCCAGATATTCACATATATATGAATAT	1144
Db	875	TATATCGAATTTAGTAAATCCATTTTGATTAATTTATTTTTCATGTATTAATTT	816
Qy	1142	TTTTTGGGAAACACCTCAATGCTGAGAGAAAAATATATCGAGAAAAAATCATGATTTAC	1203
Db	815	TTTTTGAATAAATATATCAATATATATAAAAAAATGTCGATAGATTAATTAATTTGGTCT	756
Qy	1202	AGTTCCTAATTTGAAACCACTGACTGAT	1230
Db	755	ATGTTTCTGCAAAACACAGAAATGAT	727

```

RESULT 12
US-08-107-755A-8/C
; Sequence 8, Application US/08107755A
; Patent No. 5721352
;
; GENERAL INFORMATION:
; APPLICANT: Meyer, Richard W.
; APPLICANT: Hall, Richard L.
; APPLICANT: Grudl, Michael E.
; TITLE OF INVENTION: Novel 5721352e1 Entomopoxvirus Expression System

```

NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: U.S.A.
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,755A
FILING DATE: 19-AUG-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,658
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF114.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1511 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Amsacta moorei entemopoxvirus
FEATURE:
NAME/KEY: CDS
LOCATION: complement (18..218)
FEATURE:
NAME/KEY: CDS
LOCATION: complement (234..782)
FEATURE:
NAME/KEY: CDS
LOCATION: 852..1511
US-08-107-755A-8

Query Match 2.8%; Score 37; DB 2; Length 1511;
Best Local Similarity 46.1%; Pred. No. 0.38; Mismatches 145; Indels 0; Gaps 0;
Matches 124; Conservative 0;
QY 962 AATAACACATCTTTTGGCTGACAGATGAAGTTGATGTAAGTCAACACCTTCCG 1021
DB 995 ATATATATATGCAATTCCTCTAATTAATACTATTTTATATATATATATTAAC 936
QY 1022 ACTTCTCCAGCTTTTAACATGATCCCTTAAGTTCATTCATTCATTCATTCGTCG 1081
DB 935 ATATCTCTGTTATATATATTTTAAATTAATTAATTAATTAATTAATTAAT 876
QY 1082 TCCAAACAGCTGGAACAGCGCTGATCCAGATTAATCCAGTATTAATTAAT 1141
DB 875 TATATCGAATTTAGTAATCCATTTGATTAATTTATTTTTCATTGATTAATTTT 816
QY 1142 TTTTGGAAACACTCAATCTGAGAGAAATTAATGAGAAAAAAGCTGATGTAC 1201
DB 815 TTTTGGAAAAATATATCAATATAAAAAAATGCGATGAATTAATTAATTTGTCCT 756
QY 1202 AGTTCCATTTGAAACCACTGACTGAT 1230

DB 755 ATGTTTCTGCAACACAGATTAATGAT 727

RESULT 13
US-08-544-332-8/C
Sequence 8, Application US/08544332
Patent No. 5935777
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Grudl, Michael E.
TITLE OF INVENTION: No. 5935777e1 Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gerard H. Bencen
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/544,332
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,867
FILING DATE: 07-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,755
FILING DATE: 19-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H.
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: UF114.C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1511 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Amsacta moorei entemopoxvirus
FEATURE:
NAME/KEY: CDS
LOCATION: complement (18..218)
FEATURE:
NAME/KEY: CDS
LOCATION: complement (234..782)
FEATURE:
NAME/KEY: CDS
LOCATION: 852..1511
US-08-544-332-8

Query Match 2.8%; Score 37; DB 4; Length 1511;

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 1, 2000, 05:52:42 ; Search time 610.76 Seconds
(without alignments)
8912.632 Million cell updates/sec

Title: US-09-240-675-1

Perfect score: 1343

Sequence: 1 CTCGACGAGATCTCGCGCGC.....ATACCTTAATGAGGTACC 1343

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4857316 seqs, 202611650 residues

Total number of hits satisfying chosen parameters: 9714632

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

EST:*

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106: gb_gss13:*
107: gb_gss14:*
108: gb_gss15:*
109: gb_gss16:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result

Query

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
C 1	495.4	36.9	538	80	AM366810	AM366810 CM1-HT015
C 2	491.4	35.6	505	30	AA258405	AA258405 zrf62b09.s
C 3	446.4	33.2	456	79	AM292243	AM292243 UI-H-B12
C 4	414.8	30.9	571	46	A1458581	A1458581 t397d01.x
C 5	395	29.4	403	79	AM292242	AM292242 UI-H-B12
C 6	365.8	27.2	383	31	AA308713	AA308713 EST179523
C 7	341.2	25.4	380	30	AA258750	AA258750 zrf62b09.r
C 8	277.4	20.7	504	33	AA447894	AA447894 zrl1a06.r
C 9	271	20.2	444	61	A1863225	A1863225 t239a08.x
C 10	205.6	15.3	269	21	T96831	T96831 y651d09.r1
C 11	185	13.8	452	81	AM435471	AM435471 UI-R-BJOP
C 12	174.4	13.0	563	29	AA168022	AA168022 ms66c03.r
C 13	145.8	10.9	528	85	TA0684103	TA0684103 HS.2162.B
C 14	128.8	9.6	310	43	A1178178	A1178178 EST221843
C 15	58.6	4.4	1101	82	CNS00396	AL063921 Drosophila
C 16	56.6	4.2	475	24	H70424	H70424 y603b10.r1
C 17	53.4	4.0	387	21	T96832	T96832 y651d09.s1
C 18	53.2	3.8	1101	82	CNS00396	AL063921 Drosophila
C 19	50.4	3.8	1204	83	CNS016E2	AL106628 Drosophila
C 20	48.6	3.6	697	83	CNS018M5	AL109511 Drosophila
C 21	46.2	3.4	1101	82	CNS003B6	AL064084 Drosophila
C 22	45.4	3.4	1101	82	CNS000D1	AL065414 Drosophila
C 23	45.4	3.4	1101	82	CNS000EVL	AL069706 Drosophila
C 24	44.6	3.3	928	82	CNS00C2B	AL058639 Drosophila
C 25	44.6	3.3	1101	83	CNS0174K	AL107582 Drosophila
C 26	44.2	3.3	1001	82	CNS01400	AL103554 Drosophila
C 27	44	3.3	928	82	CNS00DKY	AL071865 Drosophila
C 28	43.8	3.3	595	35	AA50690	AA50690 1927m3 gm
C 29	43.6	3.3	987	83	CNS014PQ	AL104456 Drosophila
C 30	43.6	3.2	1101	83	CNS017KX	AL108811 Drosophila
C 31	43.4	3.2	781	82	CNS009DO	AL071206 Drosophila
C 32	43.2	3.2	1101	82	CNS009RYG	AL071206 Drosophila
C 33	42.8	3.2	579	92	A0965871	A0965871 LER1F79FR
C 34	42.8	3.2	597	92	A0965869	A0965869 LER1F79FE
C 35	42.8	3.2	597	92	A0965870	A0965870 LER1F79FE
C 36	42.8	3.2	1201	83	CNS0167M	AL106396 Drosophila
C 37	42.6	3.2	1101	83	CNS0182P	AL108811 Drosophila
C 38	42.6	3.2	1225	83	CNS0161D	AL106171 Drosophila
C 39	42.2	3.1	1101	82	CNS00KAE	AL077628 Drosophila
C 40	42	3.1	1086	82	CNS00YXK	AL096307 Drosophila
C 41	41.8	3.1	1101	82	CNS00LJT	AL068307 Drosophila
C 42	41.6	3.1	524	82	CNS00079	AL085443 Arabidops
C 43	41.6	3.1	1097	82	CNS012J5	AL101650 Drosophila
C 44	41.6	3.1	1101	82	CNS0100X	AL098379 Drosophila
C 45	41.6	3.1	1101	83	CNS017ZQ	AL108704 Drosophila

ALIGNMENTS

RESULT 1
 AM366810/c 538 bp mRNA EST 04-FEB-2000
 LOCUS CM1-HT0152-041099-021-f06 HT0152 Homo sapiens cDNA, mRNA sequence.
 DEFINITION AM366810
 ACCESSION AM366810.1 GI:6871460
 VERSION
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 538)
 TITLE The FAPESP/LICR Human Cancer Genome Project
 JOURNAL Unpublished (1999)
 COMMENT On Mar 10, 1998 this sequence version replaced gi:2948481.
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil

Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM1-HT0152-041099-021-f06&t3=1999-10-04&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 19
 High quality sequence stop: 538.
 Location/Qualifiers
 1..538
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="HT0152"
 /dev_stage="Adult"
 /note="Organ: head_neck; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 157 a 87 c 107 g 187 t
 ORIGIN

Query Match 36.9%; Score 495.4; DB 80; Length 538;
 Best Local Similarity 95.2%; Pred. No. 2.7e-11;
 Matches 511; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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OY 681 CATTGATTAAGACCAAGTTGAATGAACACCTCCACGAAATATAGAGTCT 740
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DB 538 CATTGATTAAGACCAAGTTGAATGAACACCTCCACGAAATATAGAGTCT 479
OY 741 GTCCAAATCAGACTATGTTCTTAATGGATTATACATGCAACATGACCTTCAA 800
    |||||||
DB 478 GTCCAAATCAGACTATGTTCTTAATGGATTATACATGCAACATGACCTTCAA 419
OY 801 GTTCAGTGGCTCCAGCCCTTTTAAAGAGATCCTGGAAACATTTGATTAAGGAAA 860
    |||||||
DB 418 GTTCAGTGGCTCCAGCCCTTTTAAAGAGATCCTGGAAACATTTGATTAAGGAAA 359
OY 861 CAATACCGACTGTGAAATGTCAAACTACCAAGTGTCTTCCCTCAAACTTTTC 920
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DB 358 CAATACCGACTGTGAAATGTCAAACTACCAAGTGTCTTCCCTCAAACTTTTC 299
OY 921 CAAAAGGAATTTACCTCTCCGCTACAGCATCTGATGAAATACACATCTTTTGG 980
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DB 298 CAAAAGGAATTTACCTCTCCGCTACAGCATCTGATGAAATACACATCTTTTGG 239
OY 981 TCTGAAGAGATTAAGTTGATACCTGAATACAGCTTTCTCTCCCTCCAGCTTTAAC 1040
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DB 238 TCTGAAGAGATTAAGTTGATACCTGAATACAGCTTTCTCTCCCTCCAGCTTTAAC 179
OY 1041 ATTAGATCCCTAGTATGATTCATATCTATATCGTGTCTCAAAACAGTCTGGAAC 1100
    |||||||
DB 178 ATTAGATCCCTAGTATGATTCATATCTATATCGTGTCTCAAAACAGTCTGGAAC 119
OY 1101 ACGCCTGTGATCCAGATTTATCCACTGATTATGAAATATTTTGGGAAAACCTTCA 1160
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DB 118 ACGCCTGTGATCCAGATTTATCCACTGATTATGAAATATTTTGGGAAAACCTTCA 59
OY 1161 AATGCTGAGAGAAAATTAATGAGAAAAGTGAATGTTAGAGTCCATATTGAAA 1217
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DB 58 AATGCTGAGAGAAAATTAATGAGAGTAATAACTCATGTTACGTACGTACTTTGAA 2

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RESULT 2
 AA258405/c 505 bp mRNA EST 17-MAR-1997
 LOCUS AA258405.s1
 DEFINITION zrf62b09.s1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:667961.3'
 similar to gb:J03171 INTERFERON-ALPHA RECEPTOR PRECURSOR (HUMAN);

mRNA sequence.
 AA258405
 VERSION AA258405.1 GI:1893676
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 505)
 Hillier, L., Clark, N., Dubuque, T., Elliston, R., Hawkins, M.,
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
 Treaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
 Wilson, R.
 The WashU-Merck EST Project
 Unpublished (1995)
 On Sep 12, 1995 this sequence version replaced gi:1393828.
 Contact: Wilson RK
 Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estewatson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Seq primer: -41m3 fwd. ET from Amersham
 High quality sequence stop: 418.
 Location/Qualifiers
 1..505
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:667961"
 /clone_11b="Soares.NHMPU.S1"
 /tissue_type="Pooled human melanocyte, fetal heart, and
 pregnant uterus"
 /lab_host="DH10B"
 /note="Organ: mixed (see below); Vector: pT73D-Pac
 (Pharmacia) with a modified polylinker. Site 1: Not I;
 Site 2: Eco RI; Equal amounts of plasmid DNA from three
 normalized libraries (melanocyte 2NBHM, pregnant uterus
 NBHM), and fetal heart NBHM19W) were mixed, and ss circles
 were made in vitro. Following HAP purification, this DNA
 was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from pools of
 5,000 clones made from the same 3 libraries. The pools
 consisted of I.M.A.G.E. clones 260232-265223,
 340488-345479, and 484488-489479."
 BASE COUNT 151 a 79 c 106 g 169 t
 ORIGIN
 Query Match 36.6%; Score 491.4; DB 30; Length 505;
 Best Local Similarity 99.6%; Pred. No. 2.6e-110;
 Matches 503; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Db 265 TCCTCAAAACGTTTCCAAAAAGCAATTTACCTTCGCCGCTACAGCATCTGATGGAAA 206
 Qy 965 TAACACATCTTTTGTGTGTAAGAGATAAGTTTGATAGTGAATACAGCTTCTCTACT 1024
 Db 205 TAACACATCTTTTGTGTGTAAGAGATAAGTTTGATAGTGAATACAGCTTCTCTACT 146
 Qy 1025 TCCTCCAGCTTTTAAACATTAGATCCCTTAGTGATTCATTCATATATATGCGTCC 1084
 Db 145 TCCTCCAGCTTTTAAACATTAGATCCCTTAGTGATTCATTCATATATATGCGTCC 86
 Qy 1085 AAAACAGTGTGAACACGCGCTGATTCAGGATTCACAGATTTAATATATTT 1144
 Db 85 AAAACAGTGTGAACACGCGCTGATTCAGGATTCACAGATTTAATATATTT 26
 Qy 1145 TTGGGAAAACACTCAATGCTGAG 1169
 Db 25 TTGGGAAAACACTCAATGCTGAG 1
 RESULT 3
 LOCUS AM292343/C
 DEFINITION UI-H-B12-89w-a-10-0-UI.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone
 IMAGE:272554 3', mRNA sequence.
 ACCESSION AM292343
 VERSION AM292343.1 GI:6698979
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 456)
 NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 On Jun 5, 1998 this sequence version replaced gi:3188431.
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. cDNA library preparation: M.B. Soares Lab Clone distribution:
 NCI CGAP clone distribution information can be found through the
 I.M.A.G.E. Consortium/LNL at:
 www.bio.lnl.gov/db/nci/image/image.html
 Seq primer: M13 Forward
 PolyA-Tes.
 Location/Qualifiers
 1..456
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:272554"
 /clone_11b="NCI CGAP_Sub4"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker. Site 1: Not I; Site 2: Eco RI; The
 NCI CGAP_Sub4 library is a subtracted library derived from
 the NCI CGAP_Sub2 library which is a subtracted library
 derived from the NCI CGAP_Sub1 library, which is a
 subtracted library derived from B1. B1 constitutes a
 mixture of 21 normalized or subtracted NCI CGAP
 libraries: NCI CGAP C04, NCI CGAP Pr22, NCI CGAP_P28,
 NCI CGAP C010, NCI CGAP C016, NCI CGAP Pr22, NCI CGAP_P28,
 NCI CGAP_Kid12, NCI CGAP_Kid3, NCI CGAP_Kid11,
 NCI CGAP_Lym2, NCI CGAP_Br2, NCI CGAP_C08, NCI CGAP_C11,
 NCI CGAP_Lu24, NCI CGAP_Br23, NCI CGAP_Lu5,
 NCI CGAP_Lu24, NCI CGAP_Lu19, NCI CGAP_G04, NCI CGAP_G06,
 NCI CGAP_Br25. These 21 libraries were pooled and a
 single-stranded DNA preparation of the resulting mixture
 was used as a tracer in a subtractive hybridization with
 a driver whose composition is detailed below.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eutheria: Primates: Catarrhini: Hominoidea: Homo.
1 (bases 1 to 571)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Jun 5, 1998 this sequence version replaced gi:3187434.
Contact: Robert Strausberg, Ph.D.
Tel.: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E Consortium/LINL at:

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/clone_11b="NCI_CGAP_Lu24"
/tissue_type="carcinoid"
/lab_host="DH10a"
/note="Organ: lung; Vector: pRT73D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI_CGAP_Lu5 was prepared, and ss circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (clonoids
1414920-1417991 and 1520904-1522439). Subtraction by Benco
Soares and M. Fatima Bonalao."
BASE COUNT      172 a      97 c      106 g      194 t      2 others
ORIGIN

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Query Match Similarity	30.9%	Score 414.8	DB 46	Length 571
Best Local Similarity	94.9%	Pred. No. 1.6e-91		
Matches 482	Conservative	0	Mismatches 19	Indels 7
				Gaps 5

QY	820	TTTTAAAAAGGAATCCCGAAGACATTTGTATTAATAGAAACAAATACTAGCTGAAA	879
Db	562	TTTTAAAAAGGATCCCTGGAAACC--ATTGGTATATATATTAACMAATACTGCTGTGAAA	506
QY	880	ATGTCAAAACTACCCAGTGTGTCTTTCTCTCAAAACGTTTCCAAAAAGAAATTACCTTC	939
Db	505	ATG-CAAACTACCCAGTGTGTCTTTCTCTC-AAAGGTTTCCAAAAAGGAATTT-CTCT	449
QY	940	TCCCGGTNCAAGCATCTGATGGAATAACACATC-TTTTGTGTGGAAGAGATAAGTTT	998
Db	448	CCCGGTACCAAGCATCTGATGGAATAACACATCTTTTGTGTGGAAGAGATAAGTTT	389

Db 388 GATACCTGAAATACAAGCTTTTCTCTACTTCCTCCAGCTCTTTAAACATTAGATCCCTTAGTAT 329

Oy 1059 TCATTCCATATCTTATTCGGTGTCTCCAAACAGTCTGGAAACAGCGCTGTATCCAGAT 1118

QY 1119 TATCAGCTGATTGTGAATAATTATTTTTGGGAAAAACACTTAAATGCTGACAGAAAAATT 1178

Db 268 TATCAGCTGATTGTGAATAATTATTTTTGGGAAAAACACTTAAATGCTGACAGAAAAATT 209

QY 1179 ATCAGAAAAAACTGATGTTACAGTTCCTAATTGGAACCACTGACGTATATTGTGTG 1238

Db 208 ATCGAGAAAAAATGATGTTCACAGTTCTTAATTGAAACCACTGACTATATTCTGTC 149

Qy 1239 AAGCCAGACACACACATGATGAGAAAGCTGAAATAAAGACAGTCTTTTACTGACGCT 1298
|||||

Db 148 AAGCCAGACACACACATGATGAGAAAGCTGAAATAAAGACAGTCTTTTACTGACGCT 89

Qy 1299 GATGTGAGAAAAAACCAGGAATA 1326
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Db 88 GTATGTGAGAAAAAACCAGGCTCAGA 61

RESULT 5
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LOCUS UI-H-BI2-aggw-a-09-0-01.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone
DEFINITION IMAGE:2725552 3', mRNA sequence.
ACCESSION AM292342
VERSION AM292342.1 GI:6698978
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 403)
NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Jun 5, 1998 this sequence version replaced gi:3188430.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
The sequence contained an oligo-dr track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
NCI_CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LINL at:
www.bio.linal.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLA+yes.

FEATURES

Location/Qualifiers
1..403

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2725552"
/clone_1lb="NCI_CGAP_Sub4"
/1ad_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI. The
NCI_CGAP_Sub4 library is a subtracted library derived from
the NCI_CGAP_Sub2 library which is a subtracted library
derived from the NCI_CGAP_Sub1 library, which is a
subtracted library derived from B1. B1 constitutes a
mixture of 21 normalized or subtracted NCI_CGAP
libraries: NCI_CGAP_Co4, NCI_CGAP_Pr22, NCI_CGAP_Pr28,
NCI_CGAP_Co10, NCI_CGAP_Co16, NCI_CGAP_Kid5,
NCI_CGAP_Kid12, NCI_CGAP_Kid3, NCI_CGAP_Kid5,
NCI_CGAP_Lym2, NCI_CGAP_Brn23, NCI_CGAP_Lus,
NCI_CGAP_Lus42, NCI_CGAP_Brn2, NCI_CGAP_CoB, NCI_CGAP_Co11,
NCI_CGAP_Lu24, NCI_CGAP_Lu19, NCI_CGAP_Gc4, NCI_CGAP_Gc6,
NCI_CGAP_Brn25. These 21 libraries were pooled and a
single-stranded DNA preparation of the resulting mixture
was used as a tracer in a subtractive hybridization with
a driver whose composition is detailed below:
NCI_CGAP_Kid3 pool 1: LLM 3334-3337, 3662-3683,
3798-3803 (IMAGE Clonides 132276-132911,
1456008-1456775, 1500552-150855) NCI_CGAP_Kid5 pool 1:
LLM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clonides
132912-1325831, 1471368-1472903, 1492104-1493255)
NCI_CGAP_Lus pool 1: LLM 3575-3582, 3851-3854 (IMAGE
Clonides 1414920-1417991, 1520904-1522439) NCI_CGAP_Gc4
pool 1: LLM 3164-3167, 3716-3720, 3733-3735 (IMAGE

BASE COUNT 118 a 63 c 80 g 142 t
ORIGIN
TAG_SEQ-CANC"
TAG_TISSUE=Lung
TAG_LIB=NCI_CGAP_Lus
Discovery. Genome Research 6, 791-806.)
described (Bonaldo, Lennon & Soares (1986): Normalization
and Subtraction: Two Approaches To Facilitate Gene
Tagging.

Query Match 29.4%; Score 395; DB 79; Length 403;
Best Local Similarity 100.0%; Pred. NO. 1.1e-86;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 797 TCAAGTCAGTGGCTCCACGCGCTTTTAAAGAAATCTCGAAACCAATTTGTATTAATG 856
||||| Clonides 1257096-1258631, 1469064-1470983,
1475592-1476743) NCI_CGAP_Pr22 pool 1: LLM 2457-2459,
2758-2759, 3062-3068 (IMAGE Clonides 985608-986759,
1101192-1101959, 1217928-1218015) NCI_CGAP_Co10 pool 1:
LLM 2644-2653, 2871-2872 (IMAGE Clonides 1057416-1061255,
1144584-1145351) Subtraction was performed as previously
described (Bonaldo, Lennon & Soares (1986): Normalization
and Subtraction: Two Approaches To Facilitate Gene
Tagging.

Db 403 TCAAGTCAGTGGCTCCACGCGCTTTTAAAGAAATCTCGAAACCAATTTGTATTAATG 344
|||||

Qy 857 GAAACAAATACCTGACTGTGAAATGTCAAAACCTACAGTGTCTTCTCCAAAACGT 916
|||||

Db 343 GAAACAAATACCTGACTGTGAAATGTCAAAACCTACAGTGTCTTCTCCAAAACGT 284
|||||

Qy 917 TTTCAGAAAGAAATTTACCTCTCGGGGTCAACATCTGTGAAATTAACATCTTT 976
|||||

Db 283 TTTCAGAAAGAAATTTACCTCTCGGGGTCAACATCTGTGAAATTAACATCTTT 224
|||||

Qy 977 TTGCTCTGAGAGATAAATTTGATGATGAAATACAGCTTCTACTCTCTCCAGTCTT 1036
|||||

Db 223 TTGCTCTGAGAGATAAATTTGATGATGAAATACAGCTTCTACTCTCTCCAGTCTT 164
|||||

Qy 1037 TAACATTAATGCTTGTAGTATTCATTCATATCATATGCTGCTCCAAAACAGTCTGG 1096
|||||

Db 163 TAACATTAATGCTTGTAGTATTCATTCATATCATATGCTGCTCCAAAACAGTCTGG 104
|||||

Qy 1097 AATCAAGCTGATCCAGGATTCATTCATATCATATGCTGCTCCAAAACAGTCTGG 1156
|||||

Db 103 AATCAAGCTGATCCAGGATTCATTCATATCATATGCTGCTCCAAAACAGTCTGG 44
|||||

Qy 1157 TTCAATGCTGAGAAAAAATTTATGAGAAAAAA 1191
|||||

Db 43 TTCAATGCTGAGAAAAAATTTATGAGAAAAAA 9
|||||

RESULT 6
AA308713 383 bp mRNA EST 18-APR-1997
LOCUS AA308713 HCC cell line (metastasis to liver in mouse) II Homo
DEFINITION sapiens cDNA 5' end similar to interferon, alpha/Beta receptor
(GI:860459), mRNA sequence.
ACCESSION AA308713
VERSION AA308713.1 GI:1961043
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 383)
Adams M.D., Kerlavague A.R., Fleischmann R.D., Fulmer R.A.,
Bult C.J., Lee N.H., Kirkness E.F., Weinstock K.G., Gocayne J.D.,
White O., Sutton G., Blake J.A., Brannon R.C., Man-vel C.,
Clayton R.A., Cline T.R., Cotton M.D., Earle-Hughes J., Fine L.D.,
Fitzgerald L.M., Fitzhugh W.M., Fritchman J.L., Geoghegan N.S.,
Glodek A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle P.S., Jr.,
Kelley J.M., Kelley J.C., Liu L.-I., Mammoser S.M., Merriick J.M.,
Moreno-Palancas R.F., McDonald L.A., Nguyen D.T., Pelligrino S.M.,
Phillips C.A., Ryder S.E., Scott J.L., Saudek D.M., Shirley R.,
Small K.V., Spriggs T.A., Uterback T.R., Weidman J.F., Li X.,

TITLE

Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dlmke,D., Feng,D.-F., Ferris,A., Fischer,C., Hastings,G.A.,
He,W.M., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Melsner,P.S., Olsen,H.,
Raymond,L., Wei,L.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence

JOURNAL
MEDLINE

Nature 377 (6547 Suppl.), 3-174 (1995)
12140200

COMMENT

On Sep 12, 1996 this sequence version replaced gi:1392985.
Other ESTs: TNC171186
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/cdb/ng1/ng1.html>)
Seq primer: M13 Reverse.

FEATURES

Location/Qualifiers

1..383
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HCC cell line (metastasis to liver in mouse)"
/tissue_type="colon"
/cell_type="KM12C(HCC)metastasis into mouse (liver)"
/note="Vector: pBluescript SK-; Site:1: EcoRI; Site:2:
XhoI"
BASE COUNT 111 a 75 c 91 g 104 t 2 others

Query Match

Best Local Similarity 27.2%; Score 365.8; DB 31; Length 383;
Matches 378; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 16 GCGGCTCCAGATGATGTCCTCTGCGGCGGAGACCTAGTGTGTCGCGGTG 75
DB 1 GCGGCTCCAGATGATGTCCTCTGCGGCGGAGACCTAGTGTGTCGCGGTG 60
QY 76 GCCCATGGGTGTGTCGCGAGCCGAGAGTGAATAATCTCTCAAAAAGTAG 135
DB 61 GCGCATGGGTGTGTCGCGAGCCGAGAGTGAATAATCTCTCAAAAAGTAG 120
QY 136 AGCTCGCATCATGATGACAACTTTATCTGAGGTGAACAGAGCGATGCTCTG 195
DB 121 AGCTCGCATCATGATGACAACTTTATCTGAGGTGAACAGAGCGATGCTCTG 180
QY 196 GGAATGACATTTTTCATGATATCAAAAACTGGATGATGATGATGATGAT 255
DB 181 GGAATGACATTTTTCATGATATCAAAAACTGGATGATGATGATGATGAT 240
QY 256 CTGGGTGTCAAGATATAGTACCAAAATGCAACTTTTCTCACTCAAGCTGAATGTT 315
DB 241 CTGGGTGTCAAGATATAGTACCAAAATGCAACTTTTCTCACTCAAGCTGAATGTT 300
QY 316 ATGAAGAAATTAATTCGATAGAGCAAGAAACACATCTTCATGATGATGAG 375
DB 301 ATGAAGAAATTAATTCGATAGAGCAAGAAACACATCTTCATGATGATGAG 360
QY 376 -TTGACTCATTTACCACTTTCG 397
DB 361 TTGACTCATTTACCACTTTCG 383

RESULT 7

AA258750

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AA258750 380 bp mRNA EST 17-MAR-1997
zr62b09.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:667961 5'
similar to gb:J03171 INTERFERON-ALPHA RECEPTOR PRECURSOR (HUMAN);
mRNA sequence.
AA258750
AA258750.1 GI:1893873
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 380)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucada,T., Le,M., Lennon,G., Matis,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Woldmann,P. and
Wilson,R.
The Mashu-Werck EST Project
Unpublished (1995)
On Sep 12, 1996 this sequence version replaced gi:1392980.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 360.

FEATURES

source

Location/Qualifiers
1..380
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:667961"
/clone_lib="Soares_NHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site:1: Not I;
Site:2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2bHM, pregnant uterus
NBHPu, and fetal heart NBH19W) were mixed, and ss circles
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of 1 M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
BASE COUNT 109 a 72 c 98 g 101 t

Query Match

Best Local Similarity 25.4%; Score 341.2; DB 30; Length 380;
Matches 354; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 6 GGGATCTGGGGGCTCCAGATGATGTCCTCTGCGGCGGAGACCTAGTGTCTC 65
DB 1 GGGATCTGGGGGCTCCAGATGATGTCCTCTGCGGCGGAGACCTAGTGTCTC 59
QY 66 GTGCGCGTGGGCCCAATGAGGTGTGTCGCGAGCCGAGGTGGAATAATCTCTCT 125
DB 60 GTGCGCGTGGGCCCAATGAGGTGTGTCGCGAGCCGAGGTGGAATAATCTCTCT 119
QY 126 CAAAAGTAGAGTGACATCATAGTACCACTTTATCTAGGTGGAACAGAGCAT 185
DB 120 CAAAAGTAGAGTGACATCATAGTACCACTTTATCTAGGTGGAACAGAGCAT 179
QY 186 GAGTCTGTGGGGAATGTACTTTTTCATTCGATTTATCAAAAACTGGGATGATTAATTGG 245

|||||
Db 180 GAGTCGCGGAATGTCATTTTCATTCGATATCAAAAAACGCGGATGATATTGG 239
Oy 246 ATAAATGTCGGGTGAGAAATATCTAGTACCAATGCACTTTCTCATCTCAG 305
Db 240 ATAAATGTCGGGTGAGAAATATCTAGTACCAATGCACTTTCTCATCTCAG 299
Oy 306 CTGAATGTTATGAGAAATTAATTCGTATAGAGAGAAAAAACAACCTCTT 363
Db 300 CTGAATGTTATGAGAAATTAATTCGTATAGAGAGAAAAAACAACCTCTT 357
RESULT 8
LOCUS AA447894 504 bp mRNA EST 04-JUN-1997
DEFINITION zxi1a06.r1 soares.total_fetus.Nb2HF8.9w Homo sapiens cDNA clone
IMAGE:786130.5, similar to gb:J03171 INTERFERON-ALPHA RECEPTOR
PRECURSOR (HUMAN); mRNA sequence.
ACCESSION AA447894.1 GI:2161564
VERSION AA447894
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 504)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wyllie, J., Waterston, R. and Wilson, R.
WashU-Merck EST Project 1997
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1290666.
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LINT; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28mJ rev2 ET from Amersham
High quality sequence stop: 464.
Location/Qualifiers
FEATURES
source 1..504
/organism="Homo sapiens"
/db_xref="GDB:598374.9"
/db_xref="taxon:9606"
/clone="IMAGE:786130"
/clone_1lb="Soares.total_fetus.Nb2HF8.9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/note="Vector: p773D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
TGTACCAATGTCGAGCGCGCCCTTAATTTTCTTTTCTTTT 3']
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p773 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 168 a 90 c 85 g 161 t
ORIGIN
Query Match 20.7%; Score 277.4; DB 33; Length 504;
Best Local Similarity 99.6%; Pred. No. 7.4e-58;
Matches 278; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1116 GATTATCCACGATTATGAATATTTTGGGAAAACACTTCAATGCTGAGAGAAA 1175
Db 61 GATTATCCACGATTATGAATATTTTGGGAAAACACTTCAATGCTGAGAGAAA 120
Oy 1176 ATATCGAGAAAAAACTGATGTTACAGTCCATATTGAACCACTGATATTTGT 1235
Db 121 ATATCGAGAAAAAACTGATGTTACAGTCCATATTGAACCACTGATATTTGT 180
Oy 1236 GTGAAGCGAGAGACACACATGATGAAGAGCTGAATAAGCACTGTTTAGTGAC 1295
Db 181 GTGAAGCGAGAGACACACATGATGAAGAGCTGAATAAGCACTGTTTAGTGAC 240
Oy 1296 GCTGATGTGAGAAAAACAAACAGAAATACCTCTAAA 1334
Db 241 GCTGATGTGAGAAAAACAAACAGAAATACCTCTAAA 279
RESULT 9
LOCUS A1863225 444 bp mRNA EST 26-AUG-1999
DEFINITION t339a08.x1 NCI-CGAP Brn52 Homo sapiens cDNA clone IMAGE:2290934.3,
similar to gb:J03171 INTERFERON-ALPHA RECEPTOR PRECURSOR (HUMAN);
mRNA sequence.
ACCESSION A1863225 GI:5527332
VERSION A1863225
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 444)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Dec 20, 1995 this sequence version replaced gi:1135299.
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINT at:
www-bio.llnl.gov/bdrp/image/image.html
Seq primer: -40UP from G1BCO
High quality sequence stop: 420.
Location/Qualifiers
FEATURES
source 1..444
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2290934"
/clone_1lb="NCI-CGAP_Brn52"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
/note="Organ: Brain; Vector: pCMV-SPORE6; Site_1: SalI;
Site_2: NotI; This library represents the normalized
version of NCI-CGAP_Brn52. Cloned unidirectionally.
Primer: Oligo dT. Average insert size 1.19 Kb. Tumor
types include: meningioma, oligodendroglioma, astrocytoma
(grade II), medulloblastoma, astrocytoma (grade IV).
Constructed by Life Technologies."
BASE COUNT 140 a 85 c 137 t
ORIGIN
Query Match 20.2%; Score 271; DB 61; Length 444;
Best Local Similarity 100.0%; Pred. No. 2.7e-56;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AO684103 528 bp DNA GSS 28-JUN-1999
LOCUS HS_2162_B1_F08_T7C_C1T Approved Human Genomic Sperm Library D Homo
DEFINITION sapiens genomic clone plate-2162 Col-15 Row-L, genomic survey
sequence.
ACCESSION AO684103
VERSION AO684103.1 GI:5260086
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 528)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2162 Row: L Column: 15
Seq primer: 17
Class: BAC ends
High quality sequence stop: 528.
FEATURES
source
1..528
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate-2162 Col-15 Row-L"
/clone_1lb="C1T Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
E-Coli DH10B"
BASE COUNT 172 a 85 c 87 g 172 t 12 others
ORIGIN
Query Match 10.9%; Score 145.8; DB 85; Length 528;
Best Local Similarity 95.5%; Pred. No. 1.4e-25;
Matches 150; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
OY 553 TAGAGAAAGATTGAAATTTATTCAGACATAAAATTTAAACTCTCACAGAGA 612
DB 221 TAGAGAAAGATTGAAATTTATTCAGACATAAAATTTAAACTCTCACAGAGA 280
OY 613 CTACTATTGCTAAAGTTAAAGCAGCAGCACTACTAGTCATGAAATGTGTCTATA 672
DB 281 CTACTATTGCTAAAGTTAAAGCAGCAGCACTACTAGTCATGAAATGTGTCTATA 340
OY 673 GTCCAGTACTGTATTAAGACACAGCTGAAATGA 709
DB 341 GTCCAGTACTGTATTAAGACACAGCTGAAATGA 377
RESULT 14
LOCUS A1178178 310 bp mRNA EST 20-JAN-1999
DEFINITION EST22183 Normalized rat placenta, Bento Soares Rattus sp. cDNA
clone RPLCN21 3' end, mRNA sequence.
ACCESSION A1178178
VERSION A1178178.1 GI:3728816
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 310)
Lee,N.H., Gloder,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (BEST) Catalog & Rat
Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Lee, NH
ATCC
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@igf.org
Seq primer: M13-21.
FEATURES
source
1..310
/organism="Rattus sp."
/db_xref="ATCC (inhost):2033250"
/db_xref="taxon:10118"
/clone="RPLCN21"
/clone_1lb="Normalized rat placenta, Bento Soares"
/note="Organ: placenta; Vector: p773Pac; Site_1: EcorI;
Site_2: NotI"
BASE COUNT 81 a 62 c 82 g 85 t
ORIGIN

Query Match 9.6%; Score 128.8; DB 43; Length 310;
Best Local Similarity 71.6%; Pred. No. 2e-21;
Matches 169; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
OY 843 CATTGTATAATGGAACAAATACCTGACGTGAAATGTCAAAGTACCCAGTGTCTC 902
DB 265 CATTGACAAATGGAACCAATACCTGACGTGCAAAATGTCAGACTACACAGCTGTGA 206
OY 903 TTTCCTCAAAAGCTTTCCAAAGAAAGATTACCTTCCCGGTCAAGATCTGATGGA 962
DB 205 TCTCCTCGAGACATTTCCACACAGAACTTTCTCCGGTACAGACCTCAATGGA 146
OY 963 AATAACACATCTTTTGTGCTGAGAGATAAAGTTGATGATGAAATCAAGCTTCTCTA 1022
DB 145 AATAACAGCTCTTTTGTGCTGAGAGATAAAGTTGATGATGATGATGATGATGATG 86
OY 1023 GTTCTCCAGTCTTAAATAGATCCCTTAACTGATTCATTCATATCTAATCGG 1078
DB 85 CCTCCTCGGATGATGCTGTCACCCACAGGGGAGCTCTGCTGTTATGTGCG 30
RESULT 15
LOCUS CNS00396G 1101 bp DNA GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR0810 of RPLC-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL063921
VERSION AL063921.1 GI:4941778
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequence
BP 191 91006 Evry cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammosser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

SOURCE

1. 1101

/organism="Drosophila melanogaster"

/db_xref="taxon:7227"

/clone_lib="RPCI-98"

/clone="BACROBK10"

/note="end : TE13"

/note="end : TE13"

BASE COUNT 201 a 64 c 131 g 202 t 503 others

ORIGIN

Query Match 4.4% Score 58.6; DB 82; Length 1101;
Best Local Similarity 18.9%; Pred. No. 0.00034;
Matches 108; Conservative 238; Mismatches 219; Indels 6; Gaps 2;

QY 107 AAAAAATCTAAATCTCCTCAAAAAGTAGAGTCGACATCATAGACAATTATCCT 165
DB 1042 WWWWWATWTDWTKMMWATAKTDTATWTRAWRADWAGRGAGKRDADAD 983
QY 167 GAGGTGAACAGAGAGCGATGAGCTGTGCGGAATGTGACTTTTCATTGATTATCAAA 226
DB 982 GAGRRDGGRRKRDKRDGDDKGGKKKAATAKATKWDMDMDKDKMGAKDR 923
QY 227 AACTGGGATGGATATTTGGATTAATTTGCTGGGTGAGATAT--ACTAGTACCAA 284
DB 922 KADDDGAGDKDDDKGADDDTGTGTDKDDDKWDMDKAKGTWGDATWMAATDWW 863
QY 285 TGCAACTTTTCTCCTCAAGCTGATGTTATGAAGAAATTAATTCGTTAAGACA 344
DB 862 WGMADADWTDWADADWADWADWADWADWADWADWADWADWADWADWADWADW 803
QY 345 GAAAAAGAAACACTTCTTCATGATGATGAGTGAAGTGAATTTGACCAATTTGCAAGCT 404
DB 802 RDRKRAADKRDADRDADATWTTTTRTDIDDKWKTDTWMAADRTWDRDDDDR 743
QY 405 CAGATTGCTCCAGAGACTACATTAGAGCTGAAGATAAGCAATAG---TGATACA 460
DB 742 DRAGTAGRRWRTWRWRWRRDTRWDADADTDARDDRRRGDDGADAGKKTGRKRR 683
QY 461 CATCTCCTCGAACAAGAGATAGTATGTTATGCGCTTGAATGTTAAGCTTACATA 520
DB 682 RDRATWDRTDWADWADWADWADWADWADWADWADWADWADWADWADWADWADW 623
QY 521 TAGCTTACTTATCTGAAAACTCTTCAGGTGAGAGAGAGATTGAAATATTATTC 580
DB 622 WAKWMTKTRADWDRWADWADWADWADWADWADWADWADWADWADWADWADWADW 563
QY 581 CAGACATAAAATTTAATCTCAACAGAGACTACTTATTTCTAAAAAGTAAAGCAC 640
DB 562 TATWTTWAAARAAMWMAATTTATWTTTWTWTTTWTWTTTWTWTTTAAWMAWMA 503
QY 641 ACTACTAGTCATGAAAAATGTGCTAT 671
DB 502 TWAATWTAAMAAAAAAATTTTTTTTTT 472

Search completed: June 1, 2000, 10:34:30
Job time: 16908 sec

RA Lowney P., Corral J.C., Detmer K., Lebeau M.M., Deaven L.,
 RA Lawrence H.J., Laryman C.;
 RT "A human Hox 1 homeobox gene exhibits myeloid-specific expression of
 RT alternative transcripts in human hematopoietic cells.";
 RL Nucleic Acids Res. 19:3443-3449(1991).
 RN [2]
 RP SEQUENCE OF 404-486 FROM N.A.
 RX MEDLINE: 90046832.
 RA Shen W.-F., Laryman C., Lowney P., Corral J.C., Detmer K.,
 RA Hausser C.A., Simonitch T.A., Hack F.M., Lawrence H.J.;
 RT "Lineage-restricted expression of homeobox-containing genes in human
 RT hematopoietic cell lines.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8536-8540(1989).
 RN [3]
 RP SEQUENCE OF 422-487 FROM N.A.
 RX MEDLINE: 90098876.
 RA Acampora D., D'Esposito M., Falcetta A., Pannese M., Migliaccio E.,
 RA Morelli F., Stornaiuolo A., Nigro V., Simeone A., Boncinelli E.;
 RT "The human HOX gene family.";
 RL Nucleic Acids Res. 17:10385-10402(1989).
 RN [4]
 RP SEQUENCE OF 435-473 FROM N.A.
 RX MEDLINE: 94143486.
 RA Castronovo V., Kusaka M., Charlot A., Gielen J., Sobel M.;
 RT "Homeobox genes: potential candidates for the transcriptional control
 RT of the transformed and invasive phenotype.";
 RL Biochem. Pharmacol. 47:137-143(1994).
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
 CC BINDS TO THE DNA SEQUENCE 5'-AA[AT]TTTATAC-3'.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS: HOX-A10-1/PL1 (SHOWN HERE) AND
 CC HOX-A10-2/PL2; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE ABD-B FAMILY OF HOMEBOX PROTEINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X58430: -; NOT ANNOTATED_CDS.
 DR EMBL: M30598: AA36006.1: -;
 DR EMBL: S69027: AAD14030.1: -;
 DR EMBL: S69029: AAD14031.1: -;
 DR PIR: S14930: S14930.
 DR PIR: S26402: S26402.
 DR PIR: A34425: A34425.
 DR HSSP: P02833: 1SAN.
 DR TRANSFAC: T01713: -;
 DR MIM: 142957: -;
 DR PRINTS: PR00024: HOMEBOX.
 DR PROSITE: PS00027: HOMEBOX_1: 1.
 DR PROSITE: PS50071: HOMEBOX_2: 1.
 DR PIRAM: PF00046: homeobox; 1.
 KW Homeobox; DNA binding; Developmental protein; Nuclear protein;
 KW Transcription regulation; Alternative splicing.
 FT DOMAIN 181 192 POLY-GLY.
 FT DOMAIN 219 223 POLY-PRO.
 FT DOMAIN 227 236 POLY-PRO.
 FT DOMAIN 366 371 POLY-ALA.
 FT DNA_BIND 422 481 HOMEBOX.
 FT VARSPIC 1 402 MISSING (IN ISOFORM HOX-A10-2).
 FT VARSPIC 403 405 DSL -> MCQ (IN ISOFORM HOX-A10-2).
 FT CONFLICT 435 435 L -> S (IN REF. 2).
 FT CONFLICT 437 437 L -> F (IN REF. 2).
 FT CONFLICT 473 473 R -> P (IN REF. 2).
 SQ SEQUENCE 496 AA: 54733 MW: 7706F675916552F0 CRC64;

Alignment_scores:
 Quality: 59.00 Length: 24
 Ratio: 3.105 Gaps: 1
 Percent Similarity: 79.167 Percent Identity: 58.333

Alignment_block:

US-09-240-675-1_COPY_27_229 x HXAA_HUMAN

Align seg 1/1 to: HXAA_HUMAN from: 1 to: 496

15 CCTGGGGCGCAGCAGCCCTAGTGTCTGTCGCCGCGCATGGGCGGTGTGT 64
 |||||
 350 Proglytsergltuprosertllargargargproproargtrp.leua 366
 65 CCGCAGCCCGCAGGTGAAA 84
 ::|||
 366 laaiaaiaaiaaiaaarg 372

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 31, 2000, 19:06:34 ; Search time 42.08 Seconds
(without alignments)
225.716 Million cell updates/sec

Title: US-09-240-675-2_COPY_27_427

Perfect score: 2141
Sequence: 1 GKNLSPQKVEVDIIDNFI.....AHTMDEKLKSSVSDAVCE 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2141	100.0	436	R14487	Soluble interferon
2	2141	100.0	436	R28495	Sequence of a soul
3	2141	100.0	557	R11958	Human alpha-interf
4	2141	100.0	557	R14488	Complete interfero
5	2141	100.0	557	R28496	Sequence of a soul
6	2141	100.0	557	R42635	Human interferon r
7	2137	99.8	557	R75356	Human IFN receptor
8	2136	99.8	434	R21805	Spliced-deleted in
9	2136	99.8	557	R21804	Transmembranal int
10	2132	99.6	436	R71123	IFN receptor extra
11	2084	97.3	436	R21806	Spliced-deleted in
12	220	10.3	325	W52296	CRFB4 protein. New
13	199	9.3	332	R75782	IFN-gamma receptor
14	180	8.4	553	W79159	zcytoir cytokine r
15	148	6.9	337	R71035	Human IFN-gamma ac
16	146	6.8	337	R73783	Human IFN-gamma rec
17	142	6.6	574	R73781	Human cytokine rec
18	131.5	6.1	211	W97864	Human cytokine rec
19	118	5.5	227	R14642	Human interferon r
20	118	5.5	231	R14641	Gamma interferon r
21	118	5.5	473	R55749	Extracellular doma
22	118	5.5	469	R07469	Plasid PBABULB hu
23	118	5.5	942	R70113	Gamma-IFN-R-GBP 13
24	118	5.5	1005	W83147	Rat receptor tyros
25	117.5	5.5	2214	W26357	Human LDL receptor
26	115.5	5.4	210	R14643	Gamma interferon r
27	113.5	5.3	1728	R13144	Deleted in Colorec
28	111.5	5.2	1571	W42087	Human Down syndrom
29	111.5	5.2	1910	W42086	Human Down syndrom
30	111	5.2	245	R62023	Soluble human inte
31	110	5.1	2213	W26356	Rabbit LDL recepto
32	109.5	5.1	575	R57139	Interleukin-10 rec
33	109.5	5.1	575	W41803	Mouse IL-10 receptor
34	108	5.0	991	R85090	EPH-like receptor

35	107	5.0	426	1	W09822	Human Interleukin-
36	107	5.0	427	1	W24973	Human Interleukin-
37	107	5.0	753	1	W83927	Human T85 protein.
38	105.5	4.9	878	1	R78608	Murine IL-3 recept
39	105.5	4.9	1370	1	P60005	Sequence encoded b
40	104.5	4.9	596	1	R78616	Expression vector
41	104.5	4.9	600	1	R78610	Expression vector
42	104.5	4.9	600	1	R92526	Fas antigen #1. Im
43	104.5	4.9	1447	1	R68553	Deleted in colorec
44	103	4.8	17	1	R47008	IFN-alpha receptor
45	103	4.8	553	1	W35856	Human CD45 for use

ALIGNMENTS

RESULT 1
ID R14487 standard; Protein: 436 AA.
AC R14487;
DT 16-JAN-1992 (first entry)
DE Soluble interferon-alpha/beta receptor.
KM IFN: autoimmune disease; graft rejection; histocompatibility.
OS Homo sapiens.
PN FR2657881-A.
PD 09-AUG-1991.
PE 05-FEB-1990: 001298.
PR 05-FEB-1990: FR-001298.
PA (EUBI-) LAB EURO BIOTECHNO.
PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE;
PI Tovey MG, Uze G;
DR WPI: 91-31978/44.
DR N-PSDB: Q14239.
PT New water-soluble polypeptide(s) with affinity for IFN-alpha and
PT beta - used to treat e.g. lupus erythematosus, Behcet's disease,
PT aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.
PS Claim 2; Page 43; 52pp; French.
CC The transmembrane and cytoplasmic domains of the native IFN receptor
CC have been deleted to obtain a soluble, circulating form of the
CC receptor. Potentially immunogenic epitopes have thus been eliminated.
CC Derivatives obtained by substitution or deletion of this sequence
CC are also claimed as are hybrid molecules comprising the soluble
CC receptor (or deriv.) and an immunoglobulin such as IgG1.
SQ See also Q14240.
SQ Sequence 436 AA:

Query Match 100.0%; Score 2141; DB 1; Length 436;
Best Local Similarity 100.0%; Pred. No. 2.3e-185;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKNLSPQKVEVDIIDNFI LRNRSDSGVNTFSFDYOKTGMDNMKLSGQNTSTPK 60
DB 27 GKNLSPQKVEVDIIDNFI LRNRSDSGVNTFSFDYOKTGMDNMKLSGQNTSTPK 86
QY 61 CNFSKLNLYEBIKLRIRAEKENTSSWYEVDSFTPRRAQIGPPVHLAEEDKAIYIH 120
DB 87 CNFSKLNLYEBIKLRIRAEKENTSSWYEVDSFTPRRAQIGPPVHLAEEDKAIYIH 146
QY 121 SPRTKDSVMALDGLSFTSLTKNKSQVEEIEINISHRKIKYKSPETTYLTKYKAL 180
DB 147 SPRTKDSVMALDGLSFTSLTKNKSQVEEIEINISHRKIKYKSPETTYLTKYKAL 206
QY 181 LTMKIGVSPVACIKTYENELRPPEINIEVSQONNYVLKMDYTAANNTFQVQMLHAFL 240
DB 207 LTMKIGVSPVACIKTYENELRPPEINIEVSQONNYVLKMDYTAANNTFQVQMLHAFL 266
QY 241 KRNPGNHLKWKQIPDCENKTKQCVFPNVFQKGIYLLRVQASDQNNSTFSWSEIKFDI 300
DB 267 KRNPGNHLKWKQIPDCENKTKQCVFPNVFQKGIYLLRVQASDQNNSTFSWSEIKFDI 326
QY 301 EIAFAFLPPVFNIRSLSDSHIITGAPKOSGNTPVYODPLIETIFFNENTSNAEKITE 360

Db 327 EIOAFLLPVENIRSLSDSFHIIYIGAPKOSGNTPVIOYPLIYEIIFMENTSNAERKIIIE 386
OY 361 KKTDTVPNLKPLTYCYKARAHMTDEKLKSSVFSADACE 401
Db 387 KKTDTVPNLKPLTYCYKARAHMTDEKLKSSVFSADACE 427

RESULT 2

R28495
ID R28495 standard; Protein: 436 AA.
AC R28495;
DT 31-MAR-1993 (first entry)
DE Sequence of a soluble form of the interferon (IFN) receptor
with a high affinity for IFN-alpha and -beta.
KW Interferon receptor; alpha-interferon; beta-interferon.
OS Synthetic.
PN MO9218626-A.
PD 29-OCT-1992.
PR 17-APR-1991; F00318.
PR 17-APR-1991; MO-F00318.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
PI Eid P. Gresser I, Lutfalla G, Meyer F, Mogensen KE.
PI Tovey M, Uze G;
DR WPI: 92-382110/46.
DR N-PSDB: Q30532.
PT Water soluble polypeptide(s) strongly bind interferon(s) alpha
and beta - useful as immunosuppressants, for treating auto-immune
diseases and transplant rejection
PS Claim 2; Fig 1; 58pp; English.
CC DNA encoding the water-soluble polypeptide with a high affinity for
IFN-alpha and -beta is isolated by PCR, using appropriate
oligonucleotides as primers and cloned cDNA as template. For example,
bacteriophage lambda ZAP, containing the entire coding sequence of
the IFN-alpha and -beta receptor (Q30533), was incubated with oligos
Q30534 and Q30535. R28496 represents the complete receptor. R28495
lacks the transmembrane and cytoplasmic domains. Both forms bind
IFN in the same way as antibodies so are immunosuppressants e.g. for
treating autoimmune diseases and graft rejection. They lack the
toxic side-effects of known immunosuppressants such as steroids.
SO Sequence 436 AA.

Query Match 100.0%; Score 2141; DB 1; Length 436;
Best Local Similarity 100.0%; Pred. No. 2.3e-185;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GKNLKSPOKVEVDIIDDNFILRMNRSDSEVGNTFSFDYOKTGMNMKILSGCONITSTK 60
Db 27 GKNLKSPOKVEVDIIDDNFILRMNRSDSEVGNTFSFDYOKTGMNMKILSGCONITSTK 86
OY 61 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEDSFTPRKAOIGPPEVHLEADKAIVIH 120
Db 87 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEDSFTPRKAOIGPPEVHLEADKAIVIH 146
OY 121 SPGRKDSVMMALDGLSFTYSLIMKNSGVEERIEIENIYSRRKIYKLSPEPTYCLKVKAL 180
Db 147 SPGRKDSVMMALDGLSFTYSLIMKNSGVEERIEIENIYSRRKIYKLSPEPTYCLKVKAL 206
OY 181 LTSKIGIYSPVHCITKTIVENELPPENIEVSQONONYLKWDTYANNMFOVOMLAFL 240
Db 207 LTSKIGIYSPVHCITKTIVENELPPENIEVSQONONYLKWDTYANNMFOVOMLAFL 266
OY 241 KRNPGNHLKXKQKIPDCENVTTCQCFPQNFQKIGITLLRVQASDGNNTSFSSEIKFPT 300
Db 267 KRNPGNHLKXKQKIPDCENVTTCQCFPQNFQKIGITLLRVQASDGNNTSFSSEIKFPT 326
OY 301 EIOAFLLPVENIRSLSDSFHIIYIGAPKOSGNTPVIOYPLIYEIIFMENTSNAERKIIIE 360
Db 327 EIOAFLLPVENIRSLSDSFHIIYIGAPKOSGNTPVIOYPLIYEIIFMENTSNAERKIIIE 386
OY 361 KKTDTVPNLKPLTYCYKARAHMTDEKLKSSVFSADACE 401
Db 387 KKTDTVPNLKPLTYCYKARAHMTDEKLKSSVFSADACE 427

RESULT 3
R11958
ID R11958 standard; Protein: 557 AA.
AC R11958;
DT 18-JUL-1991 (first entry)
DE Human alpha-interferon receptor protein.
KW Human alpha IFN; IFN agonists; antiviral; anti tumour agent;
drug targeting.
OS Homo sapiens.
FH Key
FT peptide 1.27
PN MO9105862-A.
PD 02-MAY-1991.
PR 19-OCT-1990; F00758.
PR 20-OCT-1989; FR-013770.
PA (CNRS) CNRS CENT NAT RECH SCI.
PI Mogensen KE, Uze G, Lutfalla G, Gresser I;
DR WPI: 91-148740/20.
DR N-PSDB: Q11701.

PT New human alpha-interferon receptor protein - useful for testing
PT Interferon agonists and in treatment or diagnosis
PS Disclosure; fig 4; 30pp; French.
CC This recombinant human alpha interferon (IFN) receptor protein is
useful for the testing of IFN agonists and for treatment and diag-
nosis of viral diseases and tumours. Antibodies raised against
this protein can be used for blocking the receptor when required,
CC eg where overexpression of alpha-IFN is harmful. The Abs are
CC also useful for eg drug targeting. Variants of the protein,
CC having residue 164 (Thr) replaced by Arg and an Asp inserted
CC between residues 479 and 480, are also useful.
SO Sequence 557 AA.

Query Match 100.0%; Score 2141; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 3.3e-185;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GKNLKSPOKVEVDIIDDNFILRMNRSDSEVGNTFSFDYOKTGMNMKILSGCONITSTK 60
Db 27 GKNLKSPOKVEVDIIDDNFILRMNRSDSEVGNTFSFDYOKTGMNMKILSGCONITSTK 86
OY 61 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEDSFTPRKAOIGPPEVHLEADKAIVIH 120
Db 87 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEDSFTPRKAOIGPPEVHLEADKAIVIH 146
OY 121 SPGRKDSVMMALDGLSFTYSLIMKNSGVEERIEIENIYSRRKIYKLSPEPTYCLKVKAL 180
Db 147 SPGRKDSVMMALDGLSFTYSLIMKNSGVEERIEIENIYSRRKIYKLSPEPTYCLKVKAL 206
OY 181 LTSKIGIYSPVHCITKTIVENELPPENIEVSQONONYLKWDTYANNMFOVOMLAFL 240
Db 207 LTSKIGIYSPVHCITKTIVENELPPENIEVSQONONYLKWDTYANNMFOVOMLAFL 266
OY 241 KRNPGNHLKXKQKIPDCENVTTCQCFPQNFQKIGITLLRVQASDGNNTSFSSEIKFPT 300
Db 267 KRNPGNHLKXKQKIPDCENVTTCQCFPQNFQKIGITLLRVQASDGNNTSFSSEIKFPT 326
OY 301 EIOAFLLPVENIRSLSDSFHIIYIGAPKOSGNTPVIOYPLIYEIIFMENTSNAERKIIIE 360
Db 327 EIOAFLLPVENIRSLSDSFHIIYIGAPKOSGNTPVIOYPLIYEIIFMENTSNAERKIIIE 386
OY 361 KKTDTVPNLKPLTYCYKARAHMTDEKLKSSVFSADACE 401
Db 387 KKTDTVPNLKPLTYCYKARAHMTDEKLKSSVFSADACE 427

RESULT 4
R14488
ID R14488 standard; Protein: 557 AA.
AC R14488;

DR 16-JAN-1992 (first entry)
DE Complete interferon-alpha/beta receptor.
KW IFN, autoimmune disease; graft rejection; histocompatibility.
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 437..457
FT domain /label= transmembrane
FT domain 458..557
FT domain /label= cytoplasmic
FN FR2657881.A.
PD 09-AUG-1991.
PE 05-FEB-1990; 001298.
PR 05-FEB-1990; FR-001298.
PA (EUBI-) LAB EURO BIOTECNO.
PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE.
PI Toyey M, Uze G.
DR WPJ; 91-319778/44.
DR N-PSDB; Q14240.
PT New water-soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus, Behcet's disease, aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.
PS Disclosure: Page 47; 52pp; French.
CC The invention covers derivatives of the interferon-alpha and/or beta receptor obtained by deleting the transmembrane and cytoplasmic domains of the native receptor or by substitution. Potentially immunogenic epitopes are eliminated and the deriv. can be secreted from transformed cells. Soluble deriv.s block the activity of IFN alpha/beta and can be used to treat autoimmune diseases or to inhibit graft rejection. See also Q14239.
CC Sequence 557 AA;

Query Match 100.0%; Score 2141; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 3.3e-185;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKNLSPKQVEVDIIDDNFILRMNSDESVDGNTVTSFDYQKGMNWKISGCONITSTK 60
DB 27 GKNLSPKQVEVDIIDDNFILRMNSDESVDGNTVTSFDYQKGMNWKISGCONITSTK 86
QY 61 CNFSSKLNTVEEIKLRRAKENTSSWEVDSTPFPRKAQIGPEVHLEADKAIYIHI 120
DB 87 CNFSSKLNTVEEIKLRRAKENTSSWEVDSTPFPRKAQIGPEVHLEADKAIYIHI 146
QY 121 SPGRKDSYMAALDGLSFTYSLIMKNSGVEERINISYRHKIYKLSPEYTCCLKVAAL 180
DB 147 SPGRKDSYMAALDGLSFTYSLIMKNSGVEERINISYRHKIYKLSPEYTCCLKVAAL 206
QY 181 LTSWKIGVSPVHCIKTIVENELPPENIEVSQONVYLVKMDTYANMTFOVOMLAFL 240
DB 207 LTSWKIGVSPVHCIKTIVENELPPENIEVSQONVYLVKMDTYANMTFOVOMLAFL 266
QY 241 KRNPGNHLKXKQIPDCENVTTCQVFPONVFOKGIYLLRVOASDGNNTSFSSEIKFDT 300
DB 267 KRNPGNHLKXKQIPDCENVTTCQVFPONVFOKGIYLLRVOASDGNNTSFSSEIKFDT 326
QY 301 EIOAFLLPVPENIRSLSDSFHIYIGAPKOSGNTPIYIDYPIIYEIIFEMNTSNAERKIIIE 360
DB 327 EIOAFLLPVPENIRSLSDSFHIYIGAPKOSGNTPIYIDYPIIYEIIFEMNTSNAERKIIIE 386
QY 361 KKTDTVPNLKPLTVYCVKARAHTMDEKLKSSVFSADACE 401
DB 387 KKTDTVPNLKPLTVYCVKARAHTMDEKLKSSVFSADACE 427

RESULT 5
R28496
ID R28496 standard; Protein; 557 AA.
AC R28496;
DT 31-MAR-1993 (first entry)
DE Sequence of a soluble form of the interferon (IFN) receptor with a high affinity for IFN-alpha and -beta.
KW Interferon receptor; alpha-interferon; beta-interferon..

OS Synthetic.
FN WO9218626.A.
PD 29-OCT-1992.
PE 17-APR-1991; F00318.
PR 17-APR-1991; WO-F00318.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE.
PI Toyey M, Uze G.
DR WPJ; 92-382110/46.
DR N-PSDB; Q30533.
PT Water soluble polypeptide(s) strongly bind interferon(s) alpha and beta - useful as immunosuppressants, for treating autoimmune diseases and transplant rejection
PS Claim 3; Fig 2; 58pp; English.
CC DNA encoding the water-soluble polypeptide with a high affinity for IFN-alpha and -beta is isolated by PCR, using appropriate oligonucleotides as primers and cloned cDNA as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and -beta receptor (Q30533), was incubated with oligos Q30534 and Q30535. R28496 represents the complete receptor. R28495 lacks the transmembrane and cytoplasmic domains. Both forms bind IFN in the same way as antibodies so are immunosuppressants e.g. for treating autoimmune diseases and graft rejection. They lack the toxic side-effects of known immunosuppressants such as steroids.
CC Sequence 557 AA;

Query Match 100.0%; Score 2141; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 3.3e-185;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKNLSPKQVEVDIIDDNFILRMNSDESVDGNTVTSFDYQKGMNWKISGCONITSTK 60
DB 27 GKNLSPKQVEVDIIDDNFILRMNSDESVDGNTVTSFDYQKGMNWKISGCONITSTK 86
QY 61 CNFSSKLNTVEEIKLRRAKENTSSWEVDSTPFPRKAQIGPEVHLEADKAIYIHI 120
DB 87 CNFSSKLNTVEEIKLRRAKENTSSWEVDSTPFPRKAQIGPEVHLEADKAIYIHI 146
QY 121 SPGRKDSYMAALDGLSFTYSLIMKNSGVEERINISYRHKIYKLSPEYTCCLKVAAL 180
DB 147 SPGRKDSYMAALDGLSFTYSLIMKNSGVEERINISYRHKIYKLSPEYTCCLKVAAL 206
QY 181 LTSWKIGVSPVHCIKTIVENELPPENIEVSQONVYLVKMDTYANMTFOVOMLAFL 240
DB 207 LTSWKIGVSPVHCIKTIVENELPPENIEVSQONVYLVKMDTYANMTFOVOMLAFL 266
QY 241 KRNPGNHLKXKQIPDCENVTTCQVFPONVFOKGIYLLRVOASDGNNTSFSSEIKFDT 300
DB 267 KRNPGNHLKXKQIPDCENVTTCQVFPONVFOKGIYLLRVOASDGNNTSFSSEIKFDT 326
QY 301 EIOAFLLPVPENIRSLSDSFHIYIGAPKOSGNTPIYIDYPIIYEIIFEMNTSNAERKIIIE 360
DB 327 EIOAFLLPVPENIRSLSDSFHIYIGAPKOSGNTPIYIDYPIIYEIIFEMNTSNAERKIIIE 386
QY 361 KKTDTVPNLKPLTVYCVKARAHTMDEKLKSSVFSADACE 401
DB 387 KKTDTVPNLKPLTVYCVKARAHTMDEKLKSSVFSADACE 427

RESULT 6
R42635
ID R42635 standard; Protein; 557 AA.
AC R42635;
DT 20-APR-1994 (first entry)
DE Human interferon receptor.
KW IFN-R; extracellular domain; monoclonal antibody; viral infection; cell proliferation; allograft rejection; systemic lupus erythematosus; psoriasis; multiple sclerosis; Behcet's disease; aplastic anaemia; immunodeficiency; measles virus; interferon-alpha-beta.
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 1..436

FT /label= extracellular_domain
 FT /note= "soluble, immunogenic form of IFN-R"
 PD EP-56387-A.
 PD 06-OCT-1993.
 PD 31-MAR-1992; 400902.
 PR 31-MAR-1992; EP-400902.
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
 PI Benoit P, Maguire D, Meyer F, Plavec I, Tovey MG;
 DR WPI: 95-312951/40.
 DR P-PSDB: R42635.
 PT Monoclonal antibody to human interferon type-I receptor - having
 PT neutralising activity against human type I interferon, used for
 PT therapy and diagnosis
 PS Disclosure: Fig 3: 21pp; English.
 CC Monoclonal antibodies produced against soluble forms of the human
 CC interferon alpha-beta receptor based on the full-length human IFN-R
 CC sequence are claimed. The antibodies are useful for treatment and
 CC prophylaxis of disorders involving cell proliferation and/or viral
 CC infection.
 CC Sequence 557 AA:
 SQ
 Query Match 100.0%; Score 2141; DB 1; Length 557;
 Best Local Similarity 100.0%; Pred. No. 3.3e-185;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GKNLSPQVEVDIIDNFIILRNRSDESGVNTFSFDYOKTGMDNMKISGCONITSTR 60
 DB 27 GKNLSPQVEVDIIDNFIILRNRSDESGVNTFSFDYOKTGMDNMKISGCONITSTR 86
 QY 61 CNFSSKLNVYEIKLRIRAEKENTSSWYEVDSFTFPRKAQIGPPEVHLEADKAIVIH 120
 DB 87 CNFSSKLNVYEIKLRIRAEKENTSSWYEVDSFTFPRKAQIGPPEVHLEADKAIVIH 146
 QY 121 SPGTDSVMALDGLSTFTSLIIMKNSGVEERIENTYSHRKIKLSPEPTYCLKVKAL 180
 DB 147 SPGTDSVMALDGLSTFTSLIIMKNSGVEERIENTYSHRKIKLSPEPTYCLKVKAL 206
 QY 181 LTSWKIGVSPVHCITKTVENELPPENIEVSQNONVYLKMDTYANMTFOVOMLHAF 240
 DB 207 LTSWKIGVSPVHCITKTVENELPPENIEVSQNONVYLKMDTYANMTFOVOMLHAF 266
 QY 241 KRNPGNHLYKMKQIPDCENKTKTCVFPQNVFOKGIYLLRVQASDGNNTSFWSEIEKFD 300
 DB 267 KRNPGNHLYKMKQIPDCENKTKTCVFPQNVFOKGIYLLRVQASDGNNTSFWSEIEKFD 326
 QY 301 EIOAFLLPPVFNIRLSDSFHIYIGAPKOSGNTPIODYPLIYEIIFMENTSNAEKIIE 360
 DB 327 EIOAFLLPPVFNIRLSDSFHIYIGAPKOSGNTPIODYPLIYEIIFMENTSNAEKIIE 386
 QY 361 KKTDTVPNLKPLTVYCVKARAHMTDEKLKNSVFSDAVCE 401
 DB 387 KKTDTVPNLKPLTVYCVKARAHMTDEKLKNSVFSDAVCE 427
 RESULT 7
 ID R75356 standard; Protein: 557 AA.
 AC R75356;
 DT 16-OCT-1995 (first entry)
 DE Human IFN receptor.
 KW IFN receptor; Interferon receptor; Interferon-alpha;
 OS Interferon-beta; monoclonal antibody; immunomodulator; AIDS.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT 1..436
 FT domain /label= Extracellular_domain
 PD WO9507716-A.
 PD 23-MAR-1995.
 PD 16-SEP-1994; E03114.
 PR 17-SEP-1993; EP-402279.
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
 PI Benizri EJ, Tovey MG;

DR WPI: 95-131187/17.
 DR N-PSDB: Q86458.
 PT Compn. of monoclonal antibodies against interferon receptor -
 PT useful as immuno:modulator, eg. for treating AIDS
 PS Disclosure: Fig.3a-2b; 105pp; English.
 CC The amino acid sequence of human interferon class I receptor is
 CC given in R75356. A recombinant soluble form of the extracellular
 CC domain of this receptor (R71723) has been used to raise
 CC immunomodulatory monoclonal antibodies.
 CC Sequence 557 AA:
 SQ
 Query Match 99.8%; Score 2137; DB 1; Length 557;
 Best Local Similarity 99.8%; Pred. No. 7.6e-185;
 Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GKNLSPQVEVDIIDNFIILRNRSDESGVNTFSFDYOKTGMDNMKISGCONITSTR 60
 DB 27 GKNLSPQVEVDIIDNFIILRNRSDESGVNTFSFDYOKTGMDNMKISGCONITSTR 86
 QY 61 CNFSSKLNVYEIKLRIRAEKENTSSWYEVDSFTFPRKAQIGPPEVHLEADKAIVIH 120
 DB 87 CNFSSKLNVYEIKLRIRAEKENTSSWYEVDSFTFPRKAQIGPPEVHLEADKAIVIH 146
 QY 121 SPGTDSVMALDGLSTFTSLIIMKNSGVEERIENTYSHRKIKLSPEPTYCLKVKAL 180
 DB 147 SPGTDSVMALDGLSTFTSLIIMKNSGVEERIENTYSHRKIKLSPEPTYCLKVKAL 206
 QY 181 LTSWKIGVSPVHCITKTVENELPPENIEVSQNONVYLKMDTYANMTFOVOMLHAF 240
 DB 207 LTSWKIGVSPVHCITKTVENELPPENIEVSQNONVYLKMDTYANMTFOVOMLHAF 266
 QY 241 KRNPGNHLYKMKQIPDCENKTKTCVFPQNVFOKGIYLLRVQASDGNNTSFWSEIEKFD 300
 DB 267 KRNPGNHLYKMKQIPDCENKTKTCVFPQNVFOKGIYLLRVQASDGNNTSFWSEIEKFD 326
 QY 301 EIOAFLLPPVFNIRLSDSFHIYIGAPKOSGNTPIODYPLIYEIIFMENTSNAEKIIE 360
 DB 327 EIOAFLLPPVFNIRLSDSFHIYIGAPKOSGNTPIODYPLIYEIIFMENTSNAEKIIE 386
 QY 361 KKTDTVPNLKPLTVYCVKARAHMTDEKLKNSVFSDAVCE 401
 DB 387 KKTDTVPNLKPLTVYCVKARAHMTDEKLKNSVFSDAVCE 427
 RESULT 8
 ID W21805 standard; Protein: 434 AA.
 AC W21805;
 DT 23-SEP-1997 (first entry)
 DE Spliced-deleted interferon alpha-receptor form 1.
 KW Interferon alpha-receptor; IFNAR.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT domain 1..427
 FT /label= Extracellular_domain
 FT /note= "comprises amino acids 1-427 of the
 FT transmembrane IFNAR"
 FT 428..434
 FT domain /label= S_domain
 PD AU9475977-A.
 PD 11-MAY-1995.
 PD 20-OCT-1994; 075977.
 PR 24-OCT-1993; IL-107378.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PA (ABRA/) ABRAMOVICH C.
 PI Abramovich C, Ratovitski E, Revel M;
 DR WPI: 95-200634/27
 PT New mammalian soluble interferon alpha-receptor forms - used for
 PT inhibiting, modulating or modifying the activities of interferon(s)
 PS Example 2; Fig 7; 46pp; English.
 CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 1
 CC (W21805) is characterised by a new domain (S) which follows an

CC end-deleted extracellular domain when compared to transmembrane
CC IFNAR (W21804). There is no transmembrane domain. The amino acid
CC sequence is predicted from a cDNA clone (see also T73520) Obtd.
CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR
CC splice-deleted forms 1 and 2 (see also W21806) probably regulate
CC the response of human cells to IFNs, either by acting as IFN
CC antagonists or by regulating the activity of the multiple IFN
CC subtypes. They can be expressed in host cells and used to inhibit,
CC modulate or modify the activities of IFNs alpha and beta in cells,
CC tissues and organisms, or for diagnostic purposes.
SQ Sequence 434 AA;

Query Match 99.8%; Score 2136; DB 1; Length 434;
Best Local Similarity 99.8%; Pred. No. 6.5e-185;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GKNLSPQKVEVDIIDDNFILRMNRSDESGVNFSEFDYQKGMNWKLSGCONITSTK 60
DB 27 GKNLSPQKVEVDIIDDNFILRMNRSDESGVNFSEFDYQKGMNWKLSGCONITSTK 86
QY 61 CNFSSLKLNLYEEIKLRIRAEKENTSSWYEVDSEFTPRKAOIGPEVHLEADKAIYIHI 120
DB 87 CNFSSLKLNLYEEIKLRIRAEKENTSSWYEVDSEFTPRKAOIGPEVHLEADKAIYIHI 146
QY 121 SPGRKDSVMALDGLSFTSYLLIMKNSSGVEERIENTYSRHKIKYLSPEPTYCLKVKAL 180
DB 147 SPGRKDSVMALDGLSFTSYLLIMKNSSGVEERIENTYSRHKIKYLSPEPTYCLKVKAL 206
QY 181 LFSWKIGVSPVHCIKTTVENELPPENIEVSQVONQVYLKMDTYANMTFOVOMLAFL 240
DB 207 LFSWKIGVSPVHCIKTTVENELPPENIEVSQVONQVYLKMDTYANMTFOVOMLAFL 266
QY 241 KRPNGNHLKWKQIIPDCENKVTQCVFPONVFOKGIYLLRVOASDGNNTSFWSEIKFDT 300
DB 267 KRPNGNHLKWKQIIPDCENKVTQCVFPONVFOKGIYLLRVOASDGNNTSFWSEIKFDT 326
QY 301 EIOAFLLPVPFNIRSLSDSFHYIGAPKOSGNTPIYIDYPLIYEIIFWENTSNAERKITE 360
DB 327 EIOAFLLPVPFNIRSLSDSFHYIGAPKOSGNTPIYIDYPLIYEIIFWENTSNAERKITE 386
QY 361 KKTDTVPNLKPLTVYCVKARAHMTDEKLKNSVFSADVCE 401
DB 387 KKTDTVPNLKPLTVYCVKARAHMTDEKLKNSVFSADVCE 427

RESULT 9

ID W21804 standard; Protein; 557 AA.
AC W21804;
DT 23-SEP-1997 (first entry)
DE Transmembrane Interferon alpha-receptor.
KW Interferon alpha-receptor; IFNAR.
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 1..436
FT /label= Extracellular_domain
FT /label= 437
FT /label= Transmembrane_domain
FT /label= 458
FT domain 458..557
FT /label= Intracellular_domain
FN A09475977-A.
PD 11-MAY-1995.
PE 20-OCT-1993; 075977.
PR 24-OCT-1993; IL-107378.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (ABRA/) ABRAMOVICH C.
PI Abramovich C, Ratovitski E, Revel M;
DR WPI: 95-200634/27.
PT New mammalian soluble interferon alpha-receptor forms - used for
PS Inhibiting, modulating or modifying the activities of interferon(s)
CC Human transmembrane Interferon alpha receptor (IFNAR) (W21804)

CC Includes a 21-amino acid transmembrane region. Novel, splice-
CC deleted IFNAR forms 1 (W21805) and 2 (W21806) have been detected
CC that lack this transmembrane domain. These, soluble non-membrane
CC bound polypeptides can be expressed in host cells and used to
CC inhibit, modulate or modify the activities of interferons alpha
CC and beta in cells, tissues and organisms, or for diagnostic
CC purposes.
SQ Sequence 557 AA;

Query Match 99.8%; Score 2136; DB 1; Length 557;
Best Local Similarity 99.8%; Pred. No. 9.4e-185;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GKNLSPQKVEVDIIDDNFILRMNRSDESGVNFSEFDYQKGMNWKLSGCONITSTK 60
DB 27 GKNLSPQKVEVDIIDDNFILRMNRSDESGVNFSEFDYQKGMNWKLSGCONITSTK 86
QY 61 CNFSSLKLNLYEEIKLRIRAEKENTSSWYEVDSEFTPRKAOIGPEVHLEADKAIYIHI 120
DB 87 CNFSSLKLNLYEEIKLRIRAEKENTSSWYEVDSEFTPRKAOIGPEVHLEADKAIYIHI 146
QY 121 SPGRKDSVMALDGLSFTSYLLIMKNSSGVEERIENTYSRHKIKYLSPEPTYCLKVKAL 180
DB 147 SPGRKDSVMALDGLSFTSYLLIMKNSSGVEERIENTYSRHKIKYLSPEPTYCLKVKAL 206
QY 181 LFSWKIGVSPVHCIKTTVENELPPENIEVSQVONQVYLKMDTYANMTFOVOMLAFL 240
DB 207 LFSWKIGVSPVHCIKTTVENELPPENIEVSQVONQVYLKMDTYANMTFOVOMLAFL 266
QY 241 KRPNGNHLKWKQIIPDCENKVTQCVFPONVFOKGIYLLRVOASDGNNTSFWSEIKFDT 300
DB 267 KRPNGNHLKWKQIIPDCENKVTQCVFPONVFOKGIYLLRVOASDGNNTSFWSEIKFDT 326
QY 301 EIOAFLLPVPFNIRSLSDSFHYIGAPKOSGNTPIYIDYPLIYEIIFWENTSNAERKITE 360
DB 327 EIOAFLLPVPFNIRSLSDSFHYIGAPKOSGNTPIYIDYPLIYEIIFWENTSNAERKITE 386
QY 361 KKTDTVPNLKPLTVYCVKARAHMTDEKLKNSVFSADVCE 401
DB 387 KKTDTVPNLKPLTVYCVKARAHMTDEKLKNSVFSADVCE 427

RESULT 10

ID R71723 standard; Protein; 436 AA.
AC R71723;
DT 16-OCT-1995 (first entry)
DE IFN receptor extracellular domain.
KW IFN receptor; Interferon receptor; Interferon-alpha;
KW Interferon-beta; monoclonal antibody; Immunomodulator; AIDS.
OS Homo sapiens.
PN M09507716-A.
PD 23-MAR-1995.
PE 16-SEP-1994; E03114.
PR 17-SEP-1993; EP-402279.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
PI Benizri EJ, Tovey MG;
DR WPI: 95-131187/17.
DR N-PSDB: 086457.
FT Compn. of monoclonal antibodies against Interferon receptor -
PT useful as immuno-modulator, eg. for treating AIDS
PS Disclosure: Fig. 2A-2B; 105pp; English.
CC A recombinant soluble form of the human interferon class I receptor
CC protein extracellular domain, given in R71723, was expressed in
CC either E. coli or COS cell hosts. The protein was used to raise
CC immunomodulatory monoclonal antibodies.
SQ Sequence 436 AA;

Query Match 99.6%; Score 2137; DB 1; Length 436;
Best Local Similarity 99.3%; Pred. No. 1.5e-184;
Matches 398; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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OY 1 GKNLSPQKVEVDIIDDNFILRMNRSDSVGNVTFSPDYOKTGMDNMIKLSGCCNITSTK 60
DB 27 GKNLSPQKVEVDIIDDNFILRMNRSDSVGNVTFSPDYOKTGMDNMIKLSGCCNITSTK 86
OY 61 CNFSSLKLNVEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLAEADKAIVIH 120
DB 87 CNFSSLKLNVEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLAEADKAIVIH 146
OY 121 SPGRKDSVMALDGLSTFTSYLLIMKNSGVEERIENTYSRHKIKYLSPEITCYLKVAA 180
DB 147 SPGRKDSVMALDGLSTFTSYLLIMKNSGVEERIENTYSRHKIKYLSPEITCYLKVAA 206
OY 181 LTSWKIGYSPVHCIKTTVENELPPENIEVSQONVYLMKDYTYANMTFOVOMLHAF 240
DB 207 LTSWKIGYSPVHCIKTTVENELPPENIEVSQONVYLMKDYTYANMTFOVOMLHAF 266
OY 241 KRNPNHLYKKWQIPDCENKTTQCVFQONVFOKGIYLLRVQASDGNNTSFWSSEIKFDT 300
DB 267 KRNPNHLYKKWQIPDCENKTTQCVFQONVFOKGIYLLRVQASDGNNTSFWSSEIKFDT 326
OY 301 EIOAFLLPVPENIRSLDSFHIYIGAPKOSGNTPIYIDYPLIYEIIFEMENTSNAERK 360
DB 327 EIOAFLLPVPENIRSLDSFHIYIGAPKOSGNTPIYIDYPLIYEIIFEMENTSNAERK 386
OY 361 KRTDVTVPNLKPLTVYCVKARAHMTDEKLNKSSVSDACE 401
DB 387 KRTDVTVPNLKPLTVYCVKARAHMTDEKLNKSSVSDACE 427

RESULT 11
W21806
ID W21806 standard; Protein: 496 AA.
AC W21806;
DE 23-SEP-1997 (first entry)
DE Spliced-deleted interferon alpha-receptor form 2.
DE Interferon alpha-receptor; IFNAR.
OS Homo sapiens.
FH Key location/Qualifiers
FT domain 1, 419
FT /label= Extracellular-domain
FT /note= "comprises amino acid residues 1-413 and
FT 422-427 of transmembrane IFNAR"
FT domain 420, 496
FT /label= Intracellular domain
FT /note= "comprises amino acids 481-557 of
FT transmembrane IFNAR"
FT FT
PD A09475977-A.
PD 11-MAY-1995.
PF 20-OCT-1994: 075977.
PF 24-OCT-1993: IL-107378.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (ABRAV) ABRAMOVICH C.
PI Abramovich C, Ratovitski E, Revel M;
DR WPI: 95-20063/27.
DR New mammalian soluble interferon alpha-receptor forms - used for
PT inhibiting, modulating or modifying the activities of interferon(s)
PS Example 3; Fig 7: 46pp. English.
CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 2
CC (W21806) is characterized by a double deletion when compared to
CC transmembrane IFNAR (W21804). The extracellular domain is
CC shortened by 6 amino acid residues and is followed by a truncated
CC intracellular domain. There is no transmembrane region. The amino
CC acid sequence is predicted from a cDNA clone (see also J73521) obtd.
CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR
CC splice-deleted forms 1 (see also W21805) and 2 may regulate the
CC response of human cells to IFNs, either by acting as IFN
CC antagonists or by regulating IFN activities. They can be expressed
CC in host cells and used to inhibit, modulate or modify the
CC activities of IFNs alpha and beta in cells, tissues and organisms,
CC or for diagnostic purposes.
CC Sequence 496 AA.

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Query Match 97.3%; Score 2084; DB 1; Length 496;
Best Local Similarity 97.8%; Pred. No. 3,9e-180;
Matches 392; Conservative 0; Mismatches 1; Indels 8; Gaps 1;

OY 1 GKNLSPQKVEVDIIDDNFILRMNRSDSVGNVTFSPDYOKTGMDNMIKLSGCCNITSTK 60
DB 27 GKNLSPQKVEVDIIDDNFILRMNRSDSVGNVTFSPDYOKTGMDNMIKLSGCCNITSTK 86
OY 61 CNFSSLKLNVEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLAEADKAIVIH 120
DB 87 CNFSSLKLNVEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLAEADKAIVIH 146
OY 121 SPGRKDSVMALDGLSTFTSYLLIMKNSGVEERIENTYSRHKIKYLSPEITCYLKVAA 180
DB 147 SPGRKDSVMALDGLSTFTSYLLIMKNSGVEERIENTYSRHKIKYLSPEITCYLKVAA 206
OY 181 LTSWKIGYSPVHCIKTTVENELPPENIEVSQONVYLMKDYTYANMTFOVOMLHAF 240
DB 207 LTSWKIGYSPVHCIKTTVENELPPENIEVSQONVYLMKDYTYANMTFOVOMLHAF 266
OY 241 KRNPNHLYKKWQIPDCENKTTQCVFQONVFOKGIYLLRVQASDGNNTSFWSSEIKFDT 300
DB 267 KRNPNHLYKKWQIPDCENKTTQCVFQONVFOKGIYLLRVQASDGNNTSFWSSEIKFDT 326
OY 301 EIOAFLLPVPENIRSLDSFHIYIGAPKOSGNTPIYIDYPLIYEIIFEMENTSNAERK 360
DB 327 EIOAFLLPVPENIRSLDSFHIYIGAPKOSGNTPIYIDYPLIYEIIFEMENTSNAERK 386
OY 361 KRTDVTVPNLKPLTVYCVKARAHMTDEKLNKSSVSDACE 401
DB 387 KRTDVTVPNLKPLTVYCVKARAHMTDEKLNKSSVSDACE 419

RESULT 12
W52296
ID W52296 standard; Protein: 325 AA.
AC W52296;
DE 23-JUN-1998 (first entry)
DE CRFB4 protein.
DE CRFB4; Interleukin-10; IL-10; IL-10 receptor; allograft rejection;
KW vaccine; photosensitivity; inflammation; autoimmune disease;
KW septic shock; immune response; organ rejection; gene therapy.
OS Homo sapiens.
PN W09802542-A1.
PD 22-JAN-1998.
PF 17-JUL-1997; U12455.
PF 17-JUL-1996; US-683743.
PA (DYNE-) UNIV NEW JERSEY.
PA Kotenko SV, Pestka S;
DR WPI: 98-110590/10.
DR N-PSDB: V19874.
DR New recombinant DNA - comprises sequences encoding interleukin-10
PT and CRFB4 linked to operator, useful, e.g. preventing allograft
PT rejection
PS Claim 2; Page 7: 79pp; English.
CC This sequence is the human CRFB4 sequence, DNA encoding it is used in the
CC recombinant DNA (I) of the invention. (I) comprises a sequence (S1)
CC encoding the interleukin-10 (IL-10) receptor (IL10R) and a sequence (S2)
CC encoding CRFB4, both operably linked to expression control sequences.
CC Cells containing (I) may be used to identify agonists/antagonists of
CC IL-10. Agonists are potentially useful, e.g. for preventing allograft
CC rejection, as vaccine adjuvants, for treatment of photosensitivity,
CC inflammation, autoimmune disease and septic shock, while antagonists are
CC potentially useful for increasing immune responses against tumors,
CC viruses, bacteria and parasites (especially intracellular pathogens) and
CC for preventing organ rejection. A vector containing (I) is used to
CC restore, e.g. by gene therapy, IL-10 sensitivity to a cell that expresses
CC a dysfunctional IL10R and is able to bind IL-10 but not to transduce a
CC signal. Antisense CRFB4 sequences (especially ribozymes), can inhibit
CC IL-10 activity in cells. Antibodies specific for CRFB4 are used to
CC measure and localise CRFB4, for diagnosis of defective IL-10 activity.
CC Fragments of (I) are used as primers or probes to assay CRFB4-specific

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CC RNA. Agonists/antagonists may be administered parenterally, orally or
CC rectally especially by intravenous injection or directly into a tumour or
CC allograft.
SQ Sequence 325 AA;

Query Match 10 3%; Score 220; DB 1; Length 325;
Best Local Similarity 30.0%; Pred. No. 4.3e-12;
Matches 61; Conservative 41; Mismatches 89; Indels 12; Gaps 7;

OY 7 POKVEVDIIDNFIILRNKSDSESVGNTFSFDYOKTGMNWKLSGCONITSTKCNFSSL 66
DB 24 PEVVRNNSVNFKNILDMESAPAKGNLITFAQ----LSRIRQDKCMNTLTTECPSS- 79
OY 67 KLVNVEIKLRIRAE-KENTSSWYEVDSFTPRKAOIGPEVHLAE-EDKAIYIHISPGT 124
DB 79 -LSKYDHTLVRVAFEDSHDWNI-TECPVDITIIIGPGQVEVLADLHHRFLAPK 136
OY 125 KDSV-WMALDGL--SFTYSLILTKNSSGVBERIENTYSRKIKYKSPETTYCLKVKAALL 181
DB 137 ENYEETWTKNKNYSWTYNNQYKNGCTDEKFOITPOYDEFEVLNLEPMTTYCVQVKGFLP 196
OY 182 TSWKIGVSPVHCITKTVERELP 204
DB 197 DRNKGEMSEPVCEQTHDETVP 219

RESULT 13

R75782
ID R75782 standard; Protein: 332 AA.
AC R75782;
DT 13-NOV-1995 (first entry)
DE IFN-gamma receptor beta-subunit.
KW Interferon-gamma receptor beta subunit; mufn;
OS Interferon-gamma-antagonist.
FH Mus sp.
FT Key Location/Qualifiers
FT Peptide 1..18
FT domain /label= Sig_peptide
FT domain 19..242
FT domain /label= Extracellular_domain
FT domain 243..266
FT domain /label= Transmembrane_anchoring_domain
FT domain 267..332
FT domain /label= Cytoplasmic_domain
FN W09516036-A.
PD 15-JUN-1995.
PF 07-DEC-1994; U14277.
PR 09-DEC-1993; US-164596.
PA (AGDE/) AGOET M.
PA (BOEH/) BOEHNI R.
PA (HEMW/) HEWNI S.
PI Aguet M, Boehni R, Hemml S;
DR WPI: 95-224321/29.
DR N-PSDB: Q90808.
PT Novel Interferon gamma receptor beta chain polypeptide - for
PT treatment of inflammatory bowel disease and liver damage
PS Claim 3, Fig.2a; 86pp; English.
CC The IFN-gamma receptor beta-subunit encoded by a cDNA clone derived
CC from mouse B-cells is given in R75782. Recombinant beta-subunit,
CC prel. with the transmembrane anchoring domain deleted or
CC inactivated and with the cytoplasmic domain deleted, may be
CC used to treat pathological conditions associated with endogenous
CC IFN-gamma production.
SQ Sequence 332 AA;

Query Match 9.3%; Score 199; DB 1; Length 332;
Best Local Similarity 30.1%; Pred. No. 3.5e-10;
Matches 65; Conservative 38; Mismatches 81; Indels 32; Gaps 12;
OY 4 LKSPKVEVDIIDNFIILRNKSDSE-----VGNTFSFDYOKTGMNWKLSGCONITSTKCN 54

DB 29 LAAPLNRLHLXNDQILTWEPSSNDPRVYQVEVSF-----IDGSHRLLEPNCT 82
OY 55 NITSTKCNFESS--LKNVYE-EIKLRIRAEKEN-TSSWYEVDSFTPRKAOIGPEE-VH 108
DB 83 DITERKCDLTGGGRKRLPPEPTEFLVRVAKGNLTSKWVLEPQHYENYVGGPKNIS 142
OY 109 LEAEDKAIYIHISPGTKDSVMALDGLSFTYSLILTKNSSGVBERIENTYSRKIKY- 166
DB 143 VPPKGSLVHHSPPFD-----VFHGAFFQYLVHVMENSETQOEQVEGPFKNSYVLGNL 197
OY 167 SPETTYCLKVKAAL-LTSWKI--GVSPVHCITKT 198
DB 198 KPYRYCLOTEQOLILKNKIRPHGLLSVNSCHETT 233

RESULT 14

W79159
ID W79159 standard; Protein: 553 AA.
AC W79159;
DT 20-NOV-1998 (first entry)
DE Zcytor7 cytokine receptor polypeptide.
KW Zcytor7; cytokine receptor; ligand-binding polypeptide; kidney; pancreas;
KW type 2 cytokine receptor family; CRF2; prostate tissue; nervous tissue;
KW agonist; cell proliferation; cell differentiation; renal disease; human;
KW neutral disease; pancreatic disease.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Domain 30..250
FT Domain /note= "extracellular (ligand-binding) domain;
FT Domain /note= "sequence claimed in claim 1"
FT Domain 275..553
FT Domain /note= "intracellular domain"
FN W09837193-A1.
PD 27-AUG-1998.
PF 18-FEB-1998; U03029.
PR 02-OCT-1997; US-943087.
PR 20-FEB-1997; US-803305.
PA (ZYMO) ZYMOGENETICS INC.
PI Adams RL, Fairrah TM, Jellmeberg AC, Kho CJ, Lok S,
PI Whitmore TE;
DR WPI: 98-480798/41.
DR N-PSDB: V57515.
PT Novel human Zcytor7 DNA encodes a type 2 cytokine receptor - useful
PT for treating renal, neural, pancreatic and prostatic diseases
PS Claim 1; Pages 55-59; 72pp; English.
CC This represents the Zcytor7 cytokine receptor. Zcytor7 is a ligand-
CC binding receptor polypeptide and is a novel member of the type 2 cytokine
CC receptor family (CRF2). An expression vector containing the Zcytor
CC polynucleotide, operably linked to transcription promoter, a sequence
CC encoding a transmembrane and intracellular domain, or both, and a
CC recombinant production of the polypeptide. The sequences can be used to
CC study the Zcytor7 gene and to isolate ligands binding to it. Zcytor7 is
CC preferentially expressed in the kidney, pancreas, prostate or nervous
CC tissue. Agonists of Zcytor7 can be used to stimulate proliferation and
CC differentiation of cell in these organs. The antagonists and agonists can
CC also be used in the treatment of renal, neural, pancreatic and prostate
CC diseases.
SQ Sequence 553 AA;

Query Match 8.4%; Score 180; DB 1; Length 553;
Best Local Similarity 20.6%; Pred. No. 3.8e-08;
Matches 85; Conservative 75; Mismatches 166; Indels 86; Gaps 15;

OY 4 LKSPKVEVDIIDNFIILRNKSDSESVGNTFSFDYOKTGMNWKLSGCONITSTKCN 62
DB 37 LKRPANITFLSNMKNVLDGMPPEGLQGVKAYIVQYFYGKKMLNSECNNINRTYCD 96
OY 63 FSSIKLVNVEIKLRIRAE-KENTSSWYEVDSFTPRKAOIGPEVHLAEEDKAIYIHIS 121
DB 97 LSAETSDYEHQYAYAKAIWGTGKSMWESGAFYFLEQIOPPEVALUTDEKSTSYVLT 156

Search completed: June 1, 2000, 00:40:12
Job time: 20018 sec

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OY 122 PGT-----DSVMALDGLSTYSLIMKNSGVEERENIYSRKIYK--LSPET 170
DB 157 APERKKNRPEDLPVSMOQIYSNLKYNVSLNTKSNRTWSQCVTN---HTLVLMLEPNT 212
OY 171 TYCLKVAALLTSMKIGVSPVHCITVENE-----LPPENIEVSQONQY 218
DB 213 LYCVHSEFVGPDPRAOPSEKOCARFLKDQSSSEFKAIIFWVLP---ISITV----- 264
OY 219 VLKMDYVANTFOV-OMLHAFLRNPGNHLKWKQIIPDCENVKTQCVFPQNVFGKIY 277
DB 264 -----FLPSVVGYSIYRIYHKGKHPANLI-----LIGNEFDKRPF 301
OY 278 LLRQASDGNNTSWSEIKFTEI---QAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP 334
DB 302 V---PAEKIYINFTLINISDQSKSHQDMSLGKSSDVSLSND-----POPSGNLR 349
OY 335 VIQDYPLIYK-----IFWENTSNAEKIIEKTDV--TVPNKLPLIYV 376
DB 350 PPOEEEVKHLGVASHLMETFCDESENETGTSFTQOESLSTRTIPDKTVIEX 401
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RESULT 15

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R71035
ID R71035 standard; Protein; 337 AA.
AC R71035;
DT 11-OCT-1995 (first entry)
DE Human IFN-gamma accessory factor-1.
KM Interferon-gamma; AF-1; tumour.
OS Homo sapiens.
PN M09505847-A.
PD 02-MAR-1995.
PE 22-AUG-1994; U09438.
PR 20-AUG-1993; US-110119.
PA (UYNE-) UNIV NEW JERSEY.
PI Cook JR, Donnelly RJ, Emanuel S, Kolenko S, Mariano TM;
PI Pestka S, Schwartz B, Soh J;
DR MPI; 95-106679/14.
DR N-PSDB; Q84697.
PT Suppressing tumours in mammals with accessory factor 1 (AF-1) -
PT for interferon gamma, specifically induction of class I HLA
PT antigens. Including use of AF-1 DNA in gene therapy
PS Disclosure; Fig 21A; 114pp; English.
CC The sequence is that of human interferon-gamma accessory factor-1.
CC Incorporation of AF-1 into immune and tumour cells re-establishes
CC normal function with elimination of malignant cells.
SQ Sequence 337 AA;
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Query Match 6.98; Score 148; DB 1; Length 337;

Best Local Similarity 22.28; Pred. No. 1.4e-05; Matches 62; Conservative 49; Mismatches 104; Indels 64; Gaps 13;

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OY 4 LKSPQKVEVDIIDNFIKRW-----NRSDSVGNVTFFSPDYOKTGMNWKLS----- 52
DB 30 LPAPQHPKIRILYNAEQVLSWEPVALSNSTRPVYQVQFKYTDK-----WFTADIMSIGV 84
OY 52 GCONITSTKCNFSS-----LKLNYEEIKLRIRAKENT-SSWYEVDSTFPRKAOI 102
DB 85 NCTQITATECDFTLAASAGPMDPNV---TLRLRAELGALHSAMYTMPFOHYRNVTV 140
OY 103 GPPEVHLE--AEDKAIVIHISPGTKDSVMALDGLSTYSLIMKNSGVEERENIYS 159
DB 141 GPPE-NIEVTPGEGSLIIRFSSPDIADTSAF---FCYVHYWE--KGGIQOVKGPR 193
OY 160 RHKLY--KLSPETTYCLKVKAALLTS---WKIGVSPVHCITVENEELPPENIEVS 213
DB 194 SNSISLDNLKPSRYCLOVQOLMLNKSNIIFRGHLSISCYETMADASTELQOVILISV 253
OY 214 -----QONQYVLKMDYTYANMTFOVO 234
DB 254 GTFSLSLVLAGACFFVLVKYRGLIKYWFHPPTPIQIE 292
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 1, 2000, 00:00:26 ; Search time 23.82 Seconds

(without alignments)
243,048 Million cell updates/sec

Title: US-09-240-675-2_COPY_27_427

Perfect score: 2141
Sequence: 1 GKNLSPQKVEVDIIDNFT.....AHTMDEKLKSSVSDAVCE 401

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 145308 seqs, 14437401 residues

Total number of hits satisfying chosen parameters: 145308

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 08
Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/prodata/1/1aa/5a_COMB.pep.*
2: /cgn2_6/prodata/1/1aa/5b_COMB.pep.*
3: /cgn2_6/prodata/1/1aa/6_COMB.pep.*
4: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep.*
5: /cgn2_6/prodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2141	100.0	434	1	US-08-328-256-11 Sequence 11, Appl
2	2141	100.0	436	2	US-08-307-588-2 Sequence 2, Appl
3	2141	100.0	557	1	US-08-328-256-10 Sequence 10, Appl
4	2141	100.0	557	1	US-08-471-454-2 Sequence 2, Appl
5	2141	100.0	557	2	US-08-466-974-2 Sequence 2, Appl
6	2141	100.0	557	2	US-08-471-453-2 Sequence 2, Appl
7	2141	100.0	557	2	US-08-307-588-4 Sequence 4, Appl
8	2089	97.6	496	1	US-08-328-256-12 Sequence 12, Appl
9	490.5	22.9	202	4	PCT-US94-14277-3 Sequence 4, Appl
10	438.5	20.3	200	4	PCT-US94-14277-4 Sequence 4, Appl
11	220	10.3	325	2	US-08-683-743-4 Sequence 4, Appl
12	199	9.3	332	4	PCT-US94-14277-2 Sequence 4, Appl
13	192	9.0	223	4	PCT-US94-14277-6 Sequence 6, Appl
14	180	8.4	553	2	US-08-943-087-2 Sequence 2, Appl
15	180	8.4	553	2	US-08-943-087-14 Sequence 14, Appl
16	180	8.4	553	2	US-08-943-087-15 Sequence 15, Appl
17	180	8.4	553	2	US-08-943-087-18 Sequence 18, Appl
18	180	8.4	553	2	US-08-943-087-20 Sequence 20, Appl
19	180	8.4	553	2	US-08-943-087-22 Sequence 22, Appl
20	180	8.4	553	2	US-08-943-087-24 Sequence 24, Appl
21	180	8.4	553	2	US-08-943-087-26 Sequence 26, Appl
22	180	8.4	553	2	US-08-943-087-28 Sequence 28, Appl
23	180	8.4	553	2	US-08-943-087-30 Sequence 30, Appl
24	180	8.4	553	2	US-08-943-087-32 Sequence 32, Appl
25	180	8.4	553	2	US-08-943-087-34 Sequence 34, Appl
26	180	8.4	553	2	US-08-943-087-36 Sequence 36, Appl
27	180	8.4	553	2	US-08-943-087-38 Sequence 38, Appl
28	180	8.4	553	2	US-08-943-087-40 Sequence 40, Appl
29	180	8.4	553	2	US-08-943-087-42 Sequence 42, Appl

30	180	8.4	553	2	US-08-943-087-44 Sequence 44, Appl
31	180	8.4	553	2	US-08-943-087-46 Sequence 46, Appl
32	180	8.4	553	2	US-08-943-087-48 Sequence 48, Appl
33	172.5	8.1	221	2	US-08-943-087-56 Sequence 56, Appl
34	167.5	7.8	221	2	US-08-943-087-54 Sequence 54, Appl
35	166.5	7.8	221	2	US-08-943-087-50 Sequence 50, Appl
36	165.5	7.7	221	2	US-08-943-087-52 Sequence 52, Appl
37	163.5	7.6	221	2	US-08-943-087-60 Sequence 60, Appl
38	160.5	7.5	221	2	US-08-943-087-58 Sequence 58, Appl
39	146	6.8	337	4	PCT-US94-14277-8 Sequence 8, Appl
40	142	6.6	574	2	US-08-906-713-2 Sequence 2, Appl
41	118	5.5	489	4	PCT-US93-11110-1 Sequence 1, Appl
42	118	5.5	489	5	5221789-1 Patent No. 5221789
43	118	5.5	1005	2	US-08-469-537A-103 Sequence 103, App
44	117.5	5.5	2214	1	US-08-727-034-7 Sequence 7, Appl
45	110	5.1	2213	1	US-08-727-034-3 Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-328-256-11
; Sequence 11, Application US/08328256
; Patent No. 5643749
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: ABRAMOVICH, Carolina
; APPLICANT: RANOVITSKI, Edward
; TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEWMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,256
; FILING DATE: 24-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 107378
; FILING DATE: 24-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: REVEL-13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 434 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-328-256-11
Query Match 100.0%; Score 2141; DB 1; Length 434;
Best Local Similarity 100.0%; Pred. No. 9.4e-214;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GKNLSPQKVEVDIIDNFTILKMRSDSEVGAVTFSFDYOKTGMDNWKILSGCNTITSK 60

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Db 27 GKNLSPQKVEVDIIDNFIILRNRSDESIGNVTFSEFDYQKGTGMNMIKLSGCCNITSTK 86
Qy 61 CNFSSLKLANYEELIKLIRAKENTSSWYEDSFTFPRKAQIGPPEVHLAEADKAIYIH 120
Db 87 CNFSSLKLANYEELIKLIRAKENTSSWYEDSFTFPRKAQIGPPEVHLAEADKAIYIH 146
Qy 121 SPGKDSVMALDGLSFTYSLLIMKNSGVEERIEINYSRHKIKLSPETTYCLAKYKAL 180
Db 147 SPGKDSVMALDGLSFTYSLLIMKNSGVEERIEINYSRHKIKLSPETTYCLAKYKAL 206
Qy 181 LTSRKIGVSPVHCITKTVENELPPENIEVSQNONVYLKMDYTYANMTFOVOMLHAF 240
Db 207 LTSRKIGVSPVHCITKTVENELPPENIEVSQNONVYLKMDYTYANMTFOVOMLHAF 266
Qy 241 KRNGNHLKWKQIPDCENYKTCVFPQNVFOKGIYLLRQASDGNNTSFWSEIKFDT 300
Db 267 KRNGNHLKWKQIPDCENYKTCVFPQNVFOKGIYLLRQASDGNNTSFWSEIKFDT 326
Qy 301 EIOAFLLPVFNIRSLSDSFHITGAPKOSGNTPIODYPLIYEIIFWENTSNAEKIIE 360
Db 327 EIOAFLLPVFNIRSLSDSFHITGAPKOSGNTPIODYPLIYEIIFWENTSNAEKIIE 386
Qy 361 KKTDTVPNLKPLTYVCVKARAHMTDEKLNKSVFSDAVCE 401
Db 387 KKTDTVPNLKPLTYVCVKARAHMTDEKLNKSVFSDAVCE 427

RESULT 2
US-08-307-588-2
Sequence 2, Application US/08307588
Patent No. 5919453
GENERAL INFORMATION:
APPLICANT: BENOIT, Patrick
APPLICANT: MEYER, Francois
APPLICANT: MAGUIRE, Deborah
APPLICANT: PLAVEC, Ivan
APPLICANT: TOVEY, Michael G.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
TITLE OF INVENTION: INTERFERON
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00770
FILING DATE: 30-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92400902.0
FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 17283/117/GUPL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-307-588-2

Query Match 100.0%; Score 2141; DB 2; Length 436;
Best Local Similarity 100.0%; Pred. No. 9,5e-214;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GKNLSPQKVEVDIIDNFIILRNRSDESIGNVTFSEFDYQKGTGMNMIKLSGCCNITSTK 60
Db 27 GKNLSPQKVEVDIIDNFIILRNRSDESIGNVTFSEFDYQKGTGMNMIKLSGCCNITSTK 86
Qy 61 CNFSSLKLANYEELIKLIRAKENTSSWYEDSFTFPRKAQIGPPEVHLAEADKAIYIH 120
Db 87 CNFSSLKLANYEELIKLIRAKENTSSWYEDSFTFPRKAQIGPPEVHLAEADKAIYIH 146
Qy 121 SPGKDSVMALDGLSFTYSLLIMKNSGVEERIEINYSRHKIKLSPETTYCLAKYKAL 180
Db 147 SPGKDSVMALDGLSFTYSLLIMKNSGVEERIEINYSRHKIKLSPETTYCLAKYKAL 206
Qy 181 LTSRKIGVSPVHCITKTVENELPPENIEVSQNONVYLKMDYTYANMTFOVOMLHAF 240
Db 207 LTSRKIGVSPVHCITKTVENELPPENIEVSQNONVYLKMDYTYANMTFOVOMLHAF 266
Qy 241 KRNGNHLKWKQIPDCENYKTCVFPQNVFOKGIYLLRQASDGNNTSFWSEIKFDT 300
Db 267 KRNGNHLKWKQIPDCENYKTCVFPQNVFOKGIYLLRQASDGNNTSFWSEIKFDT 326
Qy 301 EIOAFLLPVFNIRSLSDSFHITGAPKOSGNTPIODYPLIYEIIFWENTSNAEKIIE 360
Db 327 EIOAFLLPVFNIRSLSDSFHITGAPKOSGNTPIODYPLIYEIIFWENTSNAEKIIE 386
Qy 361 KKTDTVPNLKPLTYVCVKARAHMTDEKLNKSVFSDAVCE 401
Db 387 KKTDTVPNLKPLTYVCVKARAHMTDEKLNKSVFSDAVCE 427

RESULT 3
US-08-328-256-10
Sequence 10, Application US/08328256
Patent No. 5643748
GENERAL INFORMATION:
APPLICANT: REVEL, Michel
APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
TITLE OF INVENTION: PREPARATION AND USE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: REVEL-13
REFERENCE/DOCKET NUMBER: 25,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197

TELEFAX: 207-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-328-256-10

Query Match 100.0%; Score 2141; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 1.4e-213;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKLLKSPQKVEVDIIDNFIKRNRSDESGVNTFSFDYOKTGMNWKISGCONITSTK 60
DB 27 GKRLKSPQKVEVDIIDNFIKRNRSDESGVNTFSFDYOKTGMNWKISGCONITSTK 86
QY 61 CNFSSKLNYEEIKLRIRAEKENTSSWYEVDSFTPRKAQIGPPEVHLEADKAIVIH 120
DB 87 CNFSSKLNYEEIKLRIRAEKENTSSWYEVDSFTPRKAQIGPPEVHLEADKAIVIH 146
QY 121 SPQTKSYVMALDGLSFTYSLLIMKNSSGVEERIENTYSHKIKYKSPETTYCLKYKAL 180
DB 147 SPQTKSYVMALDGLSFTYSLLIMKNSSGVEERIENTYSHKIKYKSPETTYCLKYKAL 206
QY 181 LFSMKIGVSPVHCITTYENELPPENIEVSQONONYVLKMDTYANMTFOYQMLHAF 240
DB 207 LFSMKIGVSPVHCITTYENELPPENIEVSQONONYVLKMDTYANMTFOYQMLHAF 266
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QY 301 EIOAFLLPVFNIRSLDSFHIYIGAPKOSGNTPVIODYPLIYEIIFWENTSNAERKII 360
DB 327 EIOAFLLPVFNIRSLDSFHIYIGAPKOSGNTPVIODYPLIYEIIFWENTSNAERKII 386
QY 361 KKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSADACE 401
DB 387 KKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSADACE 427

RESULT 4
US-08-471-454-2
Sequence 2, Application US/08471454
Patent No. 5731169
GENERAL INFORMATION:
APPLICANT: MOGENSEN, Knud E.
APPLICANT: UZE, Gilles
APPLICANT: LUTFALLA, Georges
APPLICANT: GRESSER, Ion
TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P. C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,454
FILING DATE: 06-JUN-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-454-2

Query Match 100.0%; Score 2141; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 1.4e-213;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKLLKSPQKVEVDIIDNFIKRNRSDESGVNTFSFDYOKTGMNWKISGCONITSTK 60
DB 27 GKRLKSPQKVEVDIIDNFIKRNRSDESGVNTFSFDYOKTGMNWKISGCONITSTK 86
QY 61 CNFSSKLNYEEIKLRIRAEKENTSSWYEVDSFTPRKAQIGPPEVHLEADKAIVIH 120
DB 87 CNFSSKLNYEEIKLRIRAEKENTSSWYEVDSFTPRKAQIGPPEVHLEADKAIVIH 146
QY 121 SPQTKSYVMALDGLSFTYSLLIMKNSSGVEERIENTYSHKIKYKSPETTYCLKYKAL 180
DB 147 SPQTKSYVMALDGLSFTYSLLIMKNSSGVEERIENTYSHKIKYKSPETTYCLKYKAL 206
QY 181 LFSMKIGVSPVHCITTYENELPPENIEVSQONONYVLKMDTYANMTFOYQMLHAF 240
DB 207 LFSMKIGVSPVHCITTYENELPPENIEVSQONONYVLKMDTYANMTFOYQMLHAF 266
QY 241 KRNPGHLYKWKQIPDCENKKTQCVFPQNVFGKGYLLRVQASDGNNTSFMSEEEKFDT 300
DB 267 KRNPGHLYKWKQIPDCENKKTQCVFPQNVFGKGYLLRVQASDGNNTSFMSEEEKFDT 326
QY 301 EIOAFLLPVFNIRSLDSFHIYIGAPKOSGNTPVIODYPLIYEIIFWENTSNAERKII 360
DB 327 EIOAFLLPVFNIRSLDSFHIYIGAPKOSGNTPVIODYPLIYEIIFWENTSNAERKII 386
QY 361 KKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSADACE 401
DB 387 KKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSADACE 427

RESULT 5
US-08-466-974-2
Sequence 2, Application US/08466974
Patent No. 5861258
GENERAL INFORMATION:
APPLICANT: MOGENSEN, Knud E.
APPLICANT: UZE, Gilles
APPLICANT: LUTFALLA, Georges
APPLICANT: GRESSER, Ion
TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P. C.
STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,974
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-466-974-2

Query Match 100.0%; Score 2141; DB 2; Length 557;
Best Local Similarity 100.0%; Pred. No. 1.4e-213;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKNLSPQKVEVDIDNFIILRNKSDSVGNVTFSFDYOKTGMWNKIKSGCONITSTK 60
DB 27 GKNLSPQKVEVDIDNFIILRNKSDSVGNVTFSFDYOKTGMWNKIKSGCONITSTK 86
QY 61 CNFSSKLNVYEEIKLIRAREKENTSSWYEVDSFTFPRKAOIGPEVHLEAEKAIYIHI 120
DB 87 CNFSSKLNVYEEIKLIRAREKENTSSWYEVDSFTFPRKAOIGPEVHLEAEKAIYIHI 146
QY 121 SPGTKDSVMALDGLSFTYSLIMKNSGVEERIENTIYSRHKIKYKLSPEYTYCLKYKAL 180
DB 147 SPGTKDSVMALDGLSFTYSLIMKNSGVEERIENTIYSRHKIKYKLSPEYTYCLKYKAL 206
QY 181 LTSWKIGVSPVHCIKTIVENELPPENIEVSQONQNTVLMKDYTYANMTFOVOMLHAF 240
DB 207 LTSWKIGVSPVHCIKTIVENELPPENIEVSQONQNTVLMKDYTYANMTFOVOMLHAF 266
QY 241 KRNPNHLYKMKOIPDCENKTTQCVFPQNVFOKGIYLLRVQASDGNNTSFWSEEEKFD 300
DB 267 KRNPNHLYKMKOIPDCENKTTQCVFPQNVFOKGIYLLRVQASDGNNTSFWSEEEKFD 326
QY 301 EIOAFLLPVPVFNIRSLSDSFHIYIGAPKOSGNTPIYDIYPLIYEIIFWENTSNAERKII 360
DB 327 EIOAFLLPVPVFNIRSLSDSFHIYIGAPKOSGNTPIYDIYPLIYEIIFWENTSNAERKII 386
QY 361 KRTDVPNLKPLTYCYVKARAHMDELNTSSVSFSDAVCE 401
DB 387 KRTDVPNLKPLTYCYVKARAHMDELNTSSVSFSDAVCE 427

RESULT 6
US-08-471-453-2
Sequence 2, Application US/08471453
Patent No. 5886153

GENERAL INFORMATION:
APPLICANT: MOGENSEN, Knud E.
APPLICANT: UZE, Gilles
APPLICANT: LUTFALLA, Georges
APPLICANT: GRESSER, Ion
TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,453
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-453-2

Query Match 100.0%; Score 2141; DB 2; Length 557;
Best Local Similarity 100.0%; Pred. No. 1.4e-213;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKNLSPQKVEVDIDNFIILRNKSDSVGNVTFSFDYOKTGMWNKIKSGCONITSTK 60
DB 27 GKNLSPQKVEVDIDNFIILRNKSDSVGNVTFSFDYOKTGMWNKIKSGCONITSTK 86
QY 61 CNFSSKLNVYEEIKLIRAREKENTSSWYEVDSFTFPRKAOIGPEVHLEAEKAIYIHI 120
DB 87 CNFSSKLNVYEEIKLIRAREKENTSSWYEVDSFTFPRKAOIGPEVHLEAEKAIYIHI 146
QY 121 SPGTKDSVMALDGLSFTYSLIMKNSGVEERIENTIYSRHKIKYKLSPEYTYCLKYKAL 180
DB 147 SPGTKDSVMALDGLSFTYSLIMKNSGVEERIENTIYSRHKIKYKLSPEYTYCLKYKAL 206
QY 181 LTSWKIGVSPVHCIKTIVENELPPENIEVSQONQNTVLMKDYTYANMTFOVOMLHAF 240
DB 207 LTSWKIGVSPVHCIKTIVENELPPENIEVSQONQNTVLMKDYTYANMTFOVOMLHAF 266
QY 241 KRNPNHLYKMKOIPDCENKTTQCVFPQNVFOKGIYLLRVQASDGNNTSFWSEEEKFD 300
DB 267 KRNPNHLYKMKOIPDCENKTTQCVFPQNVFOKGIYLLRVQASDGNNTSFWSEEEKFD 326
QY 301 EIOAFLLPVPVFNIRSLSDSFHIYIGAPKOSGNTPIYDIYPLIYEIIFWENTSNAERKII 360

DB 327 EIAFLLPPVFNIRSLSDSFHIYIGAPKOSGNTPVIODYPLIYEITFMENTSNAERKITE 386
OY 361 KKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSADAVE 401
DB 387 KKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSADAVE 427

RESULT 7
US-08-307-588-4
; Sequence 4, Application US/08307588
; Patent No. 5919453
; GENERAL INFORMATION:
; APPLICANT: BENOIT, Patrick
; APPLICANT: MEYER, Francois
; APPLICANT: MAGUIRE, Deborah
; APPLICANT: PLAVEC, Ivan
; APPLICANT: TOVEY, Michael G.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/307,588
; FILING DATE: 05-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00770
; FILING DATE: 30-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92400902.0
; FILING DATE: 31-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 17283/117/CUPL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-307-588-4

Query Match 100.0%; Score 2141; DB 2: Length 557;
Best Local Similarity 100.0%; Pred. No. 14e-213;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 GKNLSPKQVEVDIIDNFIILRNRSDESNGNTFSFDYOKTGMDNMIKLSGCONITSTR 60
DB 27 GKNLSPKQVEVDIIDNFIILRNRSDESNGNTFSFDYOKTGMDNMIKLSGCONITSTR 86
OY 61 GNFSSKLNYEEIKLIRAEKENTSSWYVDSFTPPKRAQIGPPEVHLAEADKAIYIHI 120
DB 87 GNFSSKLNYEEIKLIRAEKENTSSWYVDSFTPPKRAQIGPPEVHLAEADKAIYIHI 146
OY 121 SPGTGDSVMMALDGLSTYSLILMKNSSGVVEERENIYSHRKIKYKLSPEYTYCKAYVAL 180
DB 147 SPGTGDSVMMALDGLSTYSLILMKNSSGVVEERENIYSHRKIKYKLSPEYTYCKAYVAL 206

OY 181 LITSMKIGVSPVHCITTYENELPPPENIEVSQONONYLKMDTYANNTFOVQMLHAFI 240
DB 207 LITSMKIGVSPVHCITTYENELPPPENIEVSQONONYLKMDTYANNTFOVQMLHAFI 266
OY 241 KRNPQHNLKMKQIPDCENKTKQCVFPONVFOKGIYLLRVQASDGNNTSFMSEELKFDI 300
DB 267 KRNPQHNLKMKQIPDCENKTKQCVFPONVFOKGIYLLRVQASDGNNTSFMSEELKFDI 326
OY 301 EIAFLLPPVFNIRSLSDSFHIYIGAPKOSGNTPVIODYPLIYEITFMENTSNAERKITE 360
DB 327 EIAFLLPPVFNIRSLSDSFHIYIGAPKOSGNTPVIODYPLIYEITFMENTSNAERKITE 386
OY 361 KKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSADAVE 401
DB 387 KKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSADAVE 427

RESULT 8
US-08-328-256-12
; Sequence 12, Application US/08328256
; Patent No. 5643749
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: ABRAMOVICH, Carolina
; APPLICANT: RATOVIJSKI, Edward
; TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NETMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,256
; FILING DATE: 24-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 107378
; FILING DATE: 24-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: REVEL-13
; REFERENCE/DOCKET NUMBER: 25,618
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 496 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-328-256-12

Query Match 97.6%; Score 2089; DB 1: Length 496;
Best Local Similarity 98.0%; Pred. No. 2.9e-208;
Matches 393; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

DB 1 GKNLSPKQVEVDIIDNFIILRNRSDESNGNTFSFDYOKTGMDNMIKLSGCONITSTR 60
DB 27 GKNLSPKQVEVDIIDNFIILRNRSDESNGNTFSFDYOKTGMDNMIKLSGCONITSTR 86

Qy	61	CNFSLLKMYEEIKLRIRAKENTSSMYEVDSTPRKMOIGPPEVHLAEBAKAIYIH	130
Db	87	CNFSLLKMYEEIKLRIRAKENTSSMYEVDSTPRKMOIGPPEVHLAEBAKAIYIH	166
Qy	121	SPGRKDSYMAALDGLSTTYSLLIKRNSGVEERIENTYSRHKIYKLSPEPTYCLAKYAAAL	180
Db	147	SPGRKDSYMAALDGLSTTYSLLIKRNSGVEERIENTYSRHKIYKLSPEPTYCLAKYAAAL	206
Qy	181	LTSRKIGVSPVHGIKTTVENELPPENIEVSVOQNQYVYKMDTYANMFOVOMLAFL	240
Db	207	LTSRKIGVSPVHGIKTTVENELPPENIEVSVOQNQYVYKMDTYANMFOVOMLAFL	266
Qy	241	KRANGNHLKKKKQJPPDCENYVTCQCYFPQNYFOKGIYLLRQASDGNNTSFMSEIKFDT	300
Db	267	KRANGNHLKKKKQJPPDCENYVTCQCYFPQNYFOKGIYLLRQASDGNNTSFMSEIKFDT	326
Qy	301	EIOAFLLPPVENINISLSDSFHITYGAPKOSGNTFVIDYPLIYSEIIPMENTSNAERKIE	360
Db	327	EIOAFLLPPVENINISLSDSFHITYGAPKOSGNTFVIDYPLIYSEIIPMENTSNAERKIE	366
Qy	361	KKTDTYVNLKPLTYVCYKARAHMDLKNKSVFSFANVC 401	
Db	387	KKTDTYVNLKPLTYVCYKARAHMDLKNKSVFSFANVC 419	

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RESULT      9
PCT-US94-14277-3
: Sequence 3, Application PC/TUS9414277
GENERAL INFORMATION:
APPLICANT: Agnet, Michel
APPLICANT: Bonni, Ruth
APPLICANT: Hemmi, Silvio
TITLE OF INVENTION: Receptor Subunit Polypeptides
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy, disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: palin (genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14277
FILING DATE: 07-DEC-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/164596
FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 866PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 202 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US94-14277-3

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Query Match	22.98;	Score 490.5;	DB 4;	Length 202;
Best Local Similarity	48.58;	Pred. No. 4e-43;		
Matches 98;	Conservative 34;	Mismatches 69;	Indels 1;	Gaps 1;

[illegible]

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Query Match	20.58;	Score 438.5;	DB 4;	Length 200;
Best Local Similarity	44.08;	Pred. NO. 9.7e-38;		
Matches	88;	Conservative	35;	Mismatches 68;
				Indels 9;
				Gaps 3.

[illegible]

APPLICANT: Bohm, Ruth
APPLICANT: Hemmi, Silvio
TITLE OF INVENTION: Receptor Subunit Polypeptides
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14277
FILING DATE: 07-DEC-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/164596
FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 866PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US94-14277-6

Query Match 9.08; Score 192; DB 4; Length 223;
Best Local Similarity 29.68; Pred. No. 4.2e-12;
Matches 64; Conservative 37; Mismatches 83; Indels 32; Gaps 12;

QY 4 LKSPQXVEVDIIDNFIILNRNRSDES-----VGNVFESFDYKGTGMD-NMIXL--SGCQ 54
DB 10 LARLANRLHLYNDEQLTWEPSSNDPRVYQVEYSF-----IDGSHRLLEPCT 63
QY 55 NITSTKCNFS--LKLNYE-EIKLIRAEKEN-TSSWEVDSFTPRKAOIGPPE-VH 108
DB 64 DITETKCDLGGGRLKLFPHFTVFLNRAKRGULTSKMWGLEPFOHENTVGPKNIS 123
QY 109 LEADKAVIHISPGTDSVMALDGLSFTYSLIMKNSGVEERIEIYSRHKIY--KL 166
DB 124 VTPCKGSLVHIFSPFPD---VFHGATFOYLVHWEKSETOQOVEDGPEKSNISVLGNL 178
QY 167 SPETTYCLKVAAL-LTSMKI---GVYSPVHCITTT 198
DB 179 KPIRYVCLQTEROLILNKKIRPHGLLSNVSCHETT 214

RESULT 14
US-08-943-087-2
Sequence 2, Application US/08943087
Patent No. 5945511
GENERAL INFORMATION:
APPLICANT: Lok, S.I.
APPLICANT: Kuo, Choon J.
APPLICANT: Jelmeberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Patah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G.
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
US-08-943-087-2

Query Match 8.48; Score 180; DB 2; Length 553;
Best Local Similarity 20.68; Pred. No. 3.2e-10;
Matches 85; Conservative 75; Mismatches 166; Indels 86; Gaps 15;

QY 4 LKSPQXVEVDIIDNFIILNRNRSDES--VGFESFDYKGTGMD-NMIXL--SGCQ 62
DB 37 LKPRANITFLSIMKKNVLTQTPREGLVGYVTVYFIRGAKMLNKSCHRNINRYCD 96
QY 63 FSSILKLVYEEIKLRIRAEKEN-TSSWEVDSFTPRKAOIGPPEVHLEADKAVIYHIS 121
DB 97 LSAETSDYEHQYAKYKAWGTGCSKMAESGRYPLETOIGPEVALTTDEKSSISVLTL 156
QY 122 PGTK-----DSVMALDGLSFTYSLIMKNSGVEERIEIYSRHKIY--LSPET 170
DB 157 APEKWRNPEDLVSMQOITSNKLINVSVALNTSNRTWSQCVN-----HVLVLTWLEPNT 212
QY 171 TYCLKVAALLTSMKIGVYSPVHCITTYENE-----LPPENIEVSQONMY 218
DB 213 LYCVHVESFVGPBRPQPEKOCARTLKQOSEFAKIIFFVLP-----ISITV----- 264
QY 219 VLKMDITYAMTQY-QMLHAFILKRNPNLHYMKQIIPDCENKTKQCVPPQVFOKGIY 277
DB 264 ----FLFSVYMGYSIRYIHVGKREKHPANLI-----LTYGNEPDRFF 301
QY 278 LIRVQASDGNNTSFWSEIKFDEI---QALLPVPFNIRLSDSFHIYIGARKSGNTP 334
DB 302 V----PAKIVINFITINISDDSKISHODSLGKSSDVSLND-----PQSGNLR 349
QY 335 VIQDYPLIYEI-----LEWNTSNAERKIIETKTDV--TVPNLKPLTVY 376
DB 350 PQDEEVKHLGYASHLMEIFCDESETEGTSTQOESLSTRIPDPKTVLEY 401

RESULT 15
US-08-943-087-14

Sequence 14, Application US/08943087
Patent No. 5945511
GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Kho, Choon J.
APPLICANT: Jeimberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-943-087-14

Query Match 8.4%; Score 180; DB 2; Length 553;

Best Local Similarity 20.6%; Pred. No. 3.2e-10;

Matches 85; Conservative 75; Mismatches 166; Indels 86; Gaps 15;

OY 4 LKSPQVEVDIIDNFIILRNRSDESVG--NVTESFDYOKTGMDNWKILSGCONITSTKCN 62
DB 37 LRPANITILSLIMKKNVLOMTPEGLQGVAVTYTVQFYIGQKKWLKSECRNINRTYCD 96
OY 63 FSLKLVYEIEIKLIRI--EKENTSSMYEVSFTPRKAQIGPEVHLEAEKAVIHIS 121
DB 97 LSAETSDYEHQYAKYKALMGTKCSKMAESGRFPFLFQIGPEVALTTDEKISIVLT 156
OY 122 PGTK-----DSVMALDGLSFTYSLILKNSSGVEERINITYSRHKYK--LSPET 170
DB 157 APEKMKRNPEDLPVSMQOYISNLKYNVSVLNTKSNRTWSQCVTN---HTLVLTWLEPNT 212
OY 171 TYCLKAKALLSMKIGVSPVHCITVENE-----LPPENIEVSQONKY 218
DB 213 LCVHVESVPPGPRRAQSEKOCARTLKDQSEFRAKIIFWVLP-----ISTV----- 264
OY 219 VLKMDTYANMTQV--QMLHAFLEKRNPGNHLKXMKQIPDCENKTTQCVFPQNVFQGIY 277
DB 264 -----FLFSVMGYSIYRIHVGEKHPANLI-----LTYGNEFDKRF 301

OY 278 LLRVQASDGNNTSFMSEIEKFDTEI---QAFLLPVFNIRSLDSFHIYIGAPKOSGNT 334
DB 302 V---PAEKIVINFITLNTSDSKISHQDMSLGRSDVSLLND-----PQPSGNLR 349
OY 335 VIDDYPLIYEI-----IFMENTNAEKRIIEKTDV--TVPNLKPLTVY 376
DB 350 PQDEEVKHLGYASHLMEIFCDSEENTGTSTQOESISRTIPDKTVIEY 401

Search completed: June 1, 2000, 04:17:53
Job time: 15447 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 1, 2000, 00:37:00 ; Search time 64.83 seconds

(without alignments)
362,649 million cell updates/sec

Title: US-09-240-675-2_COPY_27_427

Perfect score: 2141
Sequence: 1 GKNLSPQKVEVDIIDDNFI.....ARTNDEKLNRKSVFSDAVCE 401

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 08
Listing first 45 summaries

Database : PIR_63:*

1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2141	100.0	557	2 A32694	interferon alpha/b
2	1384.5	64.7	560	2 S27387	interferon alpha r
3	966	45.1	590	2 A45283	interferon alpha/b
4	225	10.5	273	2 G01418	cytokine receptor
5	220	10.3	325	2 A47003	cytokine receptor
6	217.5	10.2	349	2 JC6311	interferon recepto
7	199	9.3	332	2 A49947	interferon gamma r
8	148	6.9	337	2 I38500	interferon gamma r
9	123.5	5.8	1443	2 I50600	neogenin - chicken
10	123	5.7	1375	2 T13822	frizzled gene prot
11	123	5.7	1526	2 T13823	frizzled gene prot
12	122.5	5.7	1451	2 S42167	190K protein - hum
13	118	5.5	489	2 A31555	interferon gamma r
14	118	5.5	981	2 S51604	receptor tyrosine
15	118	5.5	1005	2 S49015	receptor tyrosine
16	117.5	5.5	1283	2 A36080	insulin receptor p
17	117.5	5.5	1427	2 T31669	tumor suppressor p
18	117.5	5.5	1585	2 T19121	probable protein-t
19	117	5.4	817	2 A48721	titin, muscle - ch
20	115.5	5.4	658	2 T16040	hypothetical prote
21	115	5.4	26926	1 I38344	titin, cardiac mus
22	113	5.3	1450	2 A44027	165k myofibrillar
23	113	5.3	1615	2 B49502	protein-tyrosine-p
24	113	5.3	1767	2 A49502	protein-tyrosine-p
25	111.5	5.2	1896	2 T08851	Down syndrome cell
26	111	5.2	6831	2 T27934	hypothetical prote
27	111	5.2	6839	2 S57242	twitchin - Caenorh
28	111	5.2	7160	2 T27935	hypothetical prote
29	110.5	5.1	1898	2 S46216	leucocyte antigen-p
30	110	5.1	1912	2 A56178	protein-tyrosine-p

31	109.5	5.1	575	2 A49667	interleukin-10 rec
32	109	5.1	416	2 T25036	hypothetical prote
33	108.5	5.1	2033	2 T09123	hybrid receptor So
34	108.5	5.1	2215	2 T00348	Ir11 protein - mou
35	108	5.0	991	2 T78843	receptor protein-t
36	107.5	5.0	1372	2 A34157	insulin receptor p
37	105.5	4.9	878	1 A40091	interleukin-3 rece
38	105.5	4.9	1825	2 T32828	hypothetical prote
39	105	4.9	56	2 S41602	interferon alpha r
40	104.5	4.9	1447	2 A54100	tumor suppressor p
41	104	4.9	896	1 A35782	cytokine receptor
42	104	4.9	1239	1 A32579	neuroglial - fruit
43	104	4.9	2311	1 TVCHSR	kinase-related pro
44	103.5	4.8	896	2 I56563	interleukin-3 rece
45	103.5	4.8	1499	2 I50212	protein-tyrosine-p

ALIGNMENTS

RESULT 1

A32694
Interferon alpha/beta receptor precursor - human
C:Species: Homo sapiens (man)
C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 22-Oct-1999
C:Accession: A32694; S17112
R:Uze, G.; Lutfalla, G.; Gresser, I.
Cell 60, 225-234, 1990
A:Title: Genetic transfer of a functional human interferon alpha receptor into mouse
A:Reference number: A32694; MUID:90124632
A:Accession: A32694
A:Molecule type: mRNA
A:Residues: 1-557 <UZE>
A:Cross-references: GB:J03171; NID:q184645; PIDN:AA52730.1; PID:q306914
R:Lutfalla, G.
Submitted to the EMBL Data Library, July 1991
A:Description: The structure of the human interferon alpha/beta receptor gene.
A:Reference number: S17112
A:Accession: S17112
A:Molecule type: DNA
A:Residues: 1-16, 'A', 18-329, 'V', 343-557 <LUT>
A:Cross-references: EMBL:X60459; NID:q32671
C:Genetics:
A:Gene: GDB:IFNAR1; IFNAR; IFRC
A:Cross-references: GDB:120078; OMIM:107450
A:Map position: 21q22.1-21q22.1
A:Initons: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3
C:Keywords: cytokine receptor; glycoprotein; transmembrane protein
F:1-21/Domain: transmembrane #status predicted <TRN1>
F:437-455/Domain: transmembrane #status predicted <TRN2>
F:50,58,81,88,110,172,254,313,314,376,416,433,507,518,537/Binding site: carbohydrate

Query Match 100.0%; Score 2141; DB 2; Length 557;
Best Local Similarity 100.0%; Pred. No. 4, 2e-154;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GKNLSPQKVEVDIIDDNFIILRNRSDESYGVTSPFYOKTGMMNWKLSGCONITSTK 60
DB	27	GKNLSPQKVEVDIIDDNFIILRNRSDESYGVTSPFYOKTGMMNWKLSGCONITSTK 86
QY	61	CNFFSLKLVNVEIKLRRAERKENTSSWYEDSPFPKKAQIGPEVLEAEKAIIVHI 120
DB	87	CNFFSLKLVNVEIKLRRAERKENTSSWYEDSPFPKKAQIGPEVLEAEKAIIVHI 146
QY	121	SPGTRDSVWMLDGLSFTYSLILMKNSGVEERIEINYSRHKIYKLSPTTYCLVKVKAAL 180
DB	147	SPGTRDSVWMLDGLSFTYSLILMKNSGVEERIEINYSRHKIYKLSPTTYCLVKVKAAL 206
QY	181	LTSKILGYSPVHCIKITVENLPPENIEVSVQNONVYLKMDTYIYAMTQVQVLAFL 240
DB	207	LTSKILGYSPVHCIKITVENLPPENIEVSVQNONVYLKMDTYIYAMTQVQVLAFL 266

QY	241	KRGNHLYKKKQIPDCENKTKTCVFPVAVFKGIYLLRVQASDNNNTSFSSEIKFPT	300
Db	267	KRNGNHLYKKQIPDCENKTKTCVFPVAVFKGIYLLRVQASDNNNTSFSSEIKFPT	326
QY	301	EIOFLLPVPVNIJSLDSFHIYIGAKOSGNPVIODVPLIYEIIFFWNTSNAERKITE	360
Db	327	EIOFLLPVPVNIJSLDSFHIYIGAKOSGNPVIODVPLIYEIIFFWNTSNAERKITE	386
QY	361	KKTDTVPNLKPLTVYCVKRAAHMDEKLKSSVSFSDAYCE	401
Db	387	KKTDTVPNLKPLTVYCVKRAAHMDEKLKSSVSFSDAYCE	427

RESULT 2

interferon alpha receptor type 1 precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 13-Jan-1995 #sequenceRevision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S27387; S37370
C:Mouchel-Vielh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G.
FEBS Lett. 313: 255-259, 1992
A:Title: Specific antiviral activities of the human alpha interferons are determined at
A:Reference number: S27387; MIDB:93076908
A:Accession: S27387
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-560 <MOU>
A:Cross-references: EMBL:X68443; NID:g431; PIDN:CAA48484.1; PID:g432
A:Experimental source: MDBK cells
R:Lim, J.K.; Langer, J.A.
Biochim. Biophys. Acta 1173, 314-319, 1993
A:Title: Cloning and characterization of a bovine alpha interferon receptor.
A:Reference number: S33770; MIDB:93305725
A:Accession: S33770
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-421, 'V', 423-560 <LIM>
A:Cross-references: EMBL:U06320; NID:g163187; PIDN:AAA02571.1; PID:g163188
A:Experimental source: lung
C:Keywords: antiviral; cytokine receptor; transmembrane protein
F1-24/Domain: signal sequence <status predicted <Sig
F1-25-560/Product: interferon alpha receptor type 1 <status predicted <Mat>

	Score	DB 2:	Length
Query Match	64.78		560;
Best Local Similarity	64.08		
Best Local	5.5e-97;		
Conservative	65;		
Mismatches	78;		
Indels			5;
Gaps			5;

[illegible]

RESULT 3

Interferon alpha/beta receptor - mouse
C.Species: Mus musculus (house mouse)
C.Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C.Accession: A45283; I48423; I48424; I48425; I48426; I48427; I48428; I48429
R.Uze, G.; Lutfialla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992
A.Title: Behavior of a cloned murine interferon alpha/beta receptor expressed in homo
A.Reference number: A45283; MUID:9226522
#558;

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-590 <UE>
A:Cross-references: GB:M09641; NID:g194111; PIDN:AAA37890.1; PID:g194112
A:Note: sequence extracted from NCBI backbone (NCBIN:102354, NCBIP:102357)
R:Rutfalla, G.; Use, G.
Gene 148: 343-345; 1994
A:Title: Structure of the murine interferon alpha/beta receptor-encoding gene: high-f
A:Reference number: 148423; MUID:95047447
A:Accession: 148423
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 118-125 <RES>
A:Cross-references: EMBL:U06237; NID:g497103; PIDN:AAA65003.1; PID:g755810
A:Accession: 148424
A:Status: preliminary; translated from GB/EMBL/DDJ
A:Molecule type: DNA
A:Residues: 127-224 <RE2>
A:Cross-references: EMBL:U06238; NID:g497104; PIDN:AAC01749.1; PID:g755811
A:Accession: 148425
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 243-264 <RE3>
A:Cross-references: EMBL:U06239; NID:g497106; PIDN:AAA65004.1; PID:g510261
A:Accession: 148426
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 265-375 <RE4>
A:Cross-references: EMBL:U06240; NID:g497108; PIDN:AAA65005.1; PID:g510262
A:Accession: 148427
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 397-424 <RE5>
A:Cross-references: EMBL:U06241; NID:g497110; PIDN:AAA65006.1; PID:g755812
A:Accession: 148428
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 426-445 <RE6>
A:Cross-references: EMBL:U06242; NID:g497112; PIDN:AAA65007.1; PID:g755813
A:Accession: 148429
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 473-590 <RE7>
A:Cross-references: EMBL:U06244; NID:g497114; PIDN:AAA65008.1; PID:g510265
C:Gene: IFNAR
A:Gene: IFNAR
A:introns: 177/3; 331/1
C:Keywords: cytokine receptor; transmembrane protein

Query Match	45.18;	Score 966;	DB 2;	Length 590;
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Best Local Similarity 47.08, Freq. NO: 2.38 02,
Matches 192; Conservative 71; Mismatches 130; Indels 10; Gaps 4;

```

OY 1 GNNLKSFOQVEVDIIDDDNFI LRNRNSDESIGNVTFSDYQKTGM DNNTKLSGCONITSTK 60
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 26 GNNLKPPENIDVYIIDDDNTLTKWSHGSGMSVTFSEYRTKDEAKNLKVPEQHITTTTK 85

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0Y 61 CNFESLNLANYEETKLRIAREKEN-SSMYEVSFFPRKAOIGPEVLEEDAEAIYH 119
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 86 CEFSELLOTNYIKQFQVRYAREEGNSITSSMNEWDPIPTFTAHKSPPEVLEEDAEAIYH 145
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
0Y 120 ISPGTSDYVMALDGLSFTYSLLIWNKSSGVEERININYSRHKIYKLSPEPTYCLKRAA 179
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 146 ISPPGOGGNMALEKPEFSYTIIRIMQKSSDKKTINSTYVEKIPBELPETTYCLEVAKI 205
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
0Y 180 LLTSMKIGVYSPVHCITTYENELPREPENIEVSQONQNTVULKMDY-TYANMTFOYOMHA 238
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 206 HPSLKHSNSTVQICISTYANKMPBGNLQVDAQKSYVLKMDYIASADVLFRAQWLPBG 265
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
0Y 239 FLKRNPGNHLKWKQAPDCEWKNITTCQVPRQNTVQKGIYLLRYQASDGNNISFMSGEIKF 298
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 266 YSKSSSSGSHSKWMPRIPTCANVOQTHCFESQDPTVYGTGFFLHVAQSEGNHTSFMSGEIKF 325
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
0Y 299 DTELQALPPVFNIRLSFSFHUYIGARQOSQNTVYIDYPIYLIYIEMNTSNAEKI 358
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 326 DSOHNLPRPPVIVLTWMSDLELVYVNCODSTED-----GLNEIIMEMNTSNTKISM 378
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
0Y 359 IEKKTDTVLPKPLTYCYKARAHNIMDEKLNSVFSAYAGE 401
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 379 EKQGPETLKNLQPLVYQVQAR-LFRALLNTSNTSEKLE 420
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

```

RESULT 4
G01418
Cytokine receptor family II, member 4 - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
C:Accession: G01418
R:Jutfalla, G.
submitted to the EMBL Data Library, April 1994
A:Reference number: G06935
A:Accession: G01418
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-273 <LUT>
A:Cross-references: EMBL:U08988; NID:g571295; PID:g571296
C:Genetics:
A:Gene: GDB:CRPB4; CRF2-4
A:Cross-references: GDB:138168; OMIM:125889
A:Map position: 21q22.1-21q22.2
A:introns: 17/1; 58/2; 111/1; 166/3; 216/1

[illegible]

RESULT 5
A47003
cytokine receptor family class II protein CRF2.4 precursor - human
C.Species: Homo sapiens (man)
C.Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 10-Sep-1994
C.Accession: A47003

R: Lutfalla, G, Gardiner, K., Uze, G.
Genomics 16, 366-373, 1993
A: Title: A new member of the cytokine receptor gene family maps on chromosome 21 at
A: Reference number: A47003; MUID:93300510
A: Accession: A47003
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-325 <LUT>
A: Cross-references: GB:G17227; NID:g393378; PID:g393379
C: Genetics:
A: Map position: 21q
C: Keywords: transmembrane protein

	Query Match	10.3%	Score 220;	DB 2;	Length 325;
	Best Local Similarity	30.0%	Pred. No. 2,2e-09;		
	Matches	61;	Conservative	41;	Mismatches 89; Indels 12; Gaps 7;
QY	7	POKYEVDIIDDNFLIRKNRSDSEGVGNTPSPEDYQKTGMNWKILSGCONITSTKCNFSSL	66		
DB	24	PENVMNVSNVKNRIQIOMESPAFAKNNLTFTAAQ----	LSYRIFODKCMNTLTTECDFFS-	79	
QY	67	KLNYEEIKLRIRAE-KENTSSWYEVDSSTTPRKQAQIGPEYHLEA-EDKALVIHHSPT	124		
DB	79	LSKIGDITLTKRAFAEDHSDNVI-IFCPYDDITIIIGPGQVEYVLADSLMRFLAFLPI	136		
QY	125	KDSV-MMALDGL-SFTYSLLIWKNSSGVEERIEINYSHKIKYKLSPEYTYCLKAKALL	181		
DB	137	ENEYETMTMKNNYNSMTVNOYKMGKGTDEKFOITPOYDEVLRNLNEPMTTYCVQVGRGFLP	196		
QY	182	TSMKIGVYSPVHCITTYENELP	204		
DB	197	DRNKAGEWSEPVCEQOTTHDETVP	219		

```

RESULT      6
JC6311
interferon receptor-class II cytokine receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: JC6311
R:Gibbs, V.C.; Pennica, D.
Gene 186, 97-101, 1997
A:Title: CR2-4: isolation of cDNA clones encoding the human and mouse proteins
A:Reference number: JC6311
A:Accession: JC6311
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-349 <GIB>
A:Cross-references: GB:U53696

```

Query Match	10.2%	Score 217.5	DB 2	Length 349
Best Local Similarity	128.4%	Pred. No. 3.7e+09		
Matches	60	Conservative	45	Mismatches 79; Indels 27; Gaps 9
QY	7	POKVEVDIIDNDFILRWNRSDSEVGNVTFSEPDYQ--KTGMDMWIKLSCGONITSTKCNFS	64	
DB	24	PEKVMNNSVNFENKILQIOMEVPAFPKTNKILFTFAQYESRSPQD-----CKRTASTQCDGS	77	
QY	65	SLKLNVYEIKIRIAE--KENTSSMYEVDSPFPFKRAQGPBEVHLAEADKRVIHLS--	122	
DB	78	--HLSKYDGYTVRAVRAELADEHSEVWVN--TFQVEDTITIGPEMQQTESLAESIELETFSLP	134	
QY	122	-----PGTRDSYMAALDGL--SFYTSLLIKWNSSGVEERIEIENYSNHRKIYKLSPEPTYQ	174	
DB	135	QIENEPET-----WTLKNYIDSMAYRVQYWKNGTNEKFGVSPYDSEVLRLNDEPMTTYCI	189	
QY	175	KYKALLTSMKIGVSPYHCITYENELRP	205	
DB	190	QVQGFLLDONRTGEMSEPIC--ERTENDELTP	219	

RESULT 7
A49947
Interferon gamma receptor beta subunit - mouse
N:Alternate names: IFN-gamma R beta chain, IFN-gamma R species-specific cofactor; type I
C:Species: Mus musculus (house mouse)
C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A49947
R:Hemmi, S.; Bohni, R.; Stark, G.; Di Marco, F.; Agnet, M.
Cell 76, 803-810, 1994
A:Title: A novel member of the interferon receptor family complements functionality of
A:Reference number: A49947; MUID:94170381
A:Accession: A49947
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-332 <HEX>[†]
A:Cross-references: GEM>S59336; NID>9545841; PIDN>AAB30165.1; PID>9545842
A:Experimental source: early B-cell line Y16
A:Note: sequence extracted from NCBI backbone (NCBIN:145654, NCBIIP:145656)
C:Keywords: cytokine receptor

Query Match 9.3% Score 199 DB 2 Length 332;
 Best Local Similarity 30.1% Pred. No. 8.6e-08;
 Matches 65; Conservative 38; Mismatches 81; Indels 32; Gaps 12;

```

QY      4 LKSPQKEVDDIDDNFLIMNRSDS-----VGNTSEFSDYKGTGMD-NWIKL--SGGQ 54
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      29 LAAPLNPRHLHYNDEQILTWEPSPSSNDPRPVYQVEYSF-----IDGSHRLLEPNCT 82
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      55 NITSRKCNSS---IKLNYE-EIKLRIRAEKEN-TSSSYEVDSETPFKKAIGPPE-VH 108
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      83 DITETKCDLTGGGRLLKLPFTFLVRAKRGNLISKVGLGEPHOHENVNTVGPKNIS 142
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      109 LEADKKAIVIHISPGTKDSVMALDGLSEFTYSLLIWKNSGVEERLENITYSKKIY--KL 166
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      143 VPPGKSLVIHSPRPD-----VFHGATFOYLVIHYKESGEOQEGECPKNSIYLGNL 197
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      167 SPETTYCLKVKAAL-LTSWKI---GYSPVHCLIKTT 198
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      198 KPRVYCLOTEAOQLINKKRIKPHGLLSNVSCHETT 233
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
  
```

RESULT 8
Interferon gamma receptor accessory factor-1 precursor - human
I38500
C.Species: Homo sapiens (man)
C.Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 05-Nov-1999
C.Accession: I38500; I38501
R.Sch. J.: Donnelly, R.J.: Kotenko, S.; Mariano, T.M.; Cook, J.R.; Wang, N.; Emanuel, S.
Cell 76, 793-802, 1994
A.Title: Identification and sequence of an accessory factor required for activation of T
A.Reference number: A49946; MUID:94I70380
A.Accession: I38500
A.Molecule type: mRNA
A.Residues: 1-337 <RES>
A.Cross-References: EMBL:U05875; NID:g463549; PIDN:AAA16955.1; PID:g463550
A.Experimental source: clone pSKI
A.Accession: I38501
A.Molecule type: mRNA
A.Residues: 1-63, '0', 65-337 <RES>
A.Cross-References: EMBL:U05877; NID:g463551; PIDN:AAA16956.1; PID:g463552
A.Experimental source: clone pJS3
C.Genetics:
A.Map position: 21
C.Keywords: cytokine receptor

```
Query Match      6.98; Score 148; DB 2; Length 337;  
Best Local Similarity 22.2%; Pred.No.0.00062;  
Matches    62; Conservative   49; Mismatches 104; Indels   64; Gaps 13.  
  
QY      4 LKSPQKEVDIIDNFIILKH-----NRSDSGNGNTSFSDIOKTOMDMWIKLS----- 52  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
```

```

Db 30 LPAPQHPRILRYLNXYOVLMEPEVALSNSTRPVYRYVOFKYTDK-----WETADIMSIGV 84
QY 52 GCONITSKCNFSS-----LKNLYEEKLRIRAKENT--SWEYVDSFPPFRAQI 102
Db 85 NCTQTATCEDEFTTASPBPAGFPMDFNV---TLRLRELGALHSAMWTMPFOHRYNTV 140
QY 103 GPPEVHLE--AEDKATVIHISPTKDSVMALDGLSEFTYSLLIWNKSSGVEERIEIYIS 159
Db 141 GPPE-NIEWPGBESLIIRFSSPFDIADTSAF---FCYYVHWME--KSGIQGVKQFPR 193
QY 160 RHKTY--KLSEPTTYCLKVKALLTS---WKIGVYSPVHCIKTYVENELPPENIEVSV 213
Db 194 SNSISLDNWKFSRYCLOVOCAQLLMNKSNIFFVGHLSNISCYETMADASTELOQVILISV 253
QY 214 -----ONONYVLKMDYTYAANTFOVO 234
Db 254 GTFSLSLSTVLACGCEFFVLKRYGLIKYWFHPPSPILQIIE 292

```

RESULT 9
150600
neogenin - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996
C:Accession: 150600
R:Vilmetter, J.; Kayem, J.F.; Roman, J.M.; Dreyer, W.J.
J. Cell Biol. 127, 2009-2020, 1994
A:Title: Neogenin, an avian cell surface protein expressed during terminal neuronal d
A:Reference number: A5193; MUID:95105243
A:Accession: 150600
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 11443 <VIE>
A:Cross-references: EMBL:U07644; NID:9641965; PID:9641966

Query Match	5.8%	Score 123.5	DB 2	Length 1443
Best Local Similarity	22.0%	Pred. No. 0.32		
Matches	89	Conservative	60	Mismatches 194; Indels 61; Gaps 19;
QY	6	SPQKEVEIIDIDNEI-LRWNR--SDESGVNTFSEDOYKOTGMDNMIKLSGCONITSTKCN	62	
DB	427	ARDVAVATLVSRKIRFLRMTRTPVSDPGQGNLTIISFYTEG----	INREVEN-ISRPE	481
QY	63	FSSKLNTYEETKRIAREKENTSSNYEYDSTTPRRKAOIGPEVYHLEMDAIIYIHISP	122	
DB	482	TOVMIONLMPETVYVERVAQNRKHGE--SSAPKVAI--OPEVQLPGAPNIRAYAGS	537	
QY	123	GPKDSVMAL----DGLSFTYSLILMNKNSGVEERIENTSRKIKYKLSPEPTCYLKVA	178	
DB	538	PTSVYVYMETPISGNGEIONIKLYIMEKGQDSEODVAGLSYTTIGLKKYIEISRYVA	597	
QY	179	ALLTSMKIGVSPVHCIKTTVENELPPENIEVSQV--QNYLVKMDYIYANNTPVOYQWL	237	
DB	598	--YNNKGPVSQTQDVYVRLTSDVPSAAPONLTLEARNKSKIMLHQPPA-----	646	
QY	238	AFLRNPGHNL-----YKKKQIPDQENVKTTQCVQPNQFO--KGI-----YLRVQASD	285	
DB	646	-----GTHSQOITQKIRIKRYKRSKSDVTSVSGTQLFOLIEGEBCTENFRIAAMT	698	
QY	286	GNNT---SPWSEIKFDETEIOAFLLPV--ENISLSDSFHIYIGAPKQSGNTPIYQDY	339	
DB	699	VNGTGATQWVAEMFEESDLDESRAPEVPSLHVPLVTSI--VSWTPPENONI--VVRGY	756	
QY	340	PLIETIEIEMWNSNAER-KIIEKTKDYVYPNLKPITLYVCVKARA	382	
DB	757	ALGTGT-----GSPHAOTIKVDKORYTLENLDPSSHYYITLKA	796	

RESULT 10
T13822
frazzled gene protein - fruit fly (*Drosophila melanogaster*)
C/Species: *Drosophila melanogaster*

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T13822
 R:Kolodziej, P.A.; Tjime, L.; Mitchell, K.J.; Goodman, C.S.; Fried, S.; Jan, L.Y.; Jan, Cell 87, 197-204, 1996
 A:Title: Frazzled encodes a Drosophila member of the DCC immunoglobulin subfamily and is
 A:Reference number: 217780
 A:Accession: T13822
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1375 <KOL>
 A:Cross-references: EMBL:U71001; NID:g1621114; PID:g1621115; PIDN:AAC47314.1
 C:Genetics:
 A:Gene: frazzled
 C:Function:
 A:Map position: 2
 A:Description: may function in vivo as a receptor or component of a receptor mediating N

Query Match 5.7%; Score 123; DB 2; Length 1375;
 Best Local Similarity 16.3%; Pred. No. 0.33;
 Matches 101; Conservative 68; Mismatches 184; Indels 268; Gaps 22;

OY 1 GKLNKS-----PQVEVDIIDNFI-LRW-----NRSDESVG 31
 DB 448 GKPLDSGLQARLPSPQPDVAQIVKSRFTLSWEPLQAGDVVYVYVYKNNSEREQ 507
 OY 32 NTFSPFYQKGMNDWIKLSGQNTSTKCNFS-----LKLNYVEIKLR-----78
 DB 508 MWTSHDDQOVNIQSLPGRTYQFRVEANTFSGASAPLEVSTQPEVNIAGPPRNEG 567
 OY 78 -IRAENKTSWYE-----VD 92
 DB 568 YARSHKEIYKWEPTVTNGEILKRYVYSENDGADLYHDSALVLEAVLRLPHDTYVI 627
 OY 93 SFTPFRAQIG-----PPEVHLF-AEDKAIYIHISPTKDSVMALD 133
 DB 628 SVVPEFNNGMGDSAEIRKVTFSSTPEPPNNVTLEVTSSSITVHWPPEAEDRNGOIT 687
 OY 134 GLSTYSLLIKWSSGVEELENISRKIKYKSPETTYCLKYKAL-----TSWKIG 187
 DB 688 GYKIRYRK--FKDAPQYKSTPANI-RYFELSNLDRNAEYQKIAAMTVNGSGPTEENRA 744
 OY 188 VSPVHCIKTTVENELP-----PENIEVQONQNYVLKW 222
 DB 745 -----NLENDLDETQVPGKPIWISHPGANNIALHMGPPQHPEIKI--RNYVLGW 793
 OY 223 -----DY-----225
 DB 794 GRGIPDENTIELKETERYHILKNLESNDYVSLRARNVKGDPPIYDNIKTREDEPYDA 853
 OY 225 -----TYANMTFOVOMLHAFKLN-----PGNHLKWKQIPD 256
 DB 854 PTPLEVPVGLRAITWSSSIYVYWDIMLNKNQHVTDNRHYTVSYGIGTSNRRY-----909
 OY 257 CENVKTQCVPEPQVFOKGIYLLRVOASDGNNTSFNSEIKFDEIOAFLPVPFNIRSL 316
 DB 909 -HNTTDLNCMI-NDLRPTQYEFAYKVKGRRESSMSVLSNLTQVNPVTPP-----960
 OY 317 SDSFHIYIGAPKOSGNPIYQDYP-----LYEIIIFMENTSNAER-----KIEEKT 363
 DB 960 ---REVTVRLDENMPPTVYQWIPKHTLGOITGYNIYTTDTTKRDMDSVEAFAGEET 1016
 OY 364 DVTVPNLKPLTVYCVKARAHT 384
 DB 1017 MLMPLNKLPTTYTFKVOART 1037

RESULT 11
 T13823
 Frazzled gene protein, log isoform - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T13823

R:Kolodziej, P.A.; Tjime, L.; Mitchell, K.J.; Goodman, C.S.; Fried, S.; Jan, L.Y.; Jan, Cell 87, 197-204, 1996
 A:Title: Frazzled encodes a Drosophila member of the DCC immunoglobulin subfamily and
 A:Reference number: 217780
 A:Accession: T13823
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1526 <KOL>
 A:Cross-references: EMBL:U71002; NID:g1621116; PID:g1621117; PIDN:AAC47315.1
 C:Genetics:
 A:Gene: frazzled
 C:Function:
 A:Map position: 2

Query Match 5.7%; Score 123; DB 2; Length 1526;
 Best Local Similarity 16.3%; Pred. No. 0.38;
 Matches 101; Conservative 68; Mismatches 184; Indels 268; Gaps 22;

OY 1 GKLNKS-----PQVEVDIIDNFI-LRW-----NRSDESVG 31
 DB 599 GKPLDSGLQARLPSPQPDVAQIVKSRFTLSWEPLQAGDVVYVYVYKNNSEREQ 658
 OY 32 NTFSPFYQKGMNDWIKLSGQNTSTKCNFS-----LKLNYVEIKLR-----78
 DB 659 MWTSHDDQOVNIQSLPGRTYQFRVEANTFSGASAPLEVSTQPEVNIAGPPRNEG 718
 OY 78 -IRAENKTSWYE-----VD 92
 DB 719 YARSHKEIYKWEPTVTNGEILKRYVYSENDGADLYHDSALVLEAVLRLPHDTYVI 778
 OY 93 SFTPFRAQIG-----PPEVHLF-AEDKAIYIHISPTKDSVMALD 133
 DB 779 SVVPEFNNGMGDSAEIRKVTFSSTPEPPNNVTLEVTSSSITVHWPPEAEDRNGOIT 838
 OY 134 GLSTYSLLIKWSSGVEELENISRKIKYKSPETTYCLKYKAL-----TSWKIG 187
 DB 839 GYKIRYRK--FKDAPQYKSTPANI-RYFELSNLDRNAEYQKIAAMTVNGSGPTEENRA 895
 OY 188 VSPVHCIKTTVENELP-----PENIEVQONQNYVLKW 222
 DB 896 -----NLENDLDETQVPGKPIWISHPGANNIALHMGPPQHPEIKI--RNYVLGW 944
 OY 223 -----DY-----225
 DB 945 GRGIPDENTIELKETERYHILKNLESNDYVSLRARNVKGDPPIYDNIKTREDEPYDA 1004
 OY 225 -----TYANMTFOVOMLHAFKLN-----PGNHLKWKQIPD 256
 DB 1005 PTPLEVPVGLRAITWSSSIYVYWDIMLNKNQHVTDNRHYTVSYGIGTSNRRY-----1060
 OY 257 CENVKTQCVPEPQVFOKGIYLLRVOASDGNNTSFNSEIKFDEIOAFLPVPFNIRSL 316
 DB 1060 -HNTTDLNCMI-NDLRPTQYEFAYKVKGRRESSMSVLSNLTQVNPVTPP-----1111
 OY 317 SDSFHIYIGAPKOSGNPIYQDYP-----LYEIIIFMENTSNAER-----KIEEKT 363
 DB 1111 ---REVTVRLDENMPPTVYQWIPKHTLGOITGYNIYTTDTTKRDMDSVEAFAGEET 1167
 OY 364 DVTVPNLKPLTVYCVKARAHT 384
 DB 1168 MLMPLNKLPTTYTFKVOART 1188

RESULT 12
 S42167
 190K protein - human
 C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
 C:Accession: S42167
 R:Vinkemeier, U.; Obermann, W.; Weber, K.; Fuerst, D.O.
 J. Cell Sci. 106, 319-350, 1993
 A:Title: The globular head domain of titin extends into the center of the sarcomeric
 A:Reference number: S42166; KUID:94095665

RESULT 15

S49015

receptor tyrosine kinase Eph-1 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 28-May-1999

C:Accession: S49015; S51602

R:Malsonplante, P.C.; Baitezuela, N.X.; Yancopoulos, G.D.

Oncogene 8, 3277-3288, 1993

A:Title: Eph-1 and Eph-2: two novel members of the Eph receptor-like tyrosine kinase fam

A:Reference number: S49015; MUID:9406777

A:Accession: S49015

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1005 <MA1>

A:Cross-references: EMBL:S68024

A:Note: the authors translated the codon GAC for residue 170 as Glu

A:Accession: S51602

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-305, 'G', 359-1005 <MA2>

A:Cross-references: EMBL:S68026

A:Note: the authors translated the codon GAC for residue 170 as Glu

C:Keywords: ATP; transmembrane protein

F:675-941/Domain: protein kinase homology <KIN>

F:683-691/Region: protein kinase ATP-binding motif

Query Match 5.58; Score 118; DB 2; Length 1005;

Best Local Similarity 20.18; Pred. No. 0.51;

Matches 92; Conservative 51; Mismatches 165; Indels 150; Gaps 21;

```
OY 1 GKNLSPQKVEVDII--DDNF-----ILRMNSDESQVNT--SFQYOKTGMDNW 47
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 165 GRNKNQNOYIKIDITADESTEDLDGRVKNLNEVDVGPLSKKGYLAQDVG---- 221
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
OY 48 IKLSGCONITST---KCNFSLKLYEIEIKLIRAEKENTSSWYVDSFTFPRKAQI 102
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 221 ---ACIALVSVRYKKCPSVRLAVFPD---TITGADSSQLLEVSGSCVNHSTVD 271
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
OY 103 GPPEVHLEAEKAIYIHISPGTKDSVMALDGLSTYSLLIMKNSGVEERIENT-YSRH 161
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 272 DPKMHCSAECEMLV---PIGKCMC-----KAGYEKKNGTCQVCRP 309
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
OY 162 KIYKLSPETTYCLKVKALLSMKIGVYSPVH-----CIKTVENELPP----- 206
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 310 GFFKASPHSQTCSCPP-----HSYTHEASTSCVCEKDYFRRESDPPTMACTRP 359
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
OY 206 ---PENIEVSVOONQVYLKM-----DYTYANMTFOVQWLHAFKRNPGNHLKMK 252
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 360 PSAPRNIAISNVNETSVEFLEMIPADTGGKDVSYIILCKCN-SHAGVCECGGHR--- 416
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
OY 253 QIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEIEKFDTEIOAFLPPVFN 312
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 416 -----YLPQOIGLKNTSVMADPLAHNTYTF-----EIEA-----VNG 448
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
OY 313 IRSLSDFHIYIG---APKOSGNTPVIO-----DYP-----LYEELIF 347
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 449 VSDLSPTGRQYVSVNTTQAPSPVITNVKKGKIAKNSISLSKQEDPRPNGIITLEYELKY 508
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
OY 348 WENTSNAERKIIIE-KKTDVTVPNLKLPLVYCVKARAHT 384
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 509 FEKDOETSYTIKSKETITTAEGLKPAASVYVFOIRART 546
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
```

Search completed: June 1, 2000, 04:35:09

Job time: 14289 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 1, 2000, 00:40:17 ; Search time 34.71 Seconds

(without alignments)
351,842 Million cell updates/sec

Title: us-09-240-675-2_copy_27_427

Perfect score: 2141
Sequence: 1 GRNLSPOKVEVDIIDNFI.....AHTMDEKLNKSSVSDAYCE 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 08

Listing first 45 summaries

Database : SwissProt_38:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2141	100.0	557	1 INRL_HUMAN	P17181 homo sapien
2	1384.5	64.7	560	1 INRL_BOVIN	O04790 bos taurus
3	1382.5	64.6	560	1 INRL_SHEEP	O28589 ovis aries
4	966	45.1	590	1 INRL_MOUSE	P33896 mus musculus
5	220	10.3	325	1 CRP_HUMAN	O08324 homo sapien
6	148	6.9	337	1 INGS_HUMAN	P38484 homo sapien
7	122.5	5.7	1451	1 MYM1_HUMAN	P52179 homo sapien
8	118	5.5	489	1 INGR_HUMAN	P15260 homo sapien
9	118	5.5	1005	1 EPAS_RAT	P54757 rattus norv
10	117.5	5.5	1383	1 INSR_RAT	P15127 rattus norv
11	113	5.3	1450	1 MPST_CHICK	O02173 gallus gall
12	111.5	5.2	1447	1 DCC_MOUSE	P70211 mus musculus
13	110	5.1	1912	1 PTP_HUMAN	P23468 homo sapien
14	109.5	5.1	575	1 I10R_MOUSE	O61727 mus musculus
15	108	5.0	1037	1 EPAS_HUMAN	P54756 homo sapien
16	107.5	5.0	1372	1 INSR_MOUSE	P15208 mus musculus
17	107	5.0	427	1 I131_HUMAN	P78552 homo sapien
18	105.5	4.9	878	1 IL3B_MOUSE	P26934 mus musculus
19	104.5	4.9	1447	1 DCC_HUMAN	P43116 homo sapien
20	104	4.9	896	1 CYRB_MOUSE	P26935 mus musculus
21	104	4.9	1239	1 NRG_DROME	P20241 drosophila
22	102.5	4.8	1897	1 PTFP_HUMAN	P10566 homo sapien
23	101	4.7	1304	1 CD45_HUMAN	P08575 homo sapien
24	99.5	4.6	677	1 SPOT_HAEIN	P43811 haemophilus
25	99.5	4.6	897	1 CYRB_HUMAN	P32927 homo sapien
26	98.5	4.6	1345	1 YHOO_YEAST	P38800 saccharomyc
27	98.5	4.6	1615	1 S230_PLAFO	P03566 tobaccum mos
28	98.5	4.6	3135	1 S230_PLAFO	O08372 plasmodium
29	97.5	4.6	306	1 K128_YEAST	P06242 saccharomyc
30	97.5	4.6	1256	1 FINC_CHICK	P11722 gallus gall
31	97.5	4.6	1382	1 INSR_HUMAN	P06213 homo sapien
32	96.5	4.5	515	1 INR_HUMAN	P48551 homo sapien
33	96.5	4.5	2029	1 LAR_DROME	P16521 drosophila
34	96	4.5	662	1 I12R_HUMAN	P42701 homo sapien

ALIGNMENTS

RESULT	ID	INRL_HUMAN	STANDARD	PRT	557 AA.
35	95.5	4.5	925	1	PWP2_CAEL.
36	95.5	4.5	2280	1	YCP2_TOBAC
37	95	4.4	918	1	IL6B_HUMAN
38	94.5	4.4	1068	1	YCF0_MARPO
39	94	4.4	917	1	IL6B_MOUSE
40	94	4.4	2628	1	HAGA_PORCI
41	93.5	4.4	620	1	YMO0_YEAST
42	93.5	4.4	847	1	CD22_HUMAN
43	93.5	4.4	1091	1	CIC2_RAT
44	93	4.3	1097	1	LIFR_HUMAN
45	93	4.3	1101	1	P11G_HUMAN

35	95.5	4.5	925	1	PWP2_CAEL.	P91341 caenorhabdit
36	95.5	4.5	2280	1	YCP2_TOBAC	P09976 nicotiana t
37	95	4.4	918	1	IL6B_HUMAN	P40189 homo sapien
38	94.5	4.4	1068	1	YCF0_MARPO	P12221 marchantia
39	94	4.4	917	1	IL6B_MOUSE	O00560 mus musculus
40	94	4.4	2628	1	HAGA_PORCI	O51845 porphyromon
41	93.5	4.4	620	1	YMO0_YEAST	O03162 saccharomyc
42	93.5	4.4	847	1	CD22_HUMAN	P20273 homo sapien
43	93.5	4.4	1091	1	CIC2_RAT	P54290 rattus norv
44	93	4.3	1097	1	LIFR_HUMAN	P42702 homo sapien
45	93	4.3	1101	1	P11G_HUMAN	P48736 homo sapien

AC	INRL_HUMAN	STANDARD	PRT	557 AA.
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DE	15-FEB-2000 (Rel. 39, Last annotation update)			
DE	INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).			
GN	IFNAR1 OR IFNAR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Catarrhini; Homiidae; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	Medline: 90124632.			
RA	Uze G., Lutfalla G., Gresser I.;			
RT	"Genetic transfer of a functional human interferon alpha receptor			
RT	into mouse cells: cloning and expression of its cDNA.";			
RL	Cell 60:225-234(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	Medline: 92129376.			
RA	Lutfalla G., Gardiner K., Proudhon D., Vielh E., Uze G.;			
RT	"The structure of the human interferon alpha/beta receptor gene.";			
RL	J. Biol. Chem. 267:2802-2809(1992).			
RN	[3]			
RP	PHOSPHORYLATION BY TYK2.			
RX	Medline: 95059042.			
RA	Colamonici O., Yan H., Domanski P., Handa R., Smalley D.,			
RA	Mullerstein J., Witte M., Krishnan K., Krolewski J.;			
RT	"Direct binding to and tyrosine phosphorylation of the alpha subunit			
RT	of the type I interferon receptor by pl35tyk2 tyrosine kinase.";			
RL	Mol. Cell. Biol. 14:8133-8142(1994).			
CC	- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE			
CC	I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS			
CC	INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-			
CC	SUBUNITS THEMSELVES.			
CC	- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	- TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALL TISSUES AND			
CC	EVEN ON THE SURFACE OF MOST IFN-RESISTANT CELLS.			
CC	- PTM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYK2 TYROSINE KINASE.			
CC	- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.			
CC	- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sdb.ch/announce/			
CC	or send an email to license@sdb-sdb.ch).			
CC	-----			
DR	EMBL: J03171; AAA52730.1; -			
DR	EMBL: X60459; CAA42992.1; -			
DR	PIR: A32694; A32694.			
DR	PIR: S17112; S17112.			
DR	MIM: 107450; -			

KW Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism;
 KW Phosphorylation.
 FT SIGNAL 1 27
 FT CHAIN 28 557
 FT
 FT DOMAIN 28 436
 FT TRANSMEM 437 457
 FT DOMAIN 458 557
 FT DISULFID 79 87
 FT DISULFID 199 220
 FT MOD_RES 466 466
 FT MOD_RES 481 481
 FT CARBOHYD 50 50
 FT CARBOHYD 58 58
 FT CARBOHYD 81 81
 FT CARBOHYD 88 88
 FT CARBOHYD 110 110
 FT CARBOHYD 172 172
 FT CARBOHYD 254 254
 FT CARBOHYD 313 313
 FT CARBOHYD 314 314
 FT CARBOHYD 376 376
 FT CARBOHYD 416 416
 FT CARBOHYD 433 433
 FT VARIANT 168 168
 FT
 FT CONFLICT 17 17
 FT SEQUENCE 557 AA: 63525 MW: 0F6744CB1ADBE73 CMC64;
 G -> A (IN REF. 2).
 /FTID=VAR.002717.

Query Match 100.0%; Score 2141; DB 1; Length 557;
 Best Local Similarity 100.0%; Pred. No. 9,5e-154;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKNLSPKQVEVDIIDDNFILRMNRSDESVGNVTSFDTQKGMNWKLSGCCNITSTK 60
 DB 27 GKNLSPKQVEVDIIDDNFILRMNRSDESVGNVTSFDTQKGMNWKLSGCCNITSTK 86
 QY 61 CNFSSLKINVEEIKLRIRAEKENTSMVEVDSFTPKRAQIGPEVHLEADKAIYIHI 120
 DB 87 CNFSSLKINVEEIKLRIRAEKENTSMVEVDSFTPKRAQIGPEVHLEADKAIYIHI 146
 QY 121 SPGRDSVMMALDGLSFTYSLILMKNSGVEERENIYSRHKIKYLSPEYTCVKYKAL 180
 DB 147 SPGRDSVMMALDGLSFTYSLILMKNSGVEERENIYSRHKIKYLSPEYTCVKYKAL 206
 QY 181 LTKMIGIVSPVHCIKITVENELPPENIEVSQONQNVYKMDYTYAMTQVQVLAFL 240
 DB 207 LTKMIGIVSPVHCIKITVENELPPENIEVSQONQNVYKMDYTYAMTQVQVLAFL 266
 QY 241 KRNPNHLYKMKQIPDCEVKTQCVFQONVQKGIYLLRVOASDGNNTSEFSEIKEDT 300
 DB 267 KRNPNHLYKMKQIPDCEVKTQCVFQONVQKGIYLLRVOASDGNNTSEFSEIKEDT 326
 QY 301 EIQAFLLPPEVNIISLSFHIYIGAPKQSGTPIYDIYPLIYEIIEFMENTSNAERKIE 360
 DB 327 EIQAFLLPPEVNIISLSFHIYIGAPKQSGTPIYDIYPLIYEIIEFMENTSNAERKIE 386
 QY 361 KKTDTVPRLKPLTYCYKARAHMTDEKLNKSSVSFSDAVCE 401
 DB 387 KKTDTVPRLKPLTYCYKARAHMTDEKLNKSSVSFSDAVCE 427

RESULT 2
 INRL_BOVIN STANDARD: PRT: 560 AA.
 AC 004790;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
 GN IFNARI OR IFNAR.
 OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
 OC Bovinae; Bos.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG.
 RX MEDLINE: 93076908.
 RA Mouchel-Vleish E., Lutfalla G., Mogenssen K.E., Uze G.;
 RT "Specific antiviral activities of the human alpha interferons are
 RT determined at the level of receptor (IFNAR) structure.";
 RL FEBS Lett. 313:255-259(1992).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 93305725.
 RA Lim J.-K., Langer J.A.;
 RT "Cloning and characterization of a bovine alpha interferon receptor.";
 RL Biochim. Biophys. Acta 1173:314-319(1993).
 CC -I- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
 CC -I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
 CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
 CC SUBUNITS THEMSELVES.
 CC -I- SUBCELLULAR LOCATION: TYPE 1 MEMBRANE PROTEIN.
 CC -I- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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 CC
 CC EMBL: X68443; CAA48484.1; -;
 DR EMBL: L06320; AAA02571.1; -;
 DR PIR: S33770; S33770.
 DR PIR: S27387; S27387.
 DR PIR: PF00041; fn3; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 560
 FT
 FT DOMAIN 25 437
 FT TRANSMEM 438 458
 FT DOMAIN 459 560
 FT DISULFID 76 84
 FT DISULFID 199 220
 FT CARBOHYD 47 47
 FT CARBOHYD 55 55
 FT CARBOHYD 85 85
 FT CARBOHYD 109 109
 FT CARBOHYD 172 172
 FT CARBOHYD 254 254
 FT CARBOHYD 313 313
 FT CARBOHYD 377 377
 FT CARBOHYD 434 434
 FT CONFLICT 422 422
 FT SEQUENCE 560 AA: 63818 MW: 66D76B72861E1D11 CRC64;
 F -> V (IN REF. 2).
 Query Match 64.7%; Score 1384.5; DB 1; Length 560;
 Best Local Similarity 64.0%; Pred. No. 7e-97;
 Matches 258; Conservative 62; Mismatches 78; Indels 5; Gaps 5;

QY 3 NLKSPQVEVDIIDDNFILRMNRSDESVGNVTSFDTQKGMNWKLSGCCNITSTKCN 62
 DB 27 NLK-PEVNEIHIIDDNFILRMNRSSESVKNTTSADYIOLCTDNMKLSGCCNITSTKCN 85
 QY 63 FSSSLKLNVEEIKLRIRAEK-ENTSSMVEVDSFTPKRAQIGPEVHLEADKAIYIHI 120
 DB 86 FSSVELEVEPEKILRLRAEGNNTSMVEVPEVPLLEAOIGPDVHLEADKAIILSI 145
 QY 121 S-PGRDSVMMALDGLSFTYSLILMKNSGVEERENIYSRHKIKYLSPEYTCVKYKAA 179

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Db      146 SPFGKQDSTMMAMDDSSFFRYSVYIMWKNSSSLSEBRTETVYPEDKIYTLSPETITCLAKVME    205
Oy      180 LITSKICVYSVPHCIKTVEENLEPPPEIEVSQONQNYVLKMDITYAMTQOVOLHAF    239
Db      206 LRLQSRVGCYSVYCINTTERHKVPSPENIQINADQIIVLWKDPYEANATQAOWLRAF    265
Oy      240 LKRNDGNHLTKKKQIPDCENVKTCOCVFPONFQKGITYLLRQASDNGNTSFMSEEIKPD    299
Db      266 FKKIGNNSDKMKQIPLNCNANTSTHCVFRELYSSRKIIYVRARASNGNSTSRSEKEKN    325
Oy      300 TEIOAFLPLPVENINSLS-DSFHIIYGAPKSGCNTPIVDYDPLIYEITIENTSNAEKRI    358
Db      326 TEMKTIIFPPVVISVYDDSLHSVASGSEESENNVSNOPLYEIVIEWENTSNAEKY    385
Oy      359 IEKKTDTVAVPNLKPLTYCVKRAHTMDEKLKSSVESPAVCE    401
Db      386 LEKRTNFTFPDLKPLTYCVKRALIENDRRNKGSSESFDTJCE    428

RESULT      3
ID INR1_SHEEP STANDARD: PRT: 560 AA.
AC 028589; 095206;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC)
DE (INTERFERON ALPHA/BETA RECEPTOR-1).
DE IFNARI OR IFNAR.
OS Ovis aries (sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Caprinae; Ovis.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-ENDOMETRIUM;
RX MEDLINE; 97135690.
RA Kaluz S., Fisher P.A., Kaluzova M., Sheldrick E.L., Flint A.P.F.;
RT "Structure of an ovine interferon receptor and its expression in endometrium";
RT J. Mol. Endocrinol. 17:207-215(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-ENDOMETRIUM;
RX MEDLINE; 98006426.
RA Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.;
RT "Molecular cloning of ovine and bovine type I interferon receptor subunits from uteri, and endometrial expression of messenger ribonucleic acid for ovine receptors during the estrous cycle and pregnancy.";
RT Endocrinology 138:4757-4767(1997).
RL -1 FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-SUBUNTS THEMSELVES.
CC -1 SURCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
CC -1 TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT CONCEPTUS AT DAY 15 OF PREGNANCY.
CC -1 SIMILARITY: CONTAINS 2 FIBROBLAST TYPE III-LIKE DOMAINS.
CC -1 SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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DR EMBL; X95939; CAAG5183.1; -.
DR EMBL; U65978; AAB84231.1; -.
DR PFAM; PF00041; fn3; 1.

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Query Match	Best Local Similarity	Score	DB 1	Length
Matches 256; Conservative 65; Mismatches 77; Indels 5; Gaps 5	64.6%; 63.5%;	1382.5;	DB 1;	560;
Query	3	NLKSQKVEVDIIDNFLKRNKSDSEVGNVTFSDYCKTGMDNKLKSGCONISTKCN	62	
Db	27	NLKS-ENVEIHIIIDNFLKRNKSSSESVRNTFSADYQILGTDNNKKLPGCOHITSSKCN	85	
Query	63	FSSKL-LVYEEIKRIRAEK-ENMSWYEVDSFPFRAQIGPPEVHLEARDKAVIHI	120	
Db	86	FSSVLKQVFEIEIRIRAEBSGNSTJVEPFPFLAQIGPDVHLEADKALISLI	145	
Query	121	S-PGKDSVMALDLSFTYSLILKNSGVEERLENIYSRRKIYKLPETTYCLKVKAA	179	
Db	146	SPGEGDSIMALDSSSRYSVVIKKNSSLEERETVYPEDKIKLSPETIYCLKVKAE	205	
Query	180	LITSKIKIVISPVHCICKTTVENELPPENIEVSONQNTVLEKDYTYANMTFOVQMLAF	239	
Db	206	LRLOSGVCSYPCVYICNTTERHKVSPENVOINVNDQAVLEKDYPESTFOAGWLRAF	265	
Query	240	LKRNGNLLYKWKQKQPPDENKTTQCVFPQNGIYLLRQASDGNSTFSWSEIKRD	299	
Db	266	LKKIPGKSNMKQKQPPDENETTHCVPRDIFSGIYVVRASNGNSTFSWSEKEFN	325	
Query	300	TEIOFLPLPENNISLS-DSFHVIGAPKOSGNPVYODVPLIETIFEMWTSNAEKRI	358	
Db	326	TEVPIIIPPIYSKMSITDDSLHVSVSASESENMSVMDLPIVLEVFEMWTSNAEKRV	385	
Query	359	IEKTDVTVPNLKPLTYVCVAKARATHDEKLKNSVFSADCE 401		
Db	386	LEKRTDFEPNLKPLTYVCVAKARALIENTDRNKKSSYSDTCE 428		
RESULT 4				
INRL_MOUSE	INRL_MOUSE	STANDARD;	PRT;	590 AA.
AC	P33896;			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	15-FEB-2000 (Rel. 39, Last annotation update)			
DE	INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).			
GN	IFNAR1 OR IFNAR OR IFNAR.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
IN	[1]			
RP	SEQUENCE FROM N.A.			

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RX MEDLINE 92262522.
RA use G., Iutafalla G., Bandu M.T., Proudhon D., Moegensen K.E.;
RT "Behavior of a cloned murine interferon alpha/beta receptor expressed
RL in homo-specific or heterospecific background";
Proc. Natl. Acad. Sci. U.S.A. 89;4774-4778(1992).
CC -I- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
CC IFNPS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
CC SUBUNITS THEMSELVES.
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -I- SIMILARITY: CONTAINS 2 FIBROBLAST TYPE III-LIKE DOMAINS.
CC -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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DR EMBL: M89641: AAA37890.1; -.
DR PIR: A45283; A45283.
DR MGJ: MGI:107658; IFNR.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 590 INTERFERON-ALPHA/BETA RECEPTOR ALPHA
FT FT CHAIN.
FT DOMAIN 27 429 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 430 449 POTENTIAL.
FT DOMAIN 450 590 CYTOPLASMIC (POTENTIAL).
FT DISULFID 78 86 BY SIMILARITY.
FT DISULFID 199 220 BY SIMILARITY.
FT CARBOHYD 43 43 POTENTIAL.
FT CARBOHYD 109 109 POTENTIAL.
FT CARBOHYD 181 181 POTENTIAL.
FT CARBOHYD 214 214 POTENTIAL.
FT CARBOHYD 314 314 POTENTIAL.
FT CARBOHYD 370 370 POTENTIAL.
FT CARBOHYD 409 409 POTENTIAL.
FT CARBOHYD 413 413 POTENTIAL.
SQ SEQUENCE 590 AA: 65776 MW: 76C6DFE370185D3A CRC64;
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[illegible]

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DB 24 PENVBNMSVNFKNILQWESPAFAKGNLFTTAQY-----LSYRIFODKCMNTTTECDPSS- 79
QY 67 KLVNVEIKIRIRAE-KENTSSWYEVDSTPPFRRAQIGPEVHLEA-EDRAIVIHISPGT 124
DB 79 -LSYKGDHITRVRAEFADSDWVNI--TFCPVDDTIIGPGMQVEVLADSLHMFAPKI 136
QY 125 KDSV-MALDGL--SFYSLLIMKNSSGVEERIENTISRKIKYLSSETTYCKVKAALL 181
DB 137 ENEYETWTKNKNVSNWYNYQWNGTDEKFOITPOYDFEVLRLNLEPMYTCVQVRGFLP 196
QY 182 TSWKIGVSPVHCITVENELP 204
DB 197 DRNKAGSESPVCEQTHDETVP 219

RESULT 6
INGS_HUMAN STANDARD: PRT: 337 AA.
AC P38484;
DC 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (INTERFERON-GAMMA RECEPTOR ACCESSORY FACTOR-1) (AF-1) (INTERFERON-GAMMA TRANSDUCER-1). IFNGR2 OR IFNG1.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=LUNG FIBROBLAST;
MEDLINE: 94170380.
RA Wang N., Donnelly R.J., Kotenko S., Mariano T.M., Cook J.R.,
RA Wang N., Emanuel S.L., Schwartz B., Miki T., Pestka S.;
RT Identification and sequence of an accessory factor required for
RT activation of the human interferon gamma receptor."
RL Cell 76:793-802(1994).
CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERFERON GAMMA. REQUIRED FOR
CC SIGNAL TRANSDUCTION. THIS ACCESSORY FACTOR IS AN INTEGRAL PART OF
CC THE IFN-GAMMA SIGNAL TRANSDUCTION PATHWAY AND IS LIKELY TO
CC INTERACT WITH GAF, JAK1, AND/OR JAK2.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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CC -----
DR EMBL: U05875; AAA16955.1; -
DR EMBL: U05877; AAA16956.1; -
DR MIM: 147569; -
DR PFAM: PF00041; fn3; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT CHAIN 1 27
FT SIGNAL 28 337
FT DOMAIN 28 247
FT TRANSMEM 248 268
FT DOMAIN 269 337
FT CARBOHYD 56 56
FT CARBOHYD 85 85
FT CARBOHYD 110 110
FT CARBOHYD 137 137
FT CARBOHYD 219 219
FT CARBOHYD 231 231
FT VARIANT 64 64
FT R -> O.
FT /FRID-VAR.002718.
SO SEQUENCE 337 AA; 37834 MW; 18C61B10AD90E509 CRC64;

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Query Match 6.9%; Score 148; DB 1; Length 337;
Best Local Similarity 22.2%; Pred. No. 0.00032;
Matches 62; Conservative 49; Mismatches 104; Indels 64; Gaps 13;

QY 4 LKSPQVEVDIIDNFIWM-----NRSDSVGNVTSFQYOKGMNWILS----- 52
DB 30 LPAPQHPKIRLVNAEQVLSWEPVALSNSTRPVYRPROFYRTDSK-----WFTADIMISGV 84
QY 52 GCONITSTKCNSS-----LKLNVYEIKIRIRAEKENT-SSWYEVDSTPPFKAQI 102
DB 85 NCTQITATECDTTAASPAGFPDENV---TLRLAEALGALSAWYVPMFOHTRNTV 140
QY 103 GPEVHLE--AEKRAIVIHISPGTDSVMAALDGLSFTYSLLIMKNSSGVEERIENTIS 159
DB 141 GPPE-NIEVTPGEGSLIRFSSPFIADSTAF---FCYYHYME--KGIGQYKGPFR 193
QY 160 RKHY--KLSPETTYCKVKAALLTS---WKIGVSPVHCITVENELPPEPNIENV 213
DB 194 SNSISLDNLKPSRVYCLQVQAOQLWKNKSNIFRVGHLNSISCYETADASTELQVILLISV 253
QY 214 -----ONQNVVLKMDTYANMFQVO 234
DB 254 GTFSLSLVAGACFFLVLYLKYRGLIKYWHTPPSIPLQIE 292

RESULT 7
INGS_HUMAN STANDARD: PRT: 1451 AA.
AC P52179;
DC 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE MYOHEXIN 1 (190 KD TITIN-ASSOCIATED PROTEIN) (190 KD CONNECTIN-
DE ASSOCIATED PROTEIN).
GN MYOM1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=SKLETAL MUSCLE;
MEDLINE: 94095665.
RA Vinemeler U., Obermann W., Weber K., Fuerst D.O.;
RT The globular head domain of titin extends into the center of the
RT sarcomeric M band. cDNA cloning, epitope mapping and immunoelectron
RT microscopy of two titin-associated proteins."
RL J. Cell Sci. 106:319-330(1993).
CC -1- FUNCTION: MAJOR COMPONENT OF THE VERTEBRATE MYOFIBRILLAR M BAND.
CC BINDS MYOSIN, TITIN, AND LIGHT MEROMYOSIN. THIS BINDING IS DOSE
CC DEPENDENT.
CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 7 FIBRONECTIN TYPE III-LIKE DOMAINS.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X69090; CAA48833.1; -
DR MIM: 603508; -
DR PFAM: PF00041; fn3; 5.
DR PFAM: PF00047; fn3; 3.
DR PRINTS: PR00014; FNTPETIT.
KW Immunoglobulin domain; Muscle protein; Thick filament; Repeat.
FT DOMAIN 46 81
FT REPEAT 46 51
FT REPEAT 52 57
FT REPEAT 58 63
FT REPEAT 64 69
FT REPEAT 64 69

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OY 250 NKTQCVCEPOWFOQGITL-LRVQASDGNNSNFSNEELKFTDEIOTAFLLPRENRS--- 316
DB 79 NISHYCNISDHYGDPNSLWYKARVQCKESAFAKSEFAVCRDCKGKPPGLDKEE 138
OY 316 ---LSDSFH-IYIGAPKOSGN-TPYIDQYPLTYEIIEMENTSNAERKTIIEKTD----- 365
DB 139 KQIMIDIFHPSEVFNDEDEVDYDPEPTTCYIRINYNYVMNSSEIOYKTLITLOKREDDCDEI 198
OY 365 ---VYVPLNKPLTYICVYKARA--HTMDEKLNS-----SVFSDAV 399
DB 199 OCOLAIPIVSSLNSOYCVSAEGLVHWGCVTTEKSKEVCITIFNSSI 243

RESULT 9
EPAS_RAT STANDARD: 1 PRT: 1005 AA.
AC P54757;
DT 01-OCT-1996 (Rel. 34, created)
DT 01-OCT-1996 (Rel. 34, last sequence update)
DE 01-NOV-1997 (Rel. 35, last annotation update)
DE EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
DE KINASE RECEPTOR EHK-1) (EPH HOMOLOG KINASE-1).
GN EPHA5 OR EKH1 OR EHK-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
RA MEDLINE; 94067777.
RA Malsomierre P.C., Barrezuela N.X., Yancopoulos G.D.:
RT "Ehk-1 and Ehk-2, two novel members of the Eph receptor-like tyrosine
RT kinase family with distinctive structures and neuronal expression.";
RL Oncogene 8:3277-3288(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
RX MEDLINE; 95206467.
RX Taylor V., Pfaffr S., Miescher G.C., Honegger P., Bretschopf H.,
RA Laassmann H., Steck A.J.:
RT "Expression and developmental regulation of Ehk-1, a neuronal
RT Etk-like receptor tyrosine kinase in brain.";
RL Neuroscience 63:163-178(1994).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
CC EPHRIN-A1, -A2, -A3, -A4 AND -A5.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -> ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARE PRODUCED BY
CC ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSED IN THE NERVOUS
CC SYSTEM. PREDOMINANTLY EXPRESSED IN NEURONS.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
CC -1- SIMILARITY: CONTAINS 2 FERROXYCTIN TYPE III-LIKE DOMAINS.
CC -----
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CC or send an email to license@sdb-stb.ch).
CC -----
DR EMBL; X76889; CAAS5357.1; -.
DR HSSP; P00523; ZPTK.
DR PRINTS; PRO0014; FNTYPEI11.
DR PRINTS; PRO0109; TYRKINASE.
DR PROSITE; PS00107; PROTEIN KINASE ATP. FALSE_NEG.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR. 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM. 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V.1; 1.

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DR	PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.		
DR	PROSITE: PS01186; EGF_2; UNKNOWN_1.		
DR	PFAM; PF00041; fn3; 2.		
DR	PFAM; PF00069; pkinase; 1.		
DR	PFAM; PF01404; EPH_1bd; 1.		
KW	Transferase; Tyrosine-protein kinase; Arp-binding; Phosphorylation; Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.		
FT	SIGNAL	1	?
FT	CHAIN	?	1005
FT	DOMAIN	?	575
FT	TRANSMEM	576	596
FT	DOMAIN	597	1005
FT	DOMAIN	677	938
FT	NP_BIND	683	691
FT	BINDING	709	709
FT	ACT_SITE	802	802
FT	CARBOHYD	266	266
FT	CARBOHYD	301	301
FT	CARBOHYD	371	371
FT	CARBOHYD	425	425
FT	CARBOHYD	438	438
FT	CARBOHYD	463	463
FT	VARSPLIC	10	20
FT	VARSPLIC	306	358
FT	VARSPLIC	358	470
FT	VARSPLIC	470	621
FT	VARSPLIC	621	170
FT	CONFLICT	170	170
FT	CONFLICT	566	566
FT	CONFLICT	578	578
FT	CONFLICT	669	669
FT	CONFLICT	708	708
FT	CONFLICT	979	979
FT	SEQUENCE	1005 AA; 111007 MM; LAED42CG9693C574 CRC64;	

Query Match	5.5%	Score 118;	DB 1;	Length 1005;
Best Local Similarity	20.1%	Pred. No. 0.24;		
Matches	92;	Conservative	51;	Mismatches 165; Indels 150; Gaps 21;
QY	1	GNLTKSPQKVEVDII--DDNF-----ILRWNSDSVGNVT--SFSDYOKTGMWN	47	
Db	165	GRNIDNOYIKIIDTIAADESTFELDGRVYKLNLEVDYGLSKKGYIAFDVG----	221	
QY	48	IKLSGCONITST-----KCNFSLKLNLYEIKIRIAEKENTSSWYEDSFTPRKAOI	102	
Db	221	-----ACILVSRVRYKKCPSPVRLHAFDPD-----TITGADSSOLLESGSCVHNSVTD	271	
QY	103	GPPEVLEAEEDKATYIHSPTGKDSVMMALDGLSTYSLLIMKNSGYBERIENI-YGRH	161	
Db	272	DPRKHCAGAEEMLY-----PIGKCMC-----KAGIEEKGTQVCVCRP	309	
QY	162	KIKYLSPTTYCLVKAALLTSWKIGVSPVH-----CIKTIVENELRP-----	206	
Db	310	GFFKASPSHSOTCSKCP-----HSYTHEASTSCVCEKDYFRRESDDPTMACTRP	359	
QY	206	---FENIEVSQONQNVYLKM-----DYTANMFFQVOMLHAFILKRNPGNLLYMK	252	
Db	360	PSAPRNALSNVNETSVELEWIPPADDTGGKRVSYIILCKNS-SHAGVCEEGGVR---	416	
QY	253	QIPDCENVKTTQCVFQVNFQKGIYLLRLVQAQSDGNNTSFKWSBEIKFDIEQAFLLP	312	
Db	416	-----YLPQOIGLKNISYMMADPLAHNTVTF-----EIEA-----VNG	448	
QY	313	IRLSDSDFHIYIG---APKQSGNTPVLO-----DYP-----LTYEITF	347	
Db	449	VSDLSPTGRQVSVNVTTNQAPSPVYINVKKGIKAKNISLSWQEPDPPNGIILEYIKY	508	

QY 348 WENTSNAERKIE-KTIDVTPNKLPLTYCVARAHAT 384
DB 509 FEKQDETSTYTIKSKRETTTAEGLKPAVYFQIRAHAT 546

RESULT 10
INSTR_RAT STANDARD: PRT: 1383 AA.

AC P15127: P97681;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INSULIN RECEPTOR PRECURSOR (EC 2.7.1.112) (IR).
GN INSR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN
RP SEQUENCE FROM N.A.
RX MEDLINE: 90213337.
RA Goldstein B.J., Dudley A.L.;
RT "The rat insulin receptor: primary structure and conservation of
RT tissue-specific alternative messenger RNA splicing."
RL Mol. Endocrinol. 4:235-244(1990).
RN [2]
RP PARTIAL SEQUENCE FROM N.A.
RA STRAIN-SPRAGUE-DAWLEY;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS RECEPTOR BINDS INSULIN AND HAS A TYROSINE-PROTEIN
CC KINASE ACTIVITY.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -1- ENZYME REGULATION: AUTOPHOSPHORYLATION ACTIVATES THE KINASE
CC ACTIVITY.
CC -1- SUBUNIT: TETRAMER OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE
CC BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LIGAND-
CC BINDING DOMAIN, WHILE THE BETA CHAIN CARRY THE KINASE DOMAIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC
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CC
CC -----
CC EMBL: M29014; AAA41441.1;
CC EMBL: AF005776; AAB61414.1;
CC EMBL: AF005777; AAB61415.1;
CC EMBL: U80633; AAB38746.1;
CC EMBL: U80632; AAB38968.1;
CC EMBL: U80631; AAB38968.1; JOINED.
CC EMBL: U80630; AAB38967.1;
CC EMBL: U80629; AAB38967.1; JOINED.
CC PIR: A36080; A36080.
CC HSP: P06213; IIRK.
CC PRINTS: P00014; ENTPEIIL.
CC PRINTS: P00109; TYRKINSE.
CC PROSITE: P500107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: P500109; PROTEIN_KINASE_TYR; 1.
CC PROSITE: P500239; RECEPTOR_TYR_KIN_II; 1.
CC PROSITE: P550011; PROTEIN_KINASE_DOM; 1.
CC PFAM: PF00041; fn3; 1.
CC PFAM: PF00069; pkinase; 1.
CC PFAM: PF00757; furin-like; 1.
CC PFAM: PF01030; Recep_L_domain; 1.
CC Transferrase; Tyrosine-protein kinase; Receptor; Transmembrane;
CC Glycoprotein; ATP-binding; Phosphorylation; Signal; Repeat.
KW

FT SIGNAL 1 26
FT CHAIN 27 760
FT PROPEP 761 763
FT CHAIN 764 1383
FT CHAIN 764 1383
FT TRANSMEM 958 957
FT DOMAIN 958 978
FT DOMAIN 979 1363
FT DOMAIN 619 848
FT DOMAIN 849 949
FT DOMAIN 1024 1299
FT NE_BIND 1030 1038
FT BINDING 1058 1058
FT ACT_SITE 1160 1160
FT MOD_RES 1190 1190
FT ACT_SITE 1000 1000
FT DISULFID 461 550
FT DISULFID 461 550
FT CARBOHYD 42 42
FT CARBOHYD 51 51
FT CARBOHYD 104 104
FT CARBOHYD 137 137
FT CARBOHYD 241 241
FT CARBOHYD 281 281
FT CARBOHYD 321 321
FT CARBOHYD 363 363
FT CARBOHYD 423 423
FT CARBOHYD 444 444
FT CARBOHYD 540 540
FT CARBOHYD 634 634
FT CARBOHYD 652 652
FT CARBOHYD 699 699
FT CARBOHYD 770 770
FT CARBOHYD 783 783
FT CARBOHYD 921 921
FT CARBOHYD 934 934
FT CONFLICT 1119 1119
SQ SEQUENCE 1383 AA; 156756 MW; 489195669029444A CRC64;

Query Match
Best Local Similarity 19.0%; Score 117.5; DB 1; Length 1383;
Matches 86; Conservative 50; Mismatches 146; Indels 171; Gaps 19;

QY 17 DNFLIRNRSDSEVGNVTFSEFYQKGTMDN-----WILSCGN 55
DB 481 NDILKTKTGDAQSCENELKFSFRTSFDKILLRWEYPWPPDFDLGFMLFYKEAPYON 540
QY 56 IT-----STKCNFSSLLKLVYEILRLRAKENSSWYEDSFPPKAOIGPEVHLEA 111
DB 541 VTERDGDGAC-----GNSMTVVD-----IDPQ---RS 566
QY 112 EDKALIVIHISPTKDSVYKALDGLSFTYSLILMNKSSGVEERIEINISRHKIKYRLSPETT 171
DB 567 NDPKSQTPSHG-----WLMRG-----LKPWTQ 589
QY 172 YCLKVKALILTSWK---IGVSPVHCITTYENELPPENIEVSQONQVYKLN---DYT 225
DB 590 YALFVKTLVTFSDERTYGAKSIDIIYVDATNSVPLDPIVSNSSSQILKKRPSPSD 649
QY 226 YANMTFOYQWLHAFILKRPNGHLKWL-KQIPDCENVKTTQCVFQNVFQKGIYL----- 279
DB 650 NGNIT-----HYLVYWERQADESELFEIDYCL-----KGLKLPSPRTS 687
QY 279 --LRVQASDGNNTSPWSEI-----KFTDIOAFLLPVENIRSLSDSEFIYIGAPKQ 329
DB 668 PPFESDDSQKKNQSYDSDASAECCSCPKTDQILKELESSEFR-KTFEDYLHNVFVPRK 746
QY 330 --SGN-----TPVIQDTPILYIELIENFNSNAERKIEK--- 362
DB 747 TSSGGAEDTRPSRRKRLSEEVGNVYATTPILPDPFNISSTI--APTSHEHRPFERYVN 804
QY 362 KTDVTPNKLPLTYCVARAHATNDEKLNKSSV 394

Db 805 KESLVISGLRHTGRTGRIELQACNODSPERSGV 837

RESULT 11
MPSE CHICK STANDARD: PRT: 1450 AA.

Id MPSE CHICK
002173;
Dt 01-JUN-1994 (Rel. 29, Created)
Dt 01-JUN-1994 (Rel. 29, Last sequence update)
Dt 15-JUN-1999 (Rel. 38, Last annotation update)
DE M-PROTEIN, STRIATED MUSCLE.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-EMBRYONIC PECTORALIS MUSCLE;
RX MEDLINE: 93015907.
RA Noguchi J., Yanagisawa M., Imamura M., Kasuya Y., Sakurai T.,
RA Tanaka T., Masaki T.;
RT "Complete primary structure and tissue expression of chicken
RT pectoralis M-protein."
RL J. Biol. Chem. 267:20302-20310(1992).
CC -1- FUNCTION: IS A STRUCTURAL CONSTITUENT OF MYOFIBRILLAR M-BAND IN
CC STRIATED MUSCLE.
CC -1- TISSUE SPECIFICITY: IS EXPRESSED IN PECTORALIS AND CARDIAC MUSCLE.
CC -1- DEVELOPMENTAL STAGE: CAN BE DETECTED BY DAY 10-13 IN OVO, THE
CC CONTENT IS GRADUALLY INCREASED THROUGHOUT THE OVO DEVELOPMENT AND
CC REACHED ITS PEAK AFTER HATCHING.
CC -1- SIMILARITY: CONTAINS 7 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC
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CC
CC EMBL: D11474; BAA02033.1;
CC PIR: A44027; A44027.
CC DR HSSP: P56276; ITLK.
CC DR PFAM: PF00041; fn3: 5.
CC DR PRINTS: PRO0014; FNTYPE11.
KM Muscle protein: Repeat: Immunoglobulin domain.
FT DOMAIN 142 238 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 266 364 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 368 464 FIBRONECTIN TYPE-III.
FT DOMAIN 496 592 FIBRONECTIN TYPE-III.
FT DOMAIN 597 693 FIBRONECTIN TYPE-III.
FT DOMAIN 696 794 FIBRONECTIN TYPE-III.
FT DOMAIN 797 898 FIBRONECTIN TYPE-III.
FT DOMAIN 899 990 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 1002 1095 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 1126 1205 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 1225 1312 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 1333 1427 IG-LIKE C2-TYPE DOMAIN.
SO SEQUENCE 1450 AA; 163400 MW; E313C7D3FE6CAC7 CRC64.

Query Match 5.3%; Score 113; DB 1; Length 1450;
Best Local Similarity 21.3%; Pred. No. 0.92;
Matches 88; Conservative 63; Mismatches 131; Indels 132; Gaps 25;

QY 6 SPOVEV-DIIDNFIEMRNSDESIGN--VTSEFDYQKGMWILSGCONITSTKCN 62
Db 373 APMQVCKHDNRDVIVITWKPNTTSONPVIGYFVDCKEVGLNEMV-----QCN 421
QY 63 FSSKLWVYEEIKL-----RIRAKENNTSMYEDSFPPKAGIGPEVHLEAD- 114
Db 422 DAPVICKIPVTGLYEGRSYIFRVA-----VNSAGISRPSSVSEVVALDPAVDL 471

QY 114 -KAIVHISPG-----TKDSVMWALDS-----LSFTYSLIMRN----- 147
Db 472 ERTQTVHVEDGRKIVISKD-----LEGDDIQPGPTNVHASESKRTYVLSWDPYPRGR 527
QY 147 -----SSGVEERENITS-----RHAKYKSPETTYLKKKALLTSWKIGVYS 190
Db 528 EPLTYFIEKSMVSGSNQORNAQVAVKSPRYAVFDEAGKPYFRV-----LSANKHGISD 583
QY 191 PVHCIKTKVENEL-----PPPENIEVSQVN-----QNVLMKD-----YTANMTFOVQ 234
Db 584 PSEITTEPQODIVVVPASAPGRVATRTKTSVYVQMDKHEHNLGYIIDYISVGSNQ 643
QY 235 WLAFLKRNPNGLHYKWKQIPDCENKTKOCVPEQVAFQKQ-ITLLRVQASDC-----NNTS 290
Db 644 W-----EPANH-----KPL-----NNR-----FVHGLEGTGEQYIRVKNVAVGSENS 684
QY 291 FMSDEIRFTDEIQAFLIPVF--NIRSL-DSFHYIG--APROSGNTPIYQDY 339
Db 685 QESEAIR-----VOAALTCPSYPHGITLLNCDGSHMTLGMKAPKPYSGSPILGY 734

RESULT 12
DCC_MOUSE STANDARD: PRT: 1447 AA.

Id DCC_MOUSE
P70211;
Dt 01-NOV-1997 (Rel. 35, Created)
Dt 01-NOV-1997 (Rel. 35, Last sequence update)
Dt 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR.
GN DCC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-BRAIN;
RX MEDLINE: 96112625.
RA Cooper H.M., Ames P., Britto J., Gad J., Wilks A.F.;
RT "Cloning of the mouse homologue of the deleted in colorectal cancer
RT gene (mDCC) and its expression in the developing mouse embryo."
RT Oncogene 11:2243-2254(1995).
RL [2]
RN REVISIONS.
RC STRAIN-BALB/C; TISSUE-BRAIN;
RA Cooper H.M.;
RL Submitted (JUN-1996) to the EMBL/Genbank/DBI databases.
CC -1- FUNCTION: IMPLICATED AS A TUMOR SUPPRESSOR GENE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: TWO FORMS OF THE PROTEIN ARE PRODUCED FROM
CC THE SAME GENE BY THE USE OF ALTERNATIVE INITIATION SITES. A THIRD
CC FORM WHICH IS EXPRESSED ONLY IN THE EMBryo IS PRODUCED BY
CC ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: IN THE EMBryo, EXPRESSED AT HIGH LEVELS IN THE
CC DEVELOPING BRAIN AND NEURAL TUBE. IN ADULT, HIGHLY EXPRESSED IN
CC BRAIN WITH VERY LOW LEVELS FOUND IN TESTIS, HEART AND THYMUS.
CC -1- DEVELOPMENTAL STAGE: LOW LEVELS IN EARLY GESTATION. HIGHEST LEVELS
CC EXPRESSED DURING MID GESTATION. LEVELS DECREASE IN LATE GESTATION
CC AND REMAIN AT THIS LEVEL IN THE ADULT.
CC -1- SIMILARITY: CONTAINS 4 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 6 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC
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CC
CC EMBL: X85788; CAA59786.1;
CC DR HSSP: P56276; ITLK.
CC DR MGD: MGI:94869; DCC.

DR PFAM: PF00041; fn3; 6.
 DR PFAM: PF00047; 1g; 4.
 DR PRINTS: PR00014; FNTYPE11.
 KW Glycoprotein; Immunoglobulin domain; Transmembrane; Signal;
 KW Anti-oncogene; Alternative Initiation; Alternative Splicing.
 FT SIGNAL 1 25
 FT CHAIN 26 1447
 FT CHAIN 85 1447
 FT CHAIN 26 1097
 FT TRANSMEM 1098 1122
 FT DOMAIN 1123 1447
 FT DOMAIN 54 124
 FT DOMAIN 154 219
 FT DOMAIN 254 317
 FT DOMAIN 345 407
 FT DOMAIN 426 522
 FT DOMAIN 525 618
 FT DOMAIN 619 716
 FT DOMAIN 722 816
 FT DOMAIN 840 940
 FT DOMAIN 941 1042
 FT DISULFID 61 117
 FT DISULFID 161 212
 FT DISULFID 261 310
 FT DISULFID 352 400
 FT CARBOHYD 60 94
 FT CARBOHYD 94 299
 FT CARBOHYD 318 318
 FT CARBOHYD 478 478
 FT CARBOHYD 628 628
 FT CARBOHYD 702 702
 FT VARSPLIC 819 838
 FT SEQUENCE 1447 AA; 158298 MW; 0D1F1097C22D559F CRC64;

Query Match 5.2%; Score 111.5; DB 1; Length 1447;
 Best Local Similarity 21.4%; Pred. No. 1.2;
 Matches 106; Conservative 63; Mismatches 174; Indels 153; Gaps 29;

QY 6 SPQKVEVDIIDNFI-LRNNSDESYGN-TSPFYQKGMNKLSCCONITSTKCNF 63
 DB 431 ARDVLPLVYSSRFVLSRRPRAEKGNITFTVFSRGRRLALNTOP----- 483
 QY 64 SLKLT--NVYEIKRLIAEKENSSWEVDSEFPFRA-----QIGPEVLEAEDKA 115
 DB 483 GSDQLVGNLKPAMTFVNAVY--EKPGSSOPIKAYATPELOVGPVENLHA----- 537
 QY 116 IVIHISPGTKDSVMA---LDGLSFTYSLIMKSSGVEERIENTYSHKIKYKLSPEPT 171
 DB 537 --VSTSP-TSILITWEPAYANGPVGGRFLCTEVEVSTGEQNIENVGLSKLEGKKFTE 593
 QY 172 YCLAKYKALLTSKIGVYSPVHCIKTTVENELPPENIEVSQN-----Q 216
 DB 594 YTLRFLA--YNRYPGVSTDDITVTLSVPSAPPNISLEVYNSRSIKVSWMLPPSGTQ 651
 QY 217 N-----YVLK-----MDITYAM-----TFQV-----QW 235
 DB 652 NGFITIKYKIRHKTRRGEMETLEPNNLM-YLTGILEKSOVSFOVSAMTVNGTGPSPMW 710
 QY 236 LHAFLKRNQGNHLYKWKQIIPDCEN---KTQCVFPQ-----NVFQKGIYLLRVOQS 284
 DB 711 --YTAETPENDLDE--SQVPDQSSLHVRPQTCIMSTWPLPNIVVRG--YIIQGVG 765
 QY 285 DGNNTSFNSEEIKFDEIQAFLLPFPFNRLSLDSFHIY-----GAP-RQSGWT 333
 DB 766 ----SPYAEYAVVDSKQ-----YSTERLESSSHYVYISLKAENNAEGVPLESAT 814
 QY 334 PVIOD-----YPLIYEIIFMENTSNAERKIEKTDVTPVPLKPLTYVCV-----KAR 381
 DB 815 RSTIDPDPDVPDYPLDDF-----PTSG-----PDVSTPRLPVGVQAVALTHEAVR 861
 QY 382 AHTMDEKLNKSSVFS 397

DB 862 VSWADNSVPRKORTSD 877
 RESULT 13
 ID PTPD_HUMAN STANDARD; PRT; 1912 AA.
 AC P23468;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (EC 3.1.3.48) (R-PTP-DELTA).
 GN PTPRD.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP MEDLINE; 95204468.
 RA Pulido R., Krueger N.X., Serra-Pages C., Salto H., Streuli M.;
 RT "Molecular characterization of the human transmembrane
 RT protein-tyrosine phosphatase delta. Evidence for tissue-specific
 RT expression of alternative human transmembrane protein-tyrosine
 RT phosphatase delta isoforms.";
 RT J. Biol. Chem. 270:6722-6728(1995).
 RL [2]
 RP SEQUENCE OF 390-1912 FROM N.A.
 RC TISSUE-PLACENTA;
 RX MEDLINE; 91006018.
 RA Krueger N.X., Streuli M., Salto H.;
 RT "Structural diversity and evolution of human receptor-like protein
 RT tyrosine phosphatases.";
 RT EMBO J. 9:3241-3252(1990).
 RL [1]
 CC CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O -
 CC PROTEIN TYROSINE + ORTHOPHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: DIFFERENT ISOFORMS ARE FOUND IN DIFFERENT
 CC TISSUES DUE TO ALTERNATIVE SPLICING.
 CC -1- PFM: A CLEAVAGE OCCURS THAT SEPARATES THE EXTRACELLULAR DOMAIN
 CC FROM THE TRANSMEMBRANE SEGMENT.
 CC -1- SIMILARITY: EXTRACELLULAR REGION TYPIC OF A CAM FAMILY (3 IG-
 CC LIKE DOMAINS FOLLOWED BY 8 FIBRONECTIN TYPE III-LIKE DOMAINS),
 CC AND A CYTOPLASMIC REGION COMPOSED OF TWO PTPASE DOMAINS.
 CC -----
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 CC -----
 DR EMBL; L36929; AAC41749.1; -;
 DR EMBL; X54133; CA8068.1; -;
 DR PIR; S12052; S12052.
 DR HSSP; P18052; IYFO.
 DR MIM; 601598; -;
 DR PRINTS; PR00014; FNTYPE11.
 DR PRINTS; PR00700; PRTYPPHASE.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PS00386; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
 DR PFAM; PF00041; fn3; 8.
 DR PFAM; PF00047; 1g; 3.
 DR PFAM; PF00102; Y-phosphatase; 2.
 DR Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane; Duplication;
 KW Immunoglobulin domain; Alternative splicing.
 FT SIGNAL 1 20
 FT CHAIN 21 1912
 FT CHAIN 21 1265
 FT TRANSMEM 1266 1290
 FT DOMAIN 1291 1912
 FT DOMAIN 1291 1912
 FT CYTOPLASMIC (POTENTIAL).

FT DOMAIN 23 115 IG-LIKE C2-TYPE DOMAIN.
 FT DOMAIN 118 225 IG-LIKE C2-TYPE DOMAIN.
 FT DOMAIN 232 318 IG-LIKE C2-TYPE DOMAIN.
 FT DOMAIN 320 414 FIBRONECTIN TYPE-III.
 FT DOMAIN 417 513 FIBRONECTIN TYPE-III.
 FT DOMAIN 516 606 FIBRONECTIN TYPE-III.
 FT DOMAIN 609 708 FIBRONECTIN TYPE-III.
 FT DOMAIN 711 822 FIBRONECTIN TYPE-III.
 FT DOMAIN 825 916 FIBRONECTIN TYPE-III.
 FT DOMAIN 918 1017 FIBRONECTIN TYPE-III.
 FT DOMAIN 1020 1137 FIBRONECTIN TYPE-III.
 FT DOMAIN 1375 1618 PROTEIN-TYROSINE PHOSPHATASE.
 FT DOMAIN 1519 1912 PROTEIN-TYROSINE PHOSPHATASE.
 FT ACT_SITE 1553 1553 BY SIMILARITY.
 FT ACT_SITE 1844 1844 CLEAVAGE (POTENTIAL).
 FT SITE 1175 1178 CLEAVAGE (POTENTIAL).
 FT CARBOHYD 254 254 POTENTIAL.
 FT CARBOHYD 299 299 POTENTIAL.
 FT CARBOHYD 724 724 POTENTIAL.
 FT CARBOHYD 832 832 POTENTIAL.
 FT VARSPLIC 181 189 MISSING (IN KIDNEY ISOFORM).
 FT VARSPLIC 226 229 MISSING (IN KIDNEY ISOFORM).
 FT VARSPLIC 775 783 MISSING (IN KIDNEY ISOFORM).
 FT VARSPLIC 609 1137 MISSING (IN FETAL BRAIN ISOFORM).
 FT MUTAGEN 1178 1178 R->A: 2.5-FOLD REDUCTION IN CLEAVAGE.
 SO SEQUENCE 1912 AA: 214759 MW: 3A86C8CD3182E26 CRC64;

Query Match 5.1%; Score 110; DB 1; Length 1912;
 Best Local Similarity 22.9%; Pred. No. 2.2; Indels 96; Gaps 11;
 Matches 60; Conservative 24; Mismatches 82;

OY 166 LSEETTCCLVKA-----ALLTSM--KIGV 188
 DB 790 LQETSYSLVATYATGKGARSKPLVSTGAVPKRLVNHQMTALLIOMHPVDT 849
 OY 189 YSVHCKITV-ENELPPNIEVSQNONVYVKMDYTNAMTFQVOMLAFKRNQNH 247
 DB 850 FGLQGYRLKFGKRDMEPLTTLFSEKEDFTADLHKHGSYVFR--LSARKVGFGE 906
 OY 248 LYMKQIPDCENKTCQVPONVFOKGIYLLRQASDGNNTSFWSSEIRFDEIQAFLL 307
 DB 907 MKVEISLP--EVPPTG---FPQMLHSGTSTVSQVS-----WO----- 941
 OY 308 PVEFNIRISDSSEHYIYGAPKQSGNTPVIODYPLIYEIIFMENTS-----AEKIIIEKK 362
 DB 941 PVLAEKN-----GIIRKYLILRDI-----NIPLLPMQOLIVPAD 976
 OY 363 TDVTVNLKRLPIYCYKARAH 384
 DB 977 TMTLTGLKRPDTTYDVYKRAHT 998

RESULT 14
 110R_MOUSE STANDARD; PRT; 575 AA.
 ID 110R_MOUSE
 AC 061727;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE INTERLEUKIN-10 RECEPTOR PRECURSOR (IL-10R).
 GN IL10RA OR IL10R.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X AJ F1; TISSUE=HEMATOPOIETIC;
 RX MEDLINE; 94068585.
 RA Ho A.S.-Y., Liu Y., Khan T.A., Hsu D.-H., Bazan J.F., Moore K.W.:
 RT "A receptor for interleukin 10 is related to interferon receptors."
 CC Proc. Natl. Acad. Sci. U.S.A. 90:11267-11271(1993).
 CC -FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
 CC
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 CC
 CC EMBL: 112120; AAA16156.1;
 DR MGD; MGI:96538; IL10RA.
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 16
 FT CHAIN 17 575
 FT DOMAIN 241 262
 FT TRANSMEM 263 575
 FT DISULFID 204 225
 FT CARBOHYD 50 50
 FT CARBOHYD 66 66
 FT CARBOHYD 113 113
 FT CARBOHYD 182 182
 FT CARBOHYD 238 238
 SO SEQUENCE 575 AA: 64248 MW: 820B9CD576F686B7 CRC64;

Query Match 5.1%; Score 109.5; DB 1; Length 575;
 Best Local Similarity 20.0%; Pred. No. 0.5;
 Matches 75; Conservative 46; Mismatches 129; Indels 125; Gaps 16;

OY 1 GKMLKSPQKVEVDIIDNFIKRM-----NRSDESGVGVTFSPDYOKTGMDNFKLSGCCONI 56
 DB 23 GIELPSPSTVWEARFQHILMKRPNQSESTYIEVAL-----KQGNSTWMDIHICRA 78
 OY 57 TSTCKNFSSKLINVEE---IKLRIRA-EKENTSSVYEYDS-FTFPRKAQIQPVEVHLEA 111
 DB 79 QALSCDLTFETLIDLHRSYGYRARRAVQNSQXSMWTTETRET 123
 OY 112 EDKATVTHISPTKQSV-WMALDGLSTYSLIMKNSGVEERINENYSRKITYLS--- 168
 DB 123 VEVVIL-----TVDSVTLKANDGIYGIHPRPRTIFPAGDEYQGVFNDLVHYKISIK 176
 OY 168 -----PE-----TYCLKYKAALLTSKIGVSPVHCKITVENEELP 205
 DB 177 ESELKNATRKVKQETFTLTPVIGVRKFCVKVLRPLESRINKAEMSEEOCLITTYOY--- 234
 OY 206 PENIEVSQNONVYVKMDYTNAMTFQV-----QMLHAFKRNPGNHLK 250
 DB 234 -----FTVYNLSILVISMILFGILVCLVQW-----YIRHFG----- 267
 OY 251 WKQIPDCENKTCQVFPON-----VFQKGIYLLRQASDGNNTS-FWS 293
 DB 267 --KLPTVLVFKKPHDFEFPANPLCPETPAIHIVDLEVPKVSLELRDSVLHGSTDSGFGS 324
 OY 294 EEIKFDTETQAFILP 308
 DB 325 GKPSQTESQPLLP 339

RESULT 15
 EPPAS_HUMAN STANDARD; PRT; 1037 AA.
 ID EPPAS_HUMAN
 AC P54756;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
 DE KINASE RECEPTOR EHK-1) (EPH HOMOLOG KINASE-1) (RECEPTOR PROTEIN-
 DE TYROSINE KINASE HEK7).
 GN EPHA5 OR EHK1 OR HEK7.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Euthera; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Mescher G.C.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 25-1037 FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 95206782.
RA Fox G.M., Holst P.L., Chute H.T., Lindberg R.A., Janssen A.M.,
RA Basu R., Welcher A.A.;
RT *cDNA cloning and tissue distribution of five human EPH-like receptor
RT protein-tyrosine kinases.";
RL Oncogene 10:897-905(1995).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
CC EPHRIN-A1, -A2, -A3, -A4 AND -A5.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
CC -1- PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARE PRODUCED BY
CC ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSED IN THE NERVOUS
CC SYSTEM.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL: X95425; GAA64700.1; -
DR EMBL: L36644; AAA74245.1; -
DR HSSP: P00523; 2PTK.
DR MIM: 600004; -
DR PRINTS: PR00014; FNTYPEIII.
DR PRINTS: PR00107; TYRKINASE.
DR PROSITE: PS00109; PROTEIN_KINASE_ATP_1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR_1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM_1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PFAM: PF00041; fn3; 2.
DR PFAM: PF00069; kinase; 1.
DR PFAM: PF00536; SAM; 1.
DR PFAM: PF01404; Eph_Lbd; 1.
DR Transferrase: Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.
FT SIGNAL 1 24
FT CHAIN 25 1037 EPHRIN TYPE-A RECEPTOR 5.
FT DOMAIN 25 573 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 574 594 POTENTIAL.
FT DOMAIN 595 1037 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 675 936 PROTEIN KINASE.
FT NP_BIND 681 689 ATP (BY SIMILARITY).
FT BINDING 707 707 ATP (BY SIMILARITY).
FT ACT_SITE 800 800 BY SIMILARITY.
FT CARBOHYD 264 264 POTENTIAL.
FT CARBOHYD 299 299 POTENTIAL.
FT CARBOHYD 369 369 POTENTIAL.
FT CARBOHYD 423 423 POTENTIAL.
FT CARBOHYD 436 436 POTENTIAL.
FT CARBOHYD 461 461 POTENTIAL.
FT VARSPLIC 597 619 SCCECGGRASSICAVAPILLIV -> R (IN ISOFORM
FT SEQUENCE 1037 AA; 114784 MM; FC2C46C959AFB699 CRC64;
2).

Query Match 5.0%; Score 108; DB 1; Length 1037;
Best Local Similarity 20.3%; Pred. No. 1.4; Indels 162; Gaps 23;
Matches 94; Conservative 49; Mismatches 159;
QY 1 GKNLKSPQVEVDII--DDNF-----ILRMNRSDSVGNV---PSFDYQKTGMNW 47
DB 163 GRNIRKNOYIKIDITLADSDSPFELDGDVYMKLNFVBDYGLSKGFLAFQDVG---- 219
QY 48 IKLSGCONITST-----KCNFSLKLVNVEEIKIRAKEMTSSMYVEDSTFPRKAKI 102
DB 219 ---ACIALVSVYVYKCKPSVVRHLAVPDP-----TITGADSSQLELVSGSCVNHSTVD 269
QY 103 GPPEVHLEADKAIVIHISPGTKDSYMMALDGLSFTYSLIMKNSGVEERIENI-YSRH 161
DB 270 EPRKMHCSAEGEVLV---PIKCMC-----KAGYEKNKGTQVCAP 307
QY 162 KIYKLSPEPTYCLKVKAALLTSWKIGVSPVH-----CIKTVENELLP----- 206
DB 308 GFFKASPHIISC-----GKCPHSTHEASTSCVCEKDYPRRSDPTACTRP 357
QY 206 ---PENIEVSQONVYVKP-----DYTY-----ANMTFQVWLHAFLEKKNPN 246
DB 358 PSAPRNKISVNETSVFLEWIPPADTGGKRDVSYTACKKCN-----HAGVCECGG 410
QY 247 HLYKKRQIPDCENVKTQCVFQPNVFOKGIYLLRVAQSDGNNTSFWSEIKFETIEIAFL 306
DB 411 HV---RILPQSGIKNTS-----VAMVDLLAHNTYTF-----ELEA--- 444
QY 307 LPVFNIRSLDSFHIYIG---APKSGNTPVIO-----DYP-----L 341
DB 444 ---VNGVSDLSGARQVSVNTTNGAAPSPVNVKGRIAKNSISLSWQEDPDPNGIIL 500
QY 342 IYELIFEMTSMARKTIE-KKTDVYVFNKPLTYCVKRAH 384
DB 501 EYEIKHFEKDOETSYTIKSKETITTAEGLEKPAVYVFOIRART 544

Search completed: June 1, 2000, 04:38:50
Job time: 14313 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 1, 2000, 00:39:48 ; Search time 69.16 Seconds

(without alignments)
402.010 Million cell updates/sec

Title: US-09-240-675-2_COPY_27_427

Perfect score: 2141
Sequence: 1 GKNKSPQKVEVDIIDNFT.....AHWDKLNKSVFSDAVCE 401

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	668.5	31.2	569	13	O9YHMO
2	216.5	10.1	349	11	O61190
3	199	9.3	332	11	O63953
4	183.5	8.6	341	13	O9YGC8
5	133.5	6.2	918	13	O9W609
6	127.5	6.0	508	13	O9YHV9
7	125	5.8	1493	11	P97798
8	123.5	5.8	1443	13	O90610
9	123	5.7	1375	5	O94537
10	123	5.7	1326	5	O94538
11	121	5.7	1461	4	O92859
12	121	5.7	1461	4	O00340
13	117.5	5.5	1427	13	O91562
14	117.5	5.5	1585	5	O17859
15	117.5	5.5	2214	4	O92673
16	117	5.5	817	13	O07784
17	116.5	5.4	1264	5	P91767
18	115.5	5.4	658	5	O09946
19	115	5.4	26926	4	O10466
20	114	5.3	1377	11	P97603

21	113	5.3	1767	5	O24495
22	112	5.2	572	6	O29117
23	111.5	5.2	1445	11	O63155
24	111.5	5.2	1571	4	O60459
25	111.5	5.2	1896	4	O60458
26	111	5.2	6048	5	O23020
27	111	5.2	6831	5	O23550
28	111	5.2	7160	5	O23551
29	110.5	5.2	484	4	O14936
30	110.5	5.2	1898	11	O64604
31	110	5.1	2213	6	O95209
32	109	5.1	416	5	O18094
33	109	5.1	427	4	O95646
34	109	5.1	873	13	O98949
35	108.5	5.1	1040	13	O9W675
36	108.5	5.1	2033	11	O54711
37	108.5	5.1	2215	11	O88307
38	107	5.0	1651	4	O9Y6N7
39	105.5	4.9	1825	5	O61210
40	105	4.9	1948	4	O13332
41	104	4.9	1239	5	O61541
42	104	4.9	1302	5	O61542
43	103.5	4.8	896	11	O64146
44	103.5	4.8	1499	13	O90815
45	103	4.8	777	4	O9Y2H6

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	569 AA.
O9YHMO	O9YHMO			
AC	O9YHMO			
DT	01-MAY-1999 (TREMBLrel. 10, Created)			
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)			
DE	01-MAY-1999 (TREMBLrel. 10, Last annotation update)			
DE	INTERFERON ALPHA/BETA RECEPTOR 1.			
GN	IFNAR1.			
OS	Gallus gallus (chicken).			
CC	Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves;			
CC	Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-LIVER:			
RA	RESOUL J. GARDINER K. MONNERON D. UZE G. LUTFALLA G.:			
RT	"Comparative genomic analysis of the interferon/interleukin-10			
RL	receptor gene cluster.";			
RL	Genome Res. 0:0-0(1999).			
DR	EMBL; AF082664; AAD13669.1; ..			
KW	Receptor.			
SO	SEQUENCE	569 AA;	6405 MW;	F99BC099 CRC32;

Query Match

Best Local Similarity 38.0%; Score 668.5; DB 13; Length 569;
Matches 158; Conservative 77; Mismatches 154; Indels 27; Gaps 12;

OY	3	NKSPQKVEVDIIDNFTILRNNSDESVGNVTFSDYQ-----KTGMDNWKISGCONIT	57
DB	31	NKSPQKVEVDIIDNFTILRNNSDESVGNVTFSDYQ-----KTGMDNWKISGCONIT	89
OY	58	STKCNFSSKLNVYEEKLRRAE-KENTSSWYVDSFTFRKQIOTPPVHLAEKAI	116
DB	90	HTEDFSFSAITAYDTHIRIRERAKSPWSSIFEMIPETIAQIDPEIATQISNGAI	149
OY	117	VHISPTKDSV--MVALDLSFTYSLILNKSNGVEERLENIYSRKIKYLSPEYTC	174
DB	150	KINSPPEANOVKRM-LISVFKNYIVINDSSNV-EKRSILIPDIVINDLAPETIYCL	207
OY	175	KYKAAALTSKIGVYSPVHCITKTV-NELPPENIEVSVOONYYLKWDTY-ANNTFO	232
DB	208	KVQATVPLEDKGIFSPICIKTKRKVNDLCLPTNVVFLNKKFYLLMDNHNHEHTYT	267

RESULT 7
P97798 PRELIMINARY: PRT: 1493 AA.
AC P97798;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, last annotation update)
DE NEOGENIN (NEOGENIN PROTEIN).
GN NEOL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97407661.
RA KEELING S.L., GAD J.M., COOPER H.M.;
RT "Mouse Neogenin, a DCC-like molecule, has four splice variants and is
expressed widely in the adult mouse and during embryogenesis."
RL Oncogene 15:691-700(1997).
DR EMBL: Y09535; CAAT0727.1; -.
DR HSSP: P02751; 1TTC.
DR MGD: MGI:1097159; Neol.
DR PFAM: PF00041; fn3; 6.
DR PFAM: PF00047; 19; 4.
DR PRINTS: PR00014; FNTYPEI1.
SQ SEQUENCE 1493 AA; 163159 MW; 98F26676 CRC32;

Query Match 5.8%; Score 125; DB 11; Length 1493;
Best Local Similarity 21.3%; Pred. No. 0.12;
Matches 86; Conservative 74; Mismatches 184; Indels 60; Gaps 20;

OY 6 SPOKVEVDIIDNFI-LRMN--RSDESVGNVTFSDYOKTGMNMIKLSGCONITSTKCN 59
DB 472 APRVVASLSTFRFKIKLWRTSPASDPDGNLTYSIFTKESVDR---ERVNLSQPGEM 527
OY 59 --TKCNFSSKLNYEEIKLIRAEKENTSSWYEVDSFTPRKAOIGPEVHLEADKAI 116
DB 528 QVTIONLMPATVYIF-----KVMQNKHGSG---ESSAPLRVET--QPEVOLPGAPAPNI 576
OY 117 VIHISPTKDSVMAL----DGLSTYSLLIMKNSGVEERIENTYSHKIKYKSPETTY 172
DB 577 RAYATSPSTIVETWETPLSGNCEIONKLYWEKGTDEKODIDVSSHYTNGLKKTLEY 636
OY 173 CLKAKALITSMKIGVSPVHCITVTENELPPRENIEVSQN--ONYVLK--DYTYAN 228
DB 637 SFRVVA--YKNHGPVSTQDVAVRFLSDVPSAAPONLSLEVRNKSSTVIHKOPSSITON 694
OY 229 --MTFOVOMLHAFILKRNPGNHLKMKQIPDCENVKTTCQVFPONVFCIGIYLLRQASD 285
DB 695 GOITGKTRKRYKASRSKSVETELVTGTL-----SGLT--BGLDRGTEYVFRVALT 744
OY 286 GNNT---SFWSEIKFDTETIAFLPPV---FNIRSLDSFHIIYIGAPKOSGNTPVODY 339
DB 745 VNGTGPATDWSAETFEESDLETRVPEVPSLHVAPLVTST--VVSMTPEPQNI--VVRGY 802
OY 340 PLIEIIFMENTSNAR-KIIEKTDVTPNKLPLTVYCVARA 382
DB 803 AIGGI-----GSPHAQITKVDYKQRYTIENTLDPSSHVYITLKA 842

RESULT 8
O90610 PRELIMINARY: PRT: 1443 AA.
AC O90610;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, last annotation update)
DE NEOGENIN (FRAGMENT).
GN Gallus gallus (Chicken).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN-WHITE LECHORN; TISSUE-BRAIN;
RX MEDLINE: 95105243.
RA VIELMEYER J., ROMAN J.M., DREYER W.J.;
RT "Neogenin, an avian cell surface protein expressed during terminal
neural differentiation, is closely related to the human tumor
suppressor molecule deleted in colorectal cancer."
RL J. Cell Biol. 127:2009-2020(1994).
DR EMBL: U07644; AAC59662.1; -.
DR HSSP: P80362; 1WTL.
DR PFAM: PF00041; fn3; 6.
DR PFAM: PF00047; 19; 4.
FT NON_TER
SQ SEQUENCE 1443 AA; 158050 MW; 270B77DC CRC32;

Query Match 5.8%; Score 123.5; DB 13; Length 1443;
Best Local Similarity 22.0%; Pred. No. 0.15;
Matches 89; Conservative 60; Mismatches 194; Indels 61; Gaps 19;

OY 6 SPOKVEVDIIDNFI-LRMN--RSDESVGNVTFSDYOKTGMNMIKLSGCONITSTKCN 62
DB 427 APRDVATLVSFRFKIKLWRTSPASDPDGNLTYSIFTKESVDR---INERVEN-TSPGE 481
OY 63 FSLKLNVEEIKLIRAEKENTSSWYEVDSFTPRKAOIGPEVHLEADKAIYIHSP 122
DB 482 TQVMIONLMPETVYVFRVVAQNKHGSG---SSAPLKVAT--QPEVOLPGAPAPNIAYGS 537
OY 123 GTFDSVMAL----DGLSTYSLLIMKNSGVEERIENTYSHKIKYKSPETTYCLKYKA 178
DB 538 PSTVATWETPLSGNCEIONKLYWEKGTDEKODIDVSSHYTNGLKKTLEYSRVVA 597
OY 179 ALLTSKIKVSPVHCITVTENELPPRENIEVSQN--ONYVLKMDYTYANTFOVOMLH 237
DB 598 --YKNHGPVSTQDVAVRFLSDVPSAAPONLTLLEARNKSIHLHQPPRA----- 646
OY 238 AFLKRNPGNHL-----YKNKQIPDCENVKTTCQVFPONVFO--KGL-----YLLRQASD 285
DB 646 -----GTHSGQITGKIRYKRSKSDTEVSGTOLFOLIEGRTEYVFRVALT 698
OY 286 GNNT---SFWSEIKFDTETIAFLPPV---FNIRSLDSFHIIYIGAPKOSGNTPVODY 339
DB 699 VNGTGPATDWSAETFEESDLETRVPEVPSLHVAPLVTST--VVSMTPEPQNI--VVRGY 756
OY 340 PLIEIIFMENTSNAR-KIIEKTDVTPNKLPLTVYCVARA 382
DB 757 AIGGI-----GSPHAQITKVDYKQRYTIENTLDPSSHVYITLKA 796

RESULT 9
O94537 PRELIMINARY: PRT: 1375 AA.
AC O94537;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, last annotation update)
DE FRAZZLED.
GN FRAZZLED.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97015076.
RA KOTLOZIER P.A., TIMPE L., MITCHELL K.J., GOODMAN C.S., FRIED S.,
VAN L.Y., VAN Y.N.;
RT "Frazzled encodes a Drosophila member of the DCC immunoglobulin
subfamily and is required for CNS and motor axon guidance."
RL Cell 87:197-204(1996).
DR EMBL: U71001; AAC47314.1; -.
DR FLYBASE: FBgn0011592; fra.
DR PFAM: PF00041; fn3; 6.

DR PFAM: PF00047; 19; 3.
DR PRINTS: PR00014; FNTYPEITI.
SQ SEQUENCE 1375 AA; 151692 MW; 43806DBC CRC32;

Query Match 5.7%; Score 123; DB 5; Length 1375;
Best Local Similarity 16.3%; Pred. No. 0.15;
Matches 101; Conservative 68; Mismatches 184; Indels 268; Gaps 22;

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QY 1 GNKLKS-----POKEVDIIDDNFI-LRW-----NRSDSVG 31
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 448 GKRLDGLGRLPSPQPRDLVAQIVKSRFTLSMVEPLQAGDVYYTYKKNNSEBCK 507
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 32 NTTFSEFDYOKTGMNWKIKSGCONITSTKCNFS-----LKLNYEEIKLR-----78
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 508 MYTKSHDDQOVNIQSLPGRTYQFRVEANTNFGSASAPLEVSTQPEVNIAGPPRNEEG 567
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 78 -IRAENKNTSSWE-----VD 92
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 568 YARSHKEIYKKEEPTVTNGEILTKRYVYSENDGADLYHDSTALEAVLTLPHTDYI 627
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 93 SEFPFRKAQIG-----PREVHLE-AEDKAIYIHISPGTKDSVMALD 133
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 628 SYVPEFRNMGDSSAEIRKFTSPSEPPNNVTLEVTSSSITVHMEPPAEEDRNGQIT 687
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 134 GLSTFTSLIKMNSSGVEERIENTYSRHKIYKLSPEPTYCLVKKALL-----TSWKIG 187
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 688 GKIRIRYK--FKDAPOVKSTPANI-RYFELSLDRNAEYQVIAAMTVNGSGPTEMNRA 744
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 188 VSPVHCITTYENELP-----PPENIEVSQNONVYK 222
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 745 -----NTLENDLDETQVPGKPIWISHPGANNIALHMGPPQHPKIKI--RNYVLGM 793
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 223 -----DY-----225
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 794 GRGIPDENTIELKETERHYILKNLESMDYVYSLARANKGDPPIYDNKTRDEPVA 853
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 225 -----TYANMFOVOMLHAFILKN-----PGNHLTKKQIPD 256
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 854 PPPELVPGVGLRAITMSSSIYVYVIMIDMLKNQHTDNRHYTVSYGITSNRYRY-----909
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 257 CENVKTCQVFPQNFQKGIYLLRQASDGNNTSPMSEELKFDTELQAFLLPVPVFNIRSL 316
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 909 -HNTDNLNCKI-NDLRPNTOFEFAVKVYKGRRESSMSVSLNSTYQNVPTPP-----960
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 317 SDSFHIYIGAPKOSGNTPIYQDP-----LIYEIIEMENTSNAER-----KIIIEKKT 363
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 960 ---REVTVRLDEMNPPTYIVQWIPPKHILGOITGINIYITDTTKRDNRMSVFAFAGEET 1016
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 364 DVTVPNLKPLTYVCYKARAHT 384
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1017 MLMPLNLKPYTYTFYFKVOART 1037
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

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RESULT 10

094538 PRELIMINARY; PRT; 1526 AA.
AC 094538;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE FRAZZLED.
GN
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN (1)
RN SEQUENCE FROM N.A.
RX MEDLINE; 97015076.
RA KOLODZIEJ P.A., TIMPE L., MITCHELL K.J., GOODMAN C.S., FRIED S.,
RA JAN L.Y., JAN Y.N.,
RT *frazzled encodes a Drosophila member of the DCC immunoglobulin

RT subfamily and is required for CNS and motor axon guidance.";
DR Cell 87:197-204(1996).
DR EMBL; U71002; AAC47315.1; -.
DR FLYBASE; FBgn0011592; fra.
DR PFAM: PF00041; fn3; 6.
DR PFAM: PF00047; 19; 3.
DR PRINTS: PR00014; FNTYPEITI.
SQ SEQUENCE 1526 AA; 168787 MW; F17B1EC9 CRC32;

Query Match 5.7%; Score 123; DB 5; Length 1526;
Best Local Similarity 16.3%; Pred. No. 0.18;
Matches 101; Conservative 68; Mismatches 184; Indels 268; Gaps 22;

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QY 1 GNKLKS-----POKEVDIIDDNFI-LRW-----NRSDSVG 31
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 599 GKRLDGLGRLPSPQPRDLVAQIVKSRFTLSMVEPLQAGDVYYTYKKNNSEBCK 658
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 32 NTTFSEFDYOKTGMNWKIKSGCONITSTKCNFS-----LKLNYEEIKLR-----78
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 659 MYTKSHDDQOVNIQSLPGRTYQFRVEANTNFGSASAPLEVSTQPEVNIAGPPRNEEG 718
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 78 -IRAENKNTSSWE-----VD 92
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 719 YARSHKEIYKKEEPTVTNGEILTKRYVYSENDGADLYHDSTALEAVLTLPHTDYI 778
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 93 SEFPFRKAQIG-----PREVHLE-AEDKAIYIHISPGTKDSVMALD 133
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 779 SYVPEFRNMGDSSAEIRKFTSPSEPPNNVTLEVTSSSITVHMEPPAEEDRNGQIT 838
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 134 GLSTFTSLIKMNSSGVEERIENTYSRHKIYKLSPEPTYCLVKKALL-----TSWKIG 187
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 839 GKIRIRYK--FKDAPOVKSTPANI-RYFELSLDRNAEYQVIAAMTVNGSGPTEMNRA 895
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 188 VSPVHCITTYENELP-----PPENIEVSQNONVYK 222
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 896 -----NTLENDLDETQVPGKPIWISHPGANNIALHMGPPQHPKIKI--RNYVLGM 944
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 223 -----DY-----225
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 945 GRGIPDENTIELKETERHYILKNLESMDYVYSLARANKGDPPIYDNKTRDEPVA 1004
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 225 -----TYANMFOVOMLHAFILKN-----PGNHLTKKQIPD 256
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1005 PPPELVPGVGLRAITMSSSIYVYVIMIDMLKNQHTDNRHYTVSYGITSNRYRY-----1060
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 257 CENVKTCQVFPQNFQKGIYLLRQASDGNNTSPMSEELKFDTELQAFLLPVPVFNIRSL 316
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1060 -HNTDNLNCKI-NDLRPNTOFEFAVKVYKGRRESSMSVSLNSTYQNVPTPP-----1111
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 317 SDSFHIYIGAPKOSGNTPIYQDP-----LIYEIIEMENTSNAER-----KIIIEKKT 363
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1111 ---REVTVRLDEMNPPTYIVQWIPPKHILGOITGINIYITDTTKRDNRMSVFAFAGEET 1167
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 364 DVTVPNLKPLTYVCYKARAHT 384
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1168 MLMPLNLKPYTYTFYFKVOART 1188
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

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RESULT 11

092859 PRELIMINARY; PRT; 1461 AA.
AC 092859;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE NEOGENIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN (1)
RN SEQUENCE FROM N.A.
RA MEYERHARDT J.A., LOOK A.T., BIGNER S.H., FEARON E.R.,

RL Oncogene 0:0-0(0).
DR EMBL: U61262; AAB17263.1; -
DR HSSP: P02751; 1TTG.
DR PFAM: PF00041; fn3; 6.
DR PFAM: PF00047; 19; 4.
DR PRINTS: PR00014; FNTYPEIII.
SQ SEQUENCE 1461 AA; 159958 MW; 0AB7247E CRC32;

Query Match 5.78; Score 121; DB 4; Length 1461;
Best Local Similarity 20.8%; Pred. No. 0.24;
Matches 83; Conservative 77; Mismatches 188; Indels 52; Gaps 19;

QY 6 SPOKVEVDIIDDNFI-LRMN--RSDESNGVNTFSFDYQKTKGM--DNWIKLSCGQNTSTK 60
DB 441 APRDVAVSLVSTRFIKLTMTTPASDPHGNDLITYSVFTKEGIANERENTSHREGMOVYI 500
QY 61 CNFSSKLNVYEEIKLRIRAEKENTSSWYVDSTFPRKAOIGPPEVHLEADKAIVIH 120
DB 501 ONLMPATVYIF-----RVMAQNKHGSG-----ESSAPLRVET--QPEVOLGPPAPNLRAYA 549
QY 121 SPTKDSVMMAL----DGLSTYSLLIMKNSGVEERENIYSRHKIYKLSPTTYCLAV 176
DB 550 ASPTSTIVTETWETPVSGNGEIONKLYMEKGTDEQDVSSHSYTLINGLKKYTEYSFRV 609
QY 177 KAALLTSMKIGVSPVHCITKTVENELPPENIEVSQN--ONYLKWMD-----ITYANMT 230
DB 610 VA--YKNGHGVSTPDVAVRTLSDVPSAAPONLSLEVRANSKSMIMHOPAPATQNGOIT 667
QY 231 -FOVOMLHAFKRNPNHLLKWKMOIPDCENVKTQCVFPONVFOKGIYLLRVOASDGNNT 289
DB 668 GYKIRYRKASRKSDVTELVSGTQ-----SGLI--EGLDRGTEYNEFRVALTINGT 717
QY 290 ---SFMSSEIKFDTETIQAFLLPV---FNIRSLDSFHIYIGAKOSGNTPIYODYPLY 343
DB 718 GPATDMLSAETFEESDDETRVPEVPSLHVRLVTSI--VSWTPPENONI--VVRGVAIGY 775
QY 344 EIFFMENTSNAER-KIIEKKTDTVTPNKLPLTVYCVKARA 382
DB 776 GI-----GSPHAQTIKVDKORYTIENLDPSSHYVITLKA 811

RESULT 12
000340
ID 000340; PRELIMINARY; PRT; 1461 AA.
AC 000340;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE NEUGENIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-BRAIN;
RX MEDLINE: 97312699.
RA VIELMEYER J., CHENG X.N., MISKEYICH F., LANE R.P., YAMAKAWA K.,
RA KOENIGBERG J.R., DREYER W.J.;
RT "Molecular characterization of human neogenin, a DCC-related protein,
RT and the mapping of its gene (NEO1) to chromosomal position 15q22.3-
RT q23."
RL Genomics 41:414-421(1997).
DR EMBL: U72391; AAC51287.1; -
DR HSSP: P02751; 1TTG.
DR PFAM: PF00041; fn3; 6.
DR PFAM: PF00047; 19; 4.
DR PRINTS: PR00014; FNTYPEIII.
SQ SEQUENCE 1461 AA; 160015 MW; 9D5AEC4 CRC32;

Query Match 5.78; Score 121; DB 4; Length 1461;
Best Local Similarity 20.8%; Pred. No. 0.24;

Matches 83; Conservative 77; Mismatches 188; Indels 52; Gaps 19;

QY 6 SPOKVEVDIIDDNFI-LRMN--RSDESNGVNTFSFDYQKTKGM--DNWIKLSCGQNTSTK 60
DB 441 APRDVAVSLVSTRFIKLTMTTPASDPHGNDLITYSVFTKEGIANERENTSHREGMOVYI 500
QY 61 CNFSSKLNVYEEIKLRIRAEKENTSSWYVDSTFPRKAOIGPPEVHLEADKAIVIH 120
DB 501 ONLMPATVYIF-----RVMAQNKHGSG-----ESSAPLRVET--QPEVOLGPPAPNLRAYA 549
QY 121 SPTKDSVMMAL----DGLSTYSLLIMKNSGVEERENIYSRHKIYKLSPTTYCLAV 176
DB 550 ASPTSTIVTETWETPVSGNGEIONKLYMEKGTDEQDVSSHSYTLINGLKKYTEYSFRV 609
QY 177 KAALLTSMKIGVSPVHCITKTVENELPPENIEVSQN--ONYLKWMD-----ITYANMT 230
DB 610 VA--YKNGHGVSTPDVAVRTLSDVPSAAPONLSLEVRANSKSMIMHOPAPATQNGOIT 667
QY 231 -FOVOMLHAFKRNPNHLLKWKMOIPDCENVKTQCVFPONVFOKGIYLLRVOASDGNNT 289
DB 668 GYKIRYRKASRKSDVTELVSGTQ-----SGLI--EGLDRGTEYNEFRVALTINGT 717
QY 290 ---SFMSSEIKFDTETIQAFLLPV---FNIRSLDSFHIYIGAKOSGNTPIYODYPLY 343
DB 718 GPATDMLSAETFEESDDETRVPEVPSLHVRLVTSI--VSWTPPENONI--VVRGVAIGY 775
QY 344 EIFFMENTSNAER-KIIEKKTDTVTPNKLPLTVYCVKARA 382
DB 776 GI-----GSPHAQTIKVDKORYTIENLDPSSHYVITLKA 811

RESULT 13
091562
ID 091562; PRELIMINARY; PRT; 1427 AA.
AC 091562;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE TUMOR SUPPRESSOR.
GN XPCCA.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae;
OC Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95113183.
RA PIERCEBALI W.E., REALE M.A., CANDIA A.F., WRIGHT C.V., CHO K.R.,
RA FEARON E.R.;
RT "Expression of a homologue of the deleted in colorectal cancer (DCC)
RT gene in the nervous system of developing xenopus embryos."
RL Dev. Biol. 166:654-665(1994).
DR EMBL: U10986; AAT70168.1; -
DR HSSP: P56276; 1TLK.
DR PFAM: PF00041; fn3; 6.
DR PFAM: PF00047; 19; 4.
DR PRINTS: PR00014; FNTYPEIII.
SQ SEQUENCE 1427 AA; 156533 MW; E50B7475 CRC32;

Query Match 5.58; Score 117.5; DB 13; Length 1427;
Best Local Similarity 22.2%; Pred. No. 0.44;
Matches 93; Conservative 70; Mismatches 163; Indels 93; Gaps 22;

QY 6 SPOKVEVDIIDDNFI-LRMNRSDESNGVNTFSFDYQKTKGMWIKLSCGQNTSTKCNF 63
DB 431 APRDVAVSLVSTRFVRSRPPESKGNITOTIYVFSKQVQAEKRAVNTSQPT----- 484
QY 64 SSKLVN-----YEEIKLRIRAEKENTSSWYVDSTFPR-----KAOIGPPEVHLEAD 113
DB 484 -SLQITVGNLTPETTYFRVAVAYNE-----WGPSSQGVAVVYQPELOVGVPEVNLQ--- 536
QY 114 KATYTHISPTKDSVMMALDGLSFT-----YSLIMKNSGVEERENIYSRHKIYKLS 167

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Db 536 ---VSTAP---TSVLISMDPPAYANGPVOCYLLFCAETFSGREQINTEVDGIYRLGLR 589
OY 168 PETTYCLKYKALLTSMKIVSPVHCIKTTVENELPPENIEVSQONONYLAKNDYTA 227
Db 590 KFEYSIRFLA--YNRGCGVSESEHTVTLSPVSAHQNSLEVAN-----636
OY 228 NMTFOVOMLHAFKRNPNHNL-----YKMKQIPDCENVKT-----OCVFPONVF-----273
Db 636 SRSIKVSW---LPPEPGTONGFITGYK-----IRHRRKTRRGELETLEPNLMLYFTG 685
OY 273 -OKGI-YLLRVOASDGNNTSFMSEIKFDT-----EIQAFLLPPVFNRLSDSHIYI 324
Db 686 LKGGSOISQVAAAMTVNGSPSSDWTATLPENDLDESQVDPQSSLHVRPLTTSI-INS 744
OY 325 GAPKOSGNTPVIODYPLIYEIFEIMENTSNAER-KIIEKTDVTPVILKPLTYCVKARA 382
Db 745 WPPPLNPNL-VVRGVIIGIV-----GSPYAEYVRVDSKORYSIENLEPSSHIVISLKA 798

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RESULT 14
ID 017859 PRELIMINARY: PRT: 1585 AA.
AC 017859: Q20137:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE C09D8.1 PROTEIN.
GN C09D8.1
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabdilita; Rhabdilitida;
OC Rhabdilita; Rhabdilitidae; Rhabdilitidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RA COLES L.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z46811; CA86842.1;
DR EMBL: Z49938; CA86842.1; JOINED.
DR EMBL: Z49938; CA86842.1; JOINED.
DR EMBL: Z46811; CA86842.1; JOINED.
DR HSP: P28827; 1RP.
DR PFAM: PF00041; fn3; 3.
SQ SEQUENCE 1585 AA; 178386 MW; E403A8DD CRC32;

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Query Match 5.5%; Score 117.5; DB 5; Length 1585;
 Best Local Similarity 19.7%; Pred No. 0.51;
 Matches 86; Conservative 74; Mismatches 171; Indels 105; Gaps 24;

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OY 7 POKVEYDIDDNFILMNRSDSEV--GNVTFSEYOKTGMWIKLSCGONITSTKCNFS 64
Db 263 PIDVQEVKAKIVSWRPSESEKRNIT-SYKAILSMND--ATADRYEQVPAPSTSS 319
OY 65 SIKLNYEIKLRIR-----EKNTSSIVEY---D 92
Db 320 TEEVNRRAVLFKVAATKKGIGPSPVLINPDADLIDNNIEEENQDPGEKTMEE 379
OY 93 SFTPEKAOIGPEVLEAEKAVIHISPGTKDSYMAALDGLSFYSLILKNSGVEE 152
Db 380 NNNPKKSIKSTADY-----SAILHAPGP-----LTHISALAKAKATTICA 423
OY 153 RIENIYSRHKIKYSPETTYCLKVKAALLTSMKIVSPVHCIKTTVENELPPENIEV- 212
Db 424 PVPAPYTTTS---TPSTLFFOVTLPMTTAMN-----RVTKLETLVGPPTVAVYE 470
OY 212 SYQONONYVUKNDYTYANM--TFQVOMLHAFKRNPNHNL--YKMKQIP-----DCENKTKTQ 264
Db 471 AISNSNAVVOQMPDESOKADSFVVKIWH-----EPGNRMDEKMKQPLPVVSIKENPKRA 525
OY 265 CVFPONVFOKGIYLLRVQASDGNNTSFMSEIEIKTFDEIOAFLLPVPFNIRSL-----SD 318
Db 526 VVSDLNAPHR--YAFCVLAVKNNRQGPCDP---PTVLES--VTPIYQONLRLVLMKTSN 578

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OY 319 SFHI---YIGAKOSG---NTPVIODYPLIYEIFEIMENTSNAE---KIIEKTDVTPVN 369
Db 579 SVQLTWEYNG--PRNVGFYNNHTRGRDY--VNHLE--QEKTMSTPGGVODEKHEVLTN 634
OY 370 LKPLVYCVKARAHNM 385
Db 635 LRPMMYTIHVGRTL 650

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RESULT 15
ID 092673 PRELIMINARY: PRT: 2214 AA.
AC 092673: Q92856;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN LR11 PRECURSOR
DE (LR11).
GN LR11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA MOERWALD S., YAMAZAKI H., BUJO H., KUSUNOKI J., KANANI T., SEIMIYA K.,
RA MORISAKI N., NIMPE J., SCHNEIDER W.J., SAITO Y.;
RA NYKJAER A., SOTTRUP-JENSEN L., GLENNAN J., PETERSEN C.M.;
RT "Molecular characterization of a novel human hybrid-type receptor that
RL binds the alpha2-macroglobulin receptor-associated protein."
RN J. Biol. Chem. 271:31379-31383(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA JACOBSEN L., MADSEN P., MOESTRUP S.K., LUND A.H., TOMMERUP N.,
RA JACOBSEN L., MADSEN P., LUND A.H., TOMMERUP N., GLENNAN J.,
RA PETERSEN C.M.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: LIKELY TO BE A MULTIFUNCTIONAL RECEPTOR. BINDS LDL, THE
CC MAJOR CHOLESTEROL-CARRYING LIPOPROTEIN OF PLASMA, AND TRANSPORTS
CC IT INTO CELLS BY ENDOCYTOSIS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: ABUNDANT IN BRAIN, LIVER, KIDNEY AND PANCREAS
CC WITH DETECTABLE LEVELS IN PLACENTA, LONG AND HEART.
CC -1- SIMILARITY: CONTAINS 11 LDL-RECEPTOR CLASS A DOMAINS.
CC EMBL: Y08110; CA69325.1;
DR EMBL: Y08110; CA69325.1;
DR HSP: P01130; 1A0J.
DR PROSITE: PS01209; LDLR_1; 10.
DR PFAM: PF00057; ldl_recept_a; 11.
DR PFAM: PF00058; ldl_recept_b; 4.
DR PFAM: PF00041; fn3; 5.
DR PRINTS: PR00261; LDLRECEPTOR.
DR PRINTS: PR00014; FNTPETIT.
KM Receptor; Transmembrane; Signal; Repeat; Glycoprotein; LDL;
KM Cholesterol metabolism; Lipid transport.
KW SIGNAL
FT CHAIN 1 28
FT DOMAIN 29 2214 LOW-DENSITY LIPOPROTEIN RECEPTOR LR11.
FT DOMAIN 29 2135 EXTRACELLULAR.
FT DOMAIN 1076 1114 LDL-RECEPTOR CLASS A 1.
FT DOMAIN 1115 1155 LDL-RECEPTOR CLASS A 2.
FT DOMAIN 1156 1194 LDL-RECEPTOR CLASS A 3.
FT DOMAIN 1197 1226 LDL-RECEPTOR CLASS A 4.
FT DOMAIN 1233 1285 LDL-RECEPTOR CLASS A 5.
FT DOMAIN 1287 1317 LDL-RECEPTOR CLASS A 6.
FT DOMAIN 1323 1361 LDL-RECEPTOR CLASS A 7.
FT DOMAIN 1366 1405 LDL-RECEPTOR CLASS A 8.

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 1, 2000, 04:17:57 ; Search time 12.38 seconds
(without alignments)
834,180 Million cell updates/sec

Title: US-09-240-675-2
Perfect score: 2313
Sequence: 1 MMYVLLGATTLVLA VGPWV.....KSVFSDAVCEKTRPGNTSK 436

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues
Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	2313	100.0	R14487	Soluble Interferon
2	2313	100.0	R28495	Sequence of a soul
3	2313	100.0	R11958	Human alpha-interf
4	2313	100.0	R14488	Complete Interfero
5	2313	100.0	R28496	Sequence of a soul
6	2313	100.0	R42635	Human Interferon r
7	2309	99.8	R75356	Human IFN receptor
8	2308	99.8	R21804	Transmembranl int
9	2304	99.6	R11723	IFN receptor extra
10	2260	97.7	R21805	Spliced-deleted in
11	2208	95.5	R21806	Spliced-deleted in
12	228.5	9.9	R52296	CREB4 protein. New
13	203	8.8	R75782	IFN-gamma receptor
14	198	8.6	R79155	cytor7 cytokine r
15	155.5	6.7	R71035	Human IFN-gamma ac
16	153.5	6.6	R75783	IFN-gamma receptor
17	151	6.5	R797861	Human cytokine rec
18	131.5	5.7	R797864	Human cytokine rec
19	118.5	5.1	R70113	Gamma-IFN-R-GP 13
20	118	5.1	R14642	Gamma interferon r
21	118	5.1	R227	Gamma interferon r
22	118	5.1	R14641	Extracellular doma
23	118	5.1	R55749	Plasmod pBABU hu
24	118	5.1	R07469	Rat receptor tyros
25	117.5	5.1	R83147	Interleukin-10 rec
26	117.5	5.1	R57139	Mouse IL-10 recept
27	117.5	5.1	R41803	Human LDL receptor
28	115.5	5.0	R26357	Gamma Interferon r
29	114.5	5.0	R14643	Soluble human inte
30	113.5	4.9	R62023	Deleted in Colorec
31	111.5	4.8	R13144	Human Down syndrom
32	111.5	4.8	R42086	Human Down syndrom
33	110	4.7	R26356	Rabbit LDL receptor
34	108	4.7	R85090	EPH-like receptor

35	107	4.6	426	1	W09822	Human Interleukin-
36	107	4.6	427	1	W24973	Human Interleukin-
37	107	4.6	753	1	W83927	Human r85 protein.
38	107	4.6	1370	1	R60005	Sequence encoded b
39	106.5	4.6	928	1	R97853	Rat RKR7 eph-relat
40	105.5	4.6	400	1	R75203	Tyrosine phosphata
41	105.5	4.6	878	1	R78608	Murine IL-3 recept
42	104.5	4.5	596	1	R78616	Expression vector
43	104.5	4.5	600	1	R78610	Expression vector
44	104.5	4.5	600	1	R25226	Fas antigen #1. Im
45	104.5	4.5	660	1	R69633	Human Interleukin-

ALIGNMENTS

RESULT 1
ID R14487 standard; Protein: 436 AA.
AC R14487:
DE 16-JAN-1992 (first entry)
KW Soluble Interferon-alpha/beta receptor.
OS IFN; autoimmune disease; graft rejection; histocompatibility.
KM Homo sapiens.
PN FR2657881-A.
PD 09-AUG-1991.
PF 05-FEB-1990; 001298.
PR 05-FEB-1990; FR-001298.
PA (EUBI-) LAB EURO BIOTECNO.
PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE;
PI Tovey MG. Use G;
DR WPI, 91-319778/44.
DR N-PSDB: Q14239.
PT New water-soluble polypeptide(s) with affinity for IFN-alpha and
PT beta - used to treat e.g. lupus erythematosus, Behcet's disease,
PT aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.
PS Claim 2; Page 45; 52pp; French.
CC The transmembrane and cytoplasmic domains of the native IFN receptor
CC have been deleted to obtain a soluble, circulating form of the
CC receptor. Potentially immunogenic epitopes have thus been eliminated.
CC Derivatives obtained by substitution or deletion of this sequence
CC are also claimed as are hybrid molecules comprising the soluble
CC receptor (or deriv.) and an immunoglobulin such as IgG1.
CC See also Q14240.
SQ Sequence 436 AA:

Query Match 100.0%; Score 2313; DB 1; Length 436;
Best Local Similarity 100.0%; Pred. No. 2.3e-203;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MMYVLLGATTLVLA VGPWVLSAAGGKNLKSPOKVEYDIIDDFILRMRSDESQVNT	60
DB	1	MMYVLLGATTLVLA VGPWVLSAAGGKNLKSPOKVEYDIIDDFILRMNSDSQVNT	60
QY	61	FSPDYQKGMNMKILSCGNTSTKCNFSLKYNVEIKLRRAEKENTSSVYEYDSF	120
DB	61	FSPDYQKGMNMKILSCGNTSTKCNFSLKYNVEIKLRRAEKENTSSVYEYDSF	120
QY	121	TPFRKAQIGPPEVHLEADKAIVIHISPGTDSVMALDGLSFTYSLIMKNSGVEERI	180
DB	121	TPFRKAQIGPPEVHLEADKAIVIHISPGTDSVMALDGLSFTYSLIMKNSGVEERI	180
QY	181	ENIYSRHKIYKLSPEYTCGLVKAALLTSKIGIVSPVHCITTYENLPPENIEVSQ	240
DB	181	ENIYSRHKIYKLSPEYTCGLVKAALLTSKIGIVSPVHCITTYENLPPENIEVSQ	240
QY	241	NONVYLKNDYTYANNTFOVOMHAFLKRNPGNHLKMKOIPDCEVNTQCFPQNVOK	300
DB	241	NONVYLKNDYTYANNTFOVOMHAFLKRNPGNHLKMKOIPDCEVNTQCFPQNVOK	300
QY	301	GYLLRVQASDGNNTSFWSEIKFDTETIOAFLLPVFNIRLSDSFHIYIGAKOSGNTP	360
DB	301	GYLLRVQASDGNNTSFWSEIKFDTETIOAFLLPVFNIRLSDSFHIYIGAKOSGNTP	360

Db 301 GYLLRQASDGNNTSFWESEIKFDTEIOAFLLPPVFNIRSLSDSFHIIYGAPKQSGNTP 360
QY 361 VIODYPLIYEIIFWENTSNAERKIIKKTDVTPVNLKPLTVYCVKARAHMDEKLNKSSV 420
Db 361 VIODYPLIYEIIFWENTSNAERKIIKKTDVTPVNLKPLTVYCVKARAHMDEKLNKSSV 420
QY 421 FSDAVCEKTPGNTSK 436
Db 421 FSDAVCEKTPGNTSK 436

RESULT 2

R28495
ID R28495 standard; Protein; 436 AA.
AC R28495;
DT 31-MAR-1993 (first entry) 1
DE Sequence of a soluble form of the interferon (IFN) receptor
KW With a high affinity for IFN-alpha and -beta.
OS Interferon receptor; alpha-interferon; beta-interferon.
PN Synthetic.
PM WO9218626-A.
PD 29-OCT-1992.
PE 17-APR-1991; F00318.
PR 17-APR-1991; WO-F00318.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,
PI Toyey M, Uze G;
DR WPI: 92-382110/46.
DR N-PSDB: Q30532.
PT Water soluble polypeptide(s) strongly bind interferon(s) alpha
PT diseases and transplant rejection
PS Claim 2; Fig 1; 58pp; English.
CC DNA encoding the water-soluble polypeptide with a high affinity for
CC IFN-alpha and -beta is isolated by PCR, using appropriate
CC oligonucleotides as primers and cloned cDNA as template. For example,
CC bacteriophage lambda ZAP, containing the entire coding sequence of
CC the IFN-alpha and -beta receptor (Q30533), was incubated with Oligos
CC Q30534 and Q30535. R28496 represents the complete receptor. R28495
CC lacks the transmembrane and cytoplasmic domains. Both forms bind
CC IFN in the same way as antibodies so are immunosuppressants e.g. for
CC treating autoimmune diseases and graft rejection. They lack the
CC toxic side-effects of known immunosuppressants such as steroids.
SQ Sequence 436 AA;

Query Match 100.0%; Score 2313; DB 1; Length 436;
Best Local Similarity 100.0%; Pred. No. 2.3e-203;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVVLGATTLVAVGPNVLSAAGGNLKSPOKVEVDIIDNFIILRNRSDESIGNVT 60
Db 1 MMVVLGATTLVAVGPNVLSAAGGNLKSPOKVEVDIIDNFIILRNRSDESIGNVT 60
QY 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSSKLNVYEIKLRIRAEKENTSSWYEVDSF 120
Db 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSSKLNVYEIKLRIRAEKENTSSWYEVDSF 120
QY 121 TPFRAQOIGPPEVHLEADKAIVIHISPGTDSVMALDGLSFTYSLLIMKSSGVEERI 180
Db 121 TPFRAQOIGPPEVHLEADKAIVIHISPGTDSVMALDGLSFTYSLLIMKSSGVEERI 180
QY 181 ENIYSRHKIYKLSPEYTCCLKVKAALLTSWKIGYSPVHCITTYENELPPENIEVSQ 240
Db 181 ENIYSRHKIYKLSPEYTCCLKVKAALLTSWKIGYSPVHCITTYENELPPENIEVSQ 240
QY 241 NONVYLKMDTYAAMTFOVOMLHAFLKRNPNHLYKKQOIPDCENVTTCQCFPQNVFOK 300
Db 241 NONVYLKMDTYAAMTFOVOMLHAFLKRNPNHLYKKQOIPDCENVTTCQCFPQNVFOK 300
QY 301 GYLLRQASDGNNTSFWESEIKFDTEIOAFLLPPVFNIRSLSDSFHIIYGAPKQSGNTP 360
Db 301 GYLLRQASDGNNTSFWESEIKFDTEIOAFLLPPVFNIRSLSDSFHIIYGAPKQSGNTP 360

QY 361 VIODYPLIYEIIFWENTSNAERKIIKKTDVTPVNLKPLTVYCVKARAHMDEKLNKSSV 420
Db 361 VIODYPLIYEIIFWENTSNAERKIIKKTDVTPVNLKPLTVYCVKARAHMDEKLNKSSV 420
QY 421 FSDAVCEKTPGNTSK 436
Db 421 FSDAVCEKTPGNTSK 436

RESULT 3

R11958
ID R11958 standard; Protein; 557 AA.
AC R11958;
DT 18-JUL-1991 (first entry)
DE Human alpha-interferon receptor protein.
KW Human alpha IFN; IFN agonists; antiviral; anti tumour agent;
OS Homo sapiens.
PN Key
PM WO9105862-A.
PD 02-MAY-1991.
PE 19-OCT-1990; F00758.
PR 20-OCT-1989; FR-013770.
PA (CNRS) CNRS CENT NAT RECH SCI.
PI Mogensen KE, Uze G, Lutfalla G, Gresser I;
DR WPI: 91-148740/20.
DR N-PSDB: Q11701.
PT New human alpha-interferon receptor protein - useful for testing
PT Interferon agonists and in treatment or diagnosis
PS Disclosure: fig 4; 30pp; French.
CC This recombinant human alpha interferon (IFN) receptor protein is
CC useful for the testing of IFN agonists and for treatment and diag-
CC nosis of viral diseases and tumours. Antibodies raised against
CC this protein can be used for blocking the receptor when required,
CC eg where overexpression of alpha-IFN is harmful. The Abs are
CC also useful for eg drug targeting. Variants of the protein,
CC having residue 164 (Thr) replaced by Arg and an Asp inserted
CC between residues 479 and 480, are also useful.
SQ Sequence 557 AA;

Query Match 100.0%; Score 2313; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 3.3e-203;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVVLGATTLVAVGPNVLSAAGGNLKSPOKVEVDIIDNFIILRNRSDESIGNVT 60
Db 1 MMVVLGATTLVAVGPNVLSAAGGNLKSPOKVEVDIIDNFIILRNRSDESIGNVT 60
QY 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSSKLNVYEIKLRIRAEKENTSSWYEVDSF 120
Db 61 FSPDYOKTGMNDWIKLSGCONITSTKCNFSSKLNVYEIKLRIRAEKENTSSWYEVDSF 120
QY 121 TPFRAQOIGPPEVHLEADKAIVIHISPGTDSVMALDGLSFTYSLLIMKSSGVEERI 180
Db 121 TPFRAQOIGPPEVHLEADKAIVIHISPGTDSVMALDGLSFTYSLLIMKSSGVEERI 180
QY 181 ENIYSRHKIYKLSPEYTCCLKVKAALLTSWKIGYSPVHCITTYENELPPENIEVSQ 240
Db 181 ENIYSRHKIYKLSPEYTCCLKVKAALLTSWKIGYSPVHCITTYENELPPENIEVSQ 240
QY 241 NONVYLKMDTYAAMTFOVOMLHAFLKRNPNHLYKKQOIPDCENVTTCQCFPQNVFOK 300
Db 241 NONVYLKMDTYAAMTFOVOMLHAFLKRNPNHLYKKQOIPDCENVTTCQCFPQNVFOK 300
QY 301 GYLLRQASDGNNTSFWESEIKFDTEIOAFLLPPVFNIRSLSDSFHIIYGAPKQSGNTP 360
Db 301 GYLLRQASDGNNTSFWESEIKFDTEIOAFLLPPVFNIRSLSDSFHIIYGAPKQSGNTP 360
QY 361 VIODYPLIYEIIFWENTSNAERKIIKKTDVTPVNLKPLTVYCVKARAHMDEKLNKSSV 420

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Db 361 VIQDPLIYEITFEIEMNTSNAERKIIETKTDVTPNKLPLTYCVKARAHITMDEKLKSSV 420
QY 421 FSDAVCEKTKPGNTSK 436
Db 421 FSDAVCEKTKPGNTSK 436

RESULT 4
R14488
ID R14488 standard; Protein: 557 AA.
AC R14488;
DT 16-JAN-1992 (first entry)
DE Complete interferon-alpha/beta receptor.
KW IFN; autoimmune disease; graft rejection; histocompatibility.
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 437..457
FT /label= transmembrane
FT 458..557
FT /label= cytoplasmic
FR2657881-A.
PN 09-AUG-1991.
PD 05-FEB-1990; 001298.
PR 05-FEB-1990; FR-001298.
PA (EUBI-) LAB EURO BIOTECHNO.
PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE;
PI Toyey MG, Uze G;
PI MPI: 91-319778/44.
DR N-PSDB: Q14240.
DR New water-soluble polypeptide(s) with affinity for IFN-alpha and
PT beta - used to treat e.g. lupus erythematosus, Behcet's disease,
PT aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.
PS Disclouse: Page 47; 52pp; French.
CC The invention covers derivatives of the interferon-alpha and/or beta
CC receptor obtained by deleting the transmembrane and cytoplasmic domains
CC of the native receptor or by substitution. Potentially immunogenic
CC epitopes are eliminated and the deriv. can be secreted from
CC transformed cells. Soluble deriv.s block the activity of IFN alpha/beta
CC and can be used to treat autoimmune diseases or to inhibit graft
CC rejection. See also Q14239.
SQ Sequence 557 AA;

Query Match 100.0%; Score 2313; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 3.3e-203;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Db 361 VIQDPLIYEITFEIEMNTSNAERKIIETKTDVTPNKLPLTYCVKARAHITMDEKLKSSV 420
QY 421 FSDAVCEKTKPGNTSK 436
Db 421 FSDAVCEKTKPGNTSK 436

RESULT 5
R28496
ID R28496 standard; Protein: 557 AA.
AC R28496;
DT 31-MAR-1993 (first entry)
DE Sequence of a soluble form of the interferon (IFN) receptor
DE with a high affinity for IFN-alpha and -beta.
KW Interferon receptor; alpha-interferon; beta-interferon.
OS Synthetic.
PN MO9218626-A.
PD 29-OCT-1992.
PR 17-APR-1991; F00318.
PR 17-APR-1991; WO-F00318.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,
PI Toyey M, Uze G;
PI MPI: 92-382110/46.
DR N-PSDB: Q30533.
DR Water soluble polypeptide(s) strongly bind interferon(s) alpha
PT and beta - useful as immunosuppressants, for treating auto-immune
PT diseases and transplant rejection
PS Claim 3; Fig 2; 58pp; English.
CC DNA encoding the water-soluble polypeptide with a high affinity for
CC IFN-alpha and -beta is isolated by PCR, using appropriate
CC oligonucleotides as primers and cloned cDNA as template. For example,
CC bacteriophage lambda ZAP, containing the entire coding sequence of
CC the IFN-alpha and -beta receptor (Q30533), was incubated with oligos
CC Q30334 and Q30535. R28496 represents the complete receptor. R28495
CC lacks the transmembrane and cytoplasmic domains. Both forms bind
CC IFN in the same way as antibodies so are immunosuppressants e.g. for
CC treating autoimmune diseases and graft rejection. They lack the
CC toxic side-effects of known immunosuppressants such as steroids.
SQ Sequence 557 AA;

Query Match 100.0%; Score 2313; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 3.3e-203;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```


Db 361 VIQDYPPLIYEIIFWENTSAERKIIIEKKTDTVTPNLKPLTYVCVAKARAHMDEKLKSSV 420
QY 421 FSDAVCEKTRKPGNTSK 436
Db 421 FSDAVCEKTRKPGNTSK 436

RESULT 6
ID R42635 standard; Protein; 557 AA.
AC R42635;
DT 20-APR-1994 (first entry)
DE Human interferon receptor.
KW IFR-R; extracellular domain; monoclonal antibody; viral infection;
cell proliferation; allograft rejection; systemic lupus erythematosus;
Kw poriasis; multiple sclerosis; Behcet's disease; aplastic anaemia;
immunodeficiency; measles virus; interferon-alpha-beta.
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 1..436
FT /label= extracellular domain
FT /note= "soluble, immunogenic form of IFN-R"
PE 563487-A.
PD 06-OCT-1993.
PF 31-MAR-1992; 400902.
PR 31-MAR-1992; EP-400902.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
PI Benoit P, Maguire D, Meyer F, Plavec I, Tovey MG;
DR WPI: 93-312951/40.
DR P-PSDB: R42635.
PT Monoclonal antibody to human interferon type-I receptor - having
neutralising activity against human type I interferon, used for
therapy and diagnosis
PS Disclosure; Fig 3; 21pp; English.
CC Monoclonal antibodies produced against soluble forms of the human
interferon alpha-beta receptor based on the full-length human IFN-R
sequence are claimed. The antibodies are useful for treatment and
CC prophylaxis of disorders involving cell proliferation and/or viral
infection.
SQ Sequence 557 AA:

Query Match 100.0%; Score 2313; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 3.3e-203;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMVVLGATTLVAVGPWVLSAAGKNTKSPQKVEVDIIDNFIILRNRSDESVGNT 60
Db 1 MMVVLGATTLVAVGPWVLSAAGKNTKSPQKVEVDIIDNFIILRNRSDESVGNT 60
QY 61 FSDYOKTGMDNMWIKLSGCONITSTKCNFSSSLKNTVEEIKIRIRAEKENTSSWYEVDSF 120
Db 61 FSDYOKTGMDNMWIKLSGCONITSTKCNFSSSLKNTVEEIKIRIRAEKENTSSWYEVDSF 120
QY 121 TFFRKAQIGPPEVHLEADKAIYIHISPGTDSVMALDGLSFTYSLLIMKNSGVEERI 180
Db 121 TFFRKAQIGPPEVHLEADKAIYIHISPGTDSVMALDGLSFTYSLLIMKNSGVEERI 180
QY 121 TFFRKAQIGPPEVHLEADKAIYIHISPGTDSVMALDGLSFTYSLLIMKNSGVEERI 180
Db 121 TFFRKAQIGPPEVHLEADKAIYIHISPGTDSVMALDGLSFTYSLLIMKNSGVEERI 180
QY 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCIKTIVENELPPENIEVSQ 240
Db 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCIKTIVENELPPENIEVSQ 240
QY 241 NONVYLKMDYTYANNMFQVOMLHAFKRNPGNHLKWKQIPOCENKTTQCVFQNVFOK 300
Db 241 NONVYLKMDYTYANNMFQVOMLHAFKRNPGNHLKWKQIPOCENKTTQCVFQNVFOK 300
QY 301 GIYLLRVOASGNNSTFSESEIKFDEIOAFLPPVFNIRSLSDSFHIYIGAPKOSGNTP 360
Db 301 GIYLLRVOASGNNSTFSESEIKFDEIOAFLPPVFNIRSLSDSFHIYIGAPKOSGNTP 360
QY 361 VIQDYPPLIYEIIFWENTSAERKIIIEKKTDTVTPNLKPLTYVCVAKARAHMDEKLKSSV 420
Db 361 VIQDYPPLIYEIIFWENTSAERKIIIEKKTDTVTPNLKPLTYVCVAKARAHMDEKLKSSV 420

QY 421 FSDAVCEKTRKPGNTSK 436
Db 421 FSDAVCEKTRKPGNTSK 436

RESULT 7
ID R75356 standard; Protein; 557 AA.
AC R75356;
DT 16-OCT-1995 (first entry)
DE Human IFN receptor.
KW IFN receptor; interferon receptor; interferon-alpha;
interferon-beta; monoclonal antibody; immunomodulator; AIDS.
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 1..436
FT /label= Extracellular domain
FT W09507716-A.
PD 23-MAR-1995.
PF 16-SEP-1994; E03114.
PR 17-SEP-1993; EP-402279.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
PI Benlzeri EJ, Tovey MG;
DR WPI: 95-131187/17.
DR N-PSDB: 086458.
PT Compn. of monoclonal antibodies against interferon receptor -
useful as immuno:modulator, eg. for treating AIDS
PS Disclosure; Fig.3A-2B; 105pp; English.
CC The amino acid sequence of human interferon class I receptor is
CC given in R75356. A recombinant soluble form of the extracellular
CC domain of this receptor (R71723) has been used to raise
CC immunomodulatory monoclonal antibodies.
SQ Sequence 557 AA:

Query Match 99.8%; Score 2309; DB 1; Length 557;
Best Local Similarity 99.8%; Pred. No. 7.7e-203;
Matches 435; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MMVVLGATTLVAVGPWVLSAAGKNTKSPQKVEVDIIDNFIILRNRSDESVGNT 60
Db 1 MMVVLGATTLVAVGPWVLSAAGKNTKSPQKVEVDIIDNFIILRNRSDESVGNT 60
QY 61 FSDYOKTGMDNMWIKLSGCONITSTKCNFSSSLKNTVEEIKIRIRAEKENTSSWYEVDSF 120
Db 61 FSDYOKTGMDNMWIKLSGCONITSTKCNFSSSLKNTVEEIKIRIRAEKENTSSWYEVDSF 120
QY 121 TFFRKAQIGPPEVHLEADKAIYIHISPGTDSVMALDGLSFTYSLLIMKNSGVEERI 180
Db 121 TFFRKAQIGPPEVHLEADKAIYIHISPGTDSVMALDGLSFTYSLLIMKNSGVEERI 180
QY 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCIKTIVENELPPENIEVSQ 240
Db 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCIKTIVENELPPENIEVSQ 240
QY 241 NONVYLKMDYTYANNMFQVOMLHAFKRNPGNHLKWKQIPOCENKTTQCVFQNVFOK 300
Db 241 NONVYLKMDYTYANNMFQVOMLHAFKRNPGNHLKWKQIPOCENKTTQCVFQNVFOK 300
QY 301 GIYLLRVOASGNNSTFSESEIKFDEIOAFLPPVFNIRSLSDSFHIYIGAPKOSGNTP 360
Db 301 GIYLLRVOASGNNSTFSESEIKFDEIOAFLPPVFNIRSLSDSFHIYIGAPKOSGNTP 360
QY 361 VIQDYPPLIYEIIFWENTSAERKIIIEKKTDTVTPNLKPLTYVCVAKARAHMDEKLKSSV 420
Db 361 VIQDYPPLIYEIIFWENTSAERKIIIEKKTDTVTPNLKPLTYVCVAKARAHMDEKLKSSV 420
QY 421 FSDAVCEKTRKPGNTSK 436
Db 421 FSDAVCEKTRKPGNTSK 436


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FH Key Location/Qualifiers
FT domain 1..427
FT /label= Extracellular domain
FT /note= "Comprises amino acids 1-427 of the
FT transmembrane IFNAR."
FT 428..434
FT domain /label= S-domain
FT
FT A09475977-A.
FT 11-MAY-1995.
FT 20-OCT-1994; 075977.
FT 24-OCT-1993; IL-107378.
FT (YEDA ) YEDA RES & DEV CO LTD.
FT (ABRA/ ) ABRAMOVICH C.
FT PI Abramovich C, Ratovitski E, Revel M;
FT WPI: 95-200634/27.
FT New mammalian soluble interferon alpha-receptor forms - used for
FT inhibiting, modulating or modifying the activities of interferon(s)
PS Example 2; Fig 7; 46pp: English.
CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 1
CC (W21805) is characterised by a new domain (S) which follows an
CC end-deleted extracellular domain when compared to transmembrane
CC IFNAR (W21804). There is no transmembrane domain. The amino acid
CC sequence is predicted from a cDNA clone (see also T73520) cdt.
CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR
CC splice-deleted forms 1 and 2 (see also W21806) probably regulate
CC the response of human cells to IFNs, either by acting as IFN
CC antagonists or by regulating the activity of the multiple IFN
CC subtypes. They can be expressed in host cells and used to inhibit,
CC modulate or modify the activities of IFNs alpha and beta in cells,
CC tissues and organisms, or for diagnostic purposes.
SQ Sequence 434 AA:

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Query Match 97.7%; Score 2260; DB 1; Length 434;
Best Local Similarity 99.8%; Pred. No. 1.6e-196;
Matches 426; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 MMVLLGATTLVAVGPMVLSAAGGKRLKSPQVEVDIIDNFIILRNRSDESIGNVT 60
DB 1 MMVLLGATTLVAVGPMVLSAAGGKRLKSPQVEVDIIDNFIILRNRSDESIGNVT 60
OY 61 FSPDYQKGMNWKILSGCONITSTKCNFSSSLKLVYEELIKIRAEKENTSSWEYDSF 120
DB 61 FSPDYQKGMNWKILSGCONITSTKCNFSSSLKLVYEELIKIRAEKENTSSWEYDSF 120
OY 121 TPFKAQIGPEVHLAEADKAIVIHISPGTKDSVMALDGLSTFYSLILKNSSGVEERI 180
DB 121 TPFKAQIGPEVHLAEADKAIVIHISPGTKDSVMALDGLSTFYSLILKNSSGVEERI 180
OY 181 ENISYRHKIYKLSPEITTYCLKVAKALLTSWKIGVSPVHCIKITVENELPPENIEVSQ 240
DB 181 ENISYRHKIYKLSPEITTYCLKVAKALLTSWKIGVSPVHCIKITVENELPPENIEVSQ 240
OY 241 NONVYLKMDTYANMTFOVOMLHAFKLRNGNHLKMKQIPDCENKTKTQCVFPONVFQK 300
DB 241 NONVYLKMDTYANMTFOVOMLHAFKLRNGNHLKMKQIPDCENKTKTQCVFPONVFQK 300
OY 301 GIYLLRVOASDGNNTSFSESEIKFDEIQAFLLPVENIRSLSDSFHIYIGAPKQSGNTP 360
DB 301 GIYLLRVOASDGNNTSFSESEIKFDEIQAFLLPVENIRSLSDSFHIYIGAPKQSGNTP 360
OY 361 VIQDYPLIYEIIIFWENTSNAERKIIIEKTDVTPNLKPLTYVCVKAHATMDKLNKSSV 420
DB 361 VIQDYPLIYEIIIFWENTSNAERKIIIEKTDVTPNLKPLTYVCVKAHATMDKLNKSSV 420
OY 421 FSDANCE 427
DB 421 FSDANCE 427

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RESULT 11
W21806
ID W21806 standard; Protein: 496 AA.

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AC W21806:
DE 23-SEP-1997 (first entry)
DE Spliced-deleted interferon alpha-receptor form 2.
KW Interferon alpha-receptor; IFNAR.
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 1..419
FT /label= Extracellular domain
FT /note= "Comprises amino acid residues 1-413 and
FT 422-427 of transmembrane IFNAR"
FT 420..496
FT domain /label= Intracellular domain
FT /note= "Comprises amino acids 481-557 of
FT transmembrane IFNAR"
FT
FT A09475977-A.
FT 11-MAY-1995.
FT 20-OCT-1994; 075977.
FT 24-OCT-1993; IL-107378.
FT (YEDA ) YEDA RES & DEV CO LTD.
FT (ABRA/ ) ABRAMOVICH C.
FT PI Abramovich C, Ratovitski E, Revel M;
FT WPI: 95-200634/27.
FT New mammalian soluble interferon alpha-receptor forms - used for
FT inhibiting, modulating or modifying the activities of interferon(s)
PS Example 3; Fig 7; 46pp: English.
CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 2
CC (W21806) is characterised by a double deletion when compared to
CC transmembrane IFNAR (W21804). The extracellular domain is
CC shortened by 6 amino acid residues and is followed by a truncated
CC intracellular domain. There is no transmembrane region. The amino
CC acid sequence is predicted from a cDNA clone (see also T73521) cdt.
CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR
CC splice-deleted forms 1 (see also W21805), and 2 may regulate the
CC response of human cells to IFNs, either by acting as IFN
CC antagonists or by regulating IFN activities. They can be expressed
CC in host cells and used to inhibit, modulate or modify the
CC activities of IFNs alpha and beta in cells, tissues and organisms,
CC or for diagnostic purposes.
SQ Sequence 496 AA:

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Query Match 95.5%; Score 2208; DB 1; Length 496;
Best Local Similarity 97.9%; Pred. No. 1.1e-193;
Matches 418; Conservative 0; Mismatches 1; Indels 8; Gaps 1;

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OY 1 MMVLLGATTLVAVGPMVLSAAGGKRLKSPQVEVDIIDNFIILRNRSDESIGNVT 60
DB 1 MMVLLGATTLVAVGPMVLSAAGGKRLKSPQVEVDIIDNFIILRNRSDESIGNVT 60
OY 61 FSPDYQKGMNWKILSGCONITSTKCNFSSSLKLVYEELIKIRAEKENTSSWEYDSF 120
DB 61 FSPDYQKGMNWKILSGCONITSTKCNFSSSLKLVYEELIKIRAEKENTSSWEYDSF 120
OY 121 TPFKAQIGPEVHLAEADKAIVIHISPGTKDSVMALDGLSTFYSLILKNSSGVEERI 180
DB 121 TPFKAQIGPEVHLAEADKAIVIHISPGTKDSVMALDGLSTFYSLILKNSSGVEERI 180
OY 181 ENISYRHKIYKLSPEITTYCLKVAKALLTSWKIGVSPVHCIKITVENELPPENIEVSQ 240
DB 181 ENISYRHKIYKLSPEITTYCLKVAKALLTSWKIGVSPVHCIKITVENELPPENIEVSQ 240
OY 241 NONVYLKMDTYANMTFOVOMLHAFKLRNGNHLKMKQIPDCENKTKTQCVFPONVFQK 300
DB 241 NONVYLKMDTYANMTFOVOMLHAFKLRNGNHLKMKQIPDCENKTKTQCVFPONVFQK 300
OY 301 GIYLLRVOASDGNNTSFSESEIKFDEIQAFLLPVENIRSLSDSFHIYIGAPKQSGNTP 360
DB 301 GIYLLRVOASDGNNTSFSESEIKFDEIQAFLLPVENIRSLSDSFHIYIGAPKQSGNTP 360
OY 361 VIQDYPLIYEIIIFWENTSNAERKIIIEKTDVTPNLKPLTYVCVKAHATMDKLNKSSV 420
DB 361 VIQDYPLIYEIIIFWENTSNAERKIIIEKTDVTPNLKPLTYVCVKAHATMDKLNKSSV 420

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OY 421 FSDVACE 427
DB 414 -SDVACE 419

RESULT 12

W52296
ID W52296 standard; Protein: 325 AA.
AC W52296;
DR 23-JUN-1998 (first entry)
DE CRFB4 protein.
KW CRFB4; interleukin-10; IL-10; IL-10 receptor; allograft rejection;
KW vaccine; photosensitivity; inflammation; autoimmune disease;
KW septic shock; immune response; organ rejection; gene therapy.
OS Homo sapiens.
PN MO9802542-A1.
PD 22-JAN-1998.
PF 17-JUL-1997; U12455.
PR 17-JUL-1996; US-683743.
PI (UYNE-) UNIV NEW JERSEY.
PI Kolenko SV, Pestka S;
DR WPI: 98-110590/10.
DR N-PSDB: V19874.
PT New recombinant DNA - comprises sequences encoding interleukin-10
PT and CRFB4 linked to operator, useful, e.g. preventing allograft
PT rejection
PS Claim 2: Page -: 79pp; English.
CC This sequence is the human CRFB4 sequence, DNA encoding it is used in the
CC recombinant DNA (1) of the invention. (1) comprises a sequence (S1)
CC encoding the interleukin-10 (IL-10) receptor (IL10R) and a sequence (S2)
CC encoding CRFB4, both operably linked to expression control sequences.
CC Cells containing (1) may be used to identify agonists/antagonist of
CC IL-10. Agonists are potentially useful, e.g. for preventing allograft
CC rejection, as vaccine adjuvants, for treatment of photosensitivity,
CC inflammation, autoimmune disease and septic shock, while antagonists are
CC potentially useful for increasing immune responses against tumours,
CC viruses, bacteria and parasites (especially intracellular pathogens) and
CC for preventing organ rejection. A vector containing (1) is used to
CC restore, e.g. by gene therapy, IL-10 sensitivity to a cell that expresses
CC a dysfunctional IL10R and is able to bind IL-10 but not to transduce a
CC signal. Antisense CRFB4 sequences (especially ribozymes), can inhibit
CC IL-10 activity in cells. Antibodies specific for CRFB4 are used to
CC measure and localise CRFB4, for diagnosis of defective IL-10 activity.
CC Fragments of (1) are used as primers or probes to assay CRFB4-specific
CC RNA. Agonists/antagonists may be administered parenterally, orally or
CC rectally especially by intravenous injection or directly into a tumour or
CC allograft.
SQ Sequence 325 AA:

Query Match 9.9%; Score 228.5; DB 1; Length 325;
Best local Similarity 29.9%; Pred. No. 5,1e-13;
Matches 67; Conservative 42; Mismatches 96; Indels 19; Gaps 8;

OY 19 WLSAAGKRLKS-----PQKVEVDIIDNFILRNNSDESVCNTEFSFYQKTGM 71
DB 3 WSGSGWGGCLLVSAIGMPPPEVRNNSVFNKIILOMESPAFKGNLITFTAG----LS 58
OY 72 NMKLSGCONITSTKCNFSSKLNVEIKLRIRAE-KENTSSVYEDSTFPFKAOIG 130
DB 59 YRIFQDKCMNTTLTECFSS--LSKIGDHTLRRAEFADEHSDVNI-TTCPPVDDTIIIG 115
OY 131 PEVHLEA-EDKAIVIHISPGTKDSV-MMALDGL--SFTYSLILWKNSSGVEERIEIENYSR 186
DB 116 PGHQVEVLADSLMHRFLAPRIENYEYWTMKKNVNSMTYVNVQYKKNIDEXFOITPQYDF 175
OY 187 HKIKLSPETTYCLAKVAALITSKIVYSPVHCITVENELP 230
DB 176 EVLRNLEPMTTYCYOVRGFLPDRNKAAGEWSEPYCEQTTDETVP 219

RESULT 13
R75782

ID R75782 standard; Protein: 332 AA.
AC R75782;
DR 13-NOV-1995 (first entry)
DE IFN-gamma receptor beta-subunit.
KW Interferon-gamma receptor beta subunit; muIFN;
KW Interferon-gamma-antagonist.
OS Mus sp.
PN
FH Key
FT peptide
FT domain
FT domain
FT domain
FT domain
FT domain

Location/Qualifiers
1..18
/label- sig_peptide
19..242
/label- Extracellular domain
243..266
/label- Transmembrane_anchoring_domain
267..332
/label- Cytoplasmic domain

PN MO9516036-A.
PD 15-JUN-1995.
PF 07-DEC-1994; U14277.
PR 09-DEC-1993; US-164596.
PA (AGUE/) AGUET M.
PA (BOEH/) BOEHNI R.
PA (HEMX/) HEMMI S.
PI Aguet M, Boehni R, Hemmi S;
DR WPI: 95-224321/29.
DR N-PSDB: Q90808.
PT Novel interferon gamma receptor beta chain polypeptide - for
PT treatment of inflammatory bowel disease and liver damage
PS Claim 3: Fig.2A; 86pp; English.
CC The IFN-gamma receptor beta subunit encoded by a cDNA clone derived
CC from mouse B-cells is given in R75782. Recombinant beta-subunit,
CC pref. with the transmembrane anchoring domain deleted or
CC inactivated and with the cytoplasmic domain deleted, may be
CC used to treat pathological conditions associated with endogenous
CC IFN-gamma production.
SQ Sequence 332 AA:

Query Match 8.8%; Score 203; DB 1; Length 332;
Best local Similarity 30.1%; Pred. No. 1,1e-10;
Matches 69; Conservative 38; Mismatches 86; Indels 36; Gaps 13;
OY 21 LSAAGC-----KNKSPQKVEVDIIDNFILRNNSDES-----VGNTEFSFYQKTGM 70
DB 16 LGAASSPDSFSQLAPLNPRLHYNDQILTEPSPSSNDPRVYQVEYSE-----I 69
OY 71 D-NMIL--SGCONITSTKCNFSS--IKLNYE-EIKIRIREKEN-TSSWEVDSFPP 122
DB 70 DSGMRLLEPNCVDITETCDLGGRLKLPFTVFLVRRAKRNGLSKWGLPEFOH 129
OY 123 FRKAQIGPPE-VHLEAEDKAIVIHISPGTKDSVMMALDGLSFTYSLILWKNSSGVEERIE 181
DB 130 YENVYTGPPKNISVTGKGSIVIHESPPD-----VFHATQYLVHYEKSSTQOEQVE 184
OY 182 NIYSRKIT--KISPETTYCLAKVAAL-ITSMKI---GYSPVHCITKT 224
DB 185 GPKKSNISIVLGNLKPFRVYCLQETQDILIKKIRPHGILSNVSCHETT 233

RESULT 14
W79159
ID W79159 standard; Protein: 553 AA.
AC W79159;
DR 20-NOV-1998 (first entry)
DE zcyto7 cytokine receptor polypeptide.
KW zcyto7; cytokine receptor; ligand-binding polypeptide; kidney; pancreas;
KW type 2 cytokine receptor family; CRF2; prostate tissue; nervous tissue;
KW agonist; cell proliferation; cell differentiation; renal disease; human;
KW neutral disease; pancreatic disease.
OS Homo sapiens.
PN
FH Key
FT Domain
Location/Qualifiers
30..250
/note= "extracellular (ligand-binding) domain";

FT Domain 275.553 sequence claimed in claim 1"
 FT /note="intracellular domain"
 PN WO9837193-A1.
 PD 27-AUG-1998.
 PF 18-FEB-1998; 003029.
 PR 20-OCT-1997; US-943087.
 PR 20-FEB-1997; US-803305.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Farrah TM, Jelmberg AC, Kho CJ, Lok S,
 PI Whitmore TE:
 DR WPI: 98-480798/41.
 DR N-PDB: V57515.
 PT Novel human zcytor7 DNA encodes a type 2 cytokine receptor - useful
 PT for treating renal, neural, pancreatic and prostatic diseases
 PS Claim 1; Pages 55-59; 72pp; English.
 CC This represents the zcytor7 cytokine receptor. zcytor7 is a ligand-
 CC binding receptor polypeptide and is a novel member of the type 2 cytokine
 CC receptor family (CRF2). An expression vector containing the zcytor
 CC polynucleotide, operably linked to transcription promoter, a sequence
 CC encoding a transmembrane and intracellular domain, or both, and a
 CC transcriptional terminator can be used to transform host cells for the
 CC recombinant production of the polypeptide. The sequences can be used to
 CC study the zcytor7 gene and to isolate ligands binding to it. zcytor7 is
 CC preferentially expressed in the kidney, pancreas, prostate or nervous
 CC tissue. Agonists of zcytor7 can be used to stimulate proliferation and
 CC differentiation of cell in these organs. The antagonists and agonists can
 CC also be used in the treatment of renal, neural, pancreatic and prostate
 CC diseases.
 SQ Sequence 553 AA:

Query Match 8.6%; Score 198; DB 1; Length 553;
 Best Local Similarity 21.0%; Pred. No. 7e-10;
 Matches 91; Conservative 79; Mismatches 173; Indels 90; Gaps 17;

QY 11 LVLVAVGPR--VLSAAGGKLNKSPQKVEVDIIDNFILRMNRSDSVG--NTFSPDYOK 67
 DB 18 LLLLLAIPMGRAVPCVSG--LPKPRNITFLINMKNVLPPEGLQGVKTYTQYPI 75
 QY 66 TQMDMKIKSGCONITSTGKNSLKLNYEIKLRIR--EKENTSSWTEVDSETPPRKA 126
 DB 76 YQCKMLNKSSEKRNINRYCDLSAETSDYEHQYAKVAKIMGTCKSKMAESGRFPFLET 135
 QY 127 QIGPEVHLAEADKAIVIHISPGTK-----DSVMALDGLSTVSLIMKSSGVE 177
 DB 136 QIGPEVALTTDEKISVYLTAPEKMKRNPEDLPVSMQIYNSLKYNNSVLTKSNRTWS 195
 QY 178 ERIENIYSRHKIYK--LSPETTYCLKVKAALLTSWKIGVSPHCIGKTVE----- 229
 DB 196 QCVTN---HTLVLMLEBNTLYCVHESFVGPPRRAQPSKQCARLTKDQSSFEKAKI 251
 QY 229 -----LPPPENIEVSQONNTYVLMKDYIYANTFOY-QMLAFLLKRNFGNHLTKKQIPD 282
 DB 252 IFWYVLP-----ISITV-----FLFSVYGYSIRYIHGKKEKHPANLI----- 290
 QY 283 CENVKTCQVFPONFQKGIYLLRVQASDGNNTSPMSEIKPDEI---QAFILPPVNI 339
 DB 290 -----LIYGNFEDKRFV---PAKIVINFTILNISDCKISHQMSLLKSSSDV 336
 QY 340 RSLSDSFHIYIGAPKQSGNTPIYDIPLYEI-----IFWENTNAERKIIEKKTDV 391
 DB 337 SSLND-----POPSGNLRPQDEEVKHLGYASHLMEIFCDSEENTEGTSFTQESL 388
 QY 392 --TVPNLKPLVY 402
 DB 389 SKTIIPDKTIVLEY 401

RESULT 15
 ID R71035
 AC R71035 standard; protein; 337 AA.
 R71035;
 R71035;

DR 11-OCT-1995 (first entry)
 DE Human IFN-gamma accessory factor-1.
 KM Interferon-gamma; Af-1; tumour.
 OS Homo sapiens.
 PN WO9505847-A.
 PD 02-MAR-1995.
 PR 22-AUG-1994; U09438.
 PR 20-AUG-1993; US-110119.
 PA (UNIV) UNIV NEW JERSEY.
 PI Cook JR, Donnelly RJ, Emanuel S, Kotenko S, Mariano TM,
 PI Pestka S, Schwartz B, Soh J;
 DR WPI: 95-106679/14.
 DR N-PDB: 084697.
 PT Suppressing tumours in mammals with accessory factor 1 (Af-1) -
 PT for interferon gamma, specifically induction of class I HLA
 PT antigens, including use of Af-1 DNA in gene therapy
 PS Disclosure: Fig 21A; 114p; English.
 CC The sequence is that of human interferon-gamma accessory factor-1.
 CC Incorporation of Af-1 into immune and tumour cells re-establishes
 CC normal function with elimination of malignant cells.
 SQ Sequence 337 AA;

Query Match 6.7%; Score 155.5; DB 1; Length 337;
 Best Local Similarity 22.3%; Pred. No. 2.6e-06;
 Matches 67; Conservative 54; Mismatches 112; Indels 67; Gaps 14;

QY 12 VLVAVGPRVLSAAGG--KNLKSPOKVEVDIIDNFILRW-----NRSDESVGNWTF 62
 DB 9 LLLLLGVFAAALAAAPDPDLSQAPQHPKIRLYNAEGLSWEPVALSNSTPRVYQVQF 68
 QY 63 FDYQKTGMDMKIKLS-----GCONITSTKCNFSS-----LKLNYEIKLRIRAEK 108
 DB 69 ITDSK-----WFTADINSIGVNCQTITATEDFTAAPSAGFPMDFNV---TLRLRAEL 119
 QY 109 ENT--SMWTEVDSETPFRKAQIGPEVHLE---AEDKAIVIHISPGTKDSVMALDGLSFT 164
 DB 120 GALSAWMTWTFQHYRNVTVGPPE-NIEVTPGEGSLIIRSSFPDIADISTAF-----FC 174
 QY 165 YSLIMKNSGVEERENIYSRHKIY--KSPETTYCLKVKAALLTS---WKIGVSPV 218
 DB 175 YVHYWE--KGIQOVKGFPRSNISLDNLEKPSRYCLOVOAQLMKNKSNIFRGHLSNI 232
 QY 219 HCITTYENELPPPENIEVS-----QONVYVLMKDYIYANTFOYQ 260
 DB 233 SCYETMADASTELQOVLISVGTFSLSVLGACFVLVLYKRGILKYWFHTPPSPIDQIE 292

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OM protein - protein search, using sw model

Run on: June 1, 2000, 04:35:21 ; Search time 12.75 Seconds
(without alignments)
493.702 Million cell updates/sec

Title: US-09-240-675-2

Perfect score: 2313
Sequence: 1 MMVVLGATTLVLAAGPMV.....KSSVFSDAVCEKTKPGNTSK 436

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 145308 seqs, 14437401 residues

Total number of hits satisfying chosen parameters: 145308

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/p/odata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/p/odata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/p/odata/1/1aa/6.COMB.pep.*
4: /cgn2_6/p/odata/1/1aa/PCrus.COMB.pep.*
5: /cgn2_6/p/odata/1/1aa/backfill1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2313	100.0	436	2	US-08-307-588-2
2	2313	100.0	557	1	US-08-328-256-10
3	2313	100.0	557	1	US-08-471-454-2
4	2313	100.0	557	2	US-08-466-974-2
5	2313	100.0	557	2	US-08-471-453-2
6	2313	100.0	557	2	US-08-307-588-4
7	2265	97.9	434	1	US-08-328-256-11
8	2213	95.7	496	1	US-08-328-256-12
9	490.5	21.2	202	4	PCT-US94-14277-3
10	466.5	20.2	200	4	PCT-US94-14277-4
11	228.5	9.9	325	2	US-08-683-743-4
12	203	8.8	332	4	PCT-US94-14277-2
13	198	8.6	553	2	US-08-943-087-2
14	198	8.6	553	2	US-08-943-087-14
15	198	8.6	553	2	US-08-943-087-16
16	198	8.6	553	2	US-08-943-087-18
17	198	8.6	553	2	US-08-943-087-20
18	198	8.6	553	2	US-08-943-087-22
19	198	8.6	553	2	US-08-943-087-24
20	198	8.6	553	2	US-08-943-087-26
21	198	8.6	553	2	US-08-943-087-28
22	198	8.6	553	2	US-08-943-087-30
23	198	8.6	553	2	US-08-943-087-32
24	198	8.6	553	2	US-08-943-087-34
25	198	8.6	553	2	US-08-943-087-36
26	198	8.6	553	2	US-08-943-087-38
27	198	8.6	553	2	US-08-943-087-40
28	198	8.6	553	2	US-08-943-087-42
29	198	8.6	553	2	US-08-943-087-44

30	198	8.6	553	2	US-08-943-087-46	Sequence 46, Appl
31	198	8.6	553	2	US-08-943-087-48	Sequence 48, Appl
32	192	8.3	223	4	PCT-US94-14277-6	Sequence 6, Appl
33	174.5	7.5	221	2	US-08-943-087-56	Sequence 56, Appl
34	169.5	7.3	221	2	US-08-943-087-54	Sequence 54, Appl
35	168.5	7.3	221	2	US-08-943-087-50	Sequence 50, Appl
36	167.5	7.2	221	2	US-08-943-087-52	Sequence 52, Appl
37	165.5	7.2	221	2	US-08-943-087-60	Sequence 60, Appl
38	162.5	7.0	221	2	US-08-943-087-58	Sequence 58, Appl
39	153.5	6.6	337	4	PCT-US94-14277-8	Sequence 8, Appl
40	151	6.5	574	2	US-08-906-713-2	Sequence 2, Appl
41	118	5.1	489	4	PCT-US93-11110-1	Sequence 1, Appl
42	118	5.1	489	5	5221789-1	Patent No. 5221789
43	118	5.1	1005	2	US-08-469-537A-103	Sequence 103, App
44	117.5	5.1	575	1	US-08-424-788-2	Sequence 2, Appl
45	117.5	5.1	575	1	US-08-110-683-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-307-588-2
Sequence 2, Application US/08307588
Patent No. 5919453
GENERAL INFORMATION:
APPLICANT: BENOIT, Patrick
APPLICANT: MEYER, Francois
APPLICANT: MAGUIRE, Deborah
APPLICANT: PLAVEC, Ivan
APPLICANT: TOVEY, Michael G.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
TITLE OF INVENTION: INTERFERON
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00770
FILING DATE: 30-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92400902.0
FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 17283/117/CUPL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-307-588-2
Query Match 100.0%; Score 2313; DB 2; Length 436;
Best Local Similarity 100.0%; Pred. No. 1.8e-230;

Matches 436: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMYVLLGATTLVLAAGPWWLSAAGKNNLSPQKVEVDIIDDNFLRMNRSDSEVGNVT 60
DB 1 MMYVLLGATTLVLAAGPWWLSAAGKNNLSPQKVEVDIIDDNFLRMNRSDSEVGNVT 60
QY 61 FSPDYOKTGMDNMWIKLSGCONITSTKCNFSSKLNYEEIKLRIRAKENTSSWYEVDSF 120
DB 61 FSPDYOKTGMDNMWIKLSGCONITSTKCNFSSKLNYEEIKLRIRAKENTSSWYEVDSF 120
QY 121 TPFKKAQIGPPEVHLEAEDEKAIVIHISPGTKDSVMMALDGLSFTYSLLIMKSSGYEERI 180
DB 121 TPFKKAQIGPPEVHLEAEDEKAIVIHISPGTKDSVMMALDGLSFTYSLLIMKSSGYEERI 180
QY 181 ENIYSRHKIKYKLSPEPTYCKLVKAAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240
DB 181 ENIYSRHKIKYKLSPEPTYCKLVKAAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240
QY 241 NONVYLKMDYTYANMTFOVOMLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300
DB 241 NONVYLKMDYTYANMTFOVOMLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300
QY 301 GIYLLRVOASDGNNTSFWSEIEKFDEIQAFLPPVFNIRSLSDSFHIYIGAPKQSGNTP 360
DB 301 GIYLLRVOASDGNNTSFWSEIEKFDEIQAFLPPVFNIRSLSDSFHIYIGAPKQSGNTP 360
QY 361 VIQDYPLIYEIIFWENTSNAERKIIKKTDTVVPNLKPLTVYCVKARAHMTDEKLNKSSV 420
DB 361 VIQDYPLIYEIIFWENTSNAERKIIKKTDTVVPNLKPLTVYCVKARAHMTDEKLNKSSV 420
QY 421 FSDAVCEKTRPGNTSK 436
DB 421 FSDAVCEKTRPGNTSK 436

RESULT 2
US-08-328-256-10
; Sequence 10, Application US/08328256
; Patent No. 5643749
GENERAL INFORMATION:
APPLICANT: REVEL, Michel
APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
TITLE OF INVENTION: PREPARATION AND USE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: REVEL-13
REFERENCE/DOCKET NUMBER: 25,618
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-328-256-10

Query Match 100.0%; Score 2313; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 2,7e-230;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMYVLLGATTLVLAAGPWWLSAAGKNNLSPQKVEVDIIDDNFLRMNRSDSEVGNVT 60
DB 1 MMYVLLGATTLVLAAGPWWLSAAGKNNLSPQKVEVDIIDDNFLRMNRSDSEVGNVT 60
QY 61 FSPDYOKTGMDNMWIKLSGCONITSTKCNFSSKLNYEEIKLRIRAKENTSSWYEVDSF 120
DB 61 FSPDYOKTGMDNMWIKLSGCONITSTKCNFSSKLNYEEIKLRIRAKENTSSWYEVDSF 120
QY 121 TPFKKAQIGPPEVHLEAEDEKAIVIHISPGTKDSVMMALDGLSFTYSLLIMKSSGYEERI 180
DB 121 TPFKKAQIGPPEVHLEAEDEKAIVIHISPGTKDSVMMALDGLSFTYSLLIMKSSGYEERI 180
QY 181 ENIYSRHKIKYKLSPEPTYCKLVKAAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240
DB 181 ENIYSRHKIKYKLSPEPTYCKLVKAAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240
QY 241 NONVYLKMDYTYANMTFOVOMLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300
DB 241 NONVYLKMDYTYANMTFOVOMLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300
QY 301 GIYLLRVOASDGNNTSFWSEIEKFDEIQAFLPPVFNIRSLSDSFHIYIGAPKQSGNTP 360
DB 301 GIYLLRVOASDGNNTSFWSEIEKFDEIQAFLPPVFNIRSLSDSFHIYIGAPKQSGNTP 360
QY 361 VIQDYPLIYEIIFWENTSNAERKIIKKTDTVVPNLKPLTVYCVKARAHMTDEKLNKSSV 420
DB 361 VIQDYPLIYEIIFWENTSNAERKIIKKTDTVVPNLKPLTVYCVKARAHMTDEKLNKSSV 420
QY 421 FSDAVCEKTRPGNTSK 436
DB 421 FSDAVCEKTRPGNTSK 436

RESULT 3
US-08-471-454-2
; Sequence 2, Application US/08471454
; Patent No. 5731169
GENERAL INFORMATION:
APPLICANT: MOGENSEN, Knud E.
APPLICANT: UZE, Gilles
APPLICANT: LUTFALLA, Georges
APPLICANT: GRESSER, Ion
TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,454

FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-454-2

Query Match 100.0%; Score 2313; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 2,7e-230;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMYVLLGATTLVAVGPMVLSAAGGNLKSPOKVEVDIIDNFILRMNSDESVCNT 60
DB 1 MMYVLLGATTLVAVGPMVLSAAGGNLKSPOKVEVDIIDNFILRMNSDESVCNT 60
QY 61 FSDYQKTGMNDWIKLSGCONITSTKCNFSSKLNVYEIKLRIRAEKENTSMYEVSF 120
DB 61 FSDYQKTGMNDWIKLSGCONITSTKCNFSSKLNVYEIKLRIRAEKENTSMYEVSF 120
QY 121 TPFRAQIGPPEVHLEADKAIVHISPTKDSVMALDGLSFTYSLIMKNSGVEERI 180
DB 121 TPFRAQIGPPEVHLEADKAIVHISPTKDSVMALDGLSFTYSLIMKNSGVEERI 180
QY 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITTYVENLPPEINIEVSQ 240
DB 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITTYVENLPPEINIEVSQ 240
QY 241 NONVYLKMDYTYANNTFOVQWLHAFLEKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFOK 300
DB 241 NONVYLKMDYTYANNTFOVQWLHAFLEKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFOK 300
QY 301 GYLLRVQASDGNNTSFWESEIKFDTLQAFLLPVPFNIRSLDSFHIYIGAPKOSGNTP 360
DB 301 GYLLRVQASDGNNTSFWESEIKFDTLQAFLLPVPFNIRSLDSFHIYIGAPKOSGNTP 360
QY 361 VIQDPLIYEITFWENTSNAERKIIIEKTDVTPNLPKLTYYCVKARAHNTDEKLNKSSV 420
DB 361 VIQDPLIYEITFWENTSNAERKIIIEKTDVTPNLPKLTYYCVKARAHNTDEKLNKSSV 420
QY 421 FSDAVCEKTPGNTSK 436
DB 421 FSDAVCEKTPGNTSK 436

RESULT 4
US-08-466-974-2
Sequence 2, Application US/08466974
Patent No. 5861258

GENERAL INFORMATION:
APPLICANT: MOGENSEN, Knud E.
APPLICANT: UZE, Gilles
APPLICANT: LUTFALLA, Georges
APPLICANT: GRESSER, Ion
TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE

TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P. C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,974
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-466-974-2

Query Match 100.0%; Score 2313; DB 2; Length 557;
Best Local Similarity 100.0%; Pred. No. 2,7e-230;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMYVLLGATTLVAVGPMVLSAAGGNLKSPOKVEVDIIDNFILRMNSDESVCNT 60
DB 1 MMYVLLGATTLVAVGPMVLSAAGGNLKSPOKVEVDIIDNFILRMNSDESVCNT 60
QY 61 FSDYQKTGMNDWIKLSGCONITSTKCNFSSKLNVYEIKLRIRAEKENTSMYEVSF 120
DB 61 FSDYQKTGMNDWIKLSGCONITSTKCNFSSKLNVYEIKLRIRAEKENTSMYEVSF 120
QY 121 TPFRAQIGPPEVHLEADKAIVHISPTKDSVMALDGLSFTYSLIMKNSGVEERI 180
DB 121 TPFRAQIGPPEVHLEADKAIVHISPTKDSVMALDGLSFTYSLIMKNSGVEERI 180
QY 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITTYVENLPPEINIEVSQ 240
DB 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITTYVENLPPEINIEVSQ 240
QY 241 NONVYLKMDYTYANNTFOVQWLHAFLEKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFOK 300
DB 241 NONVYLKMDYTYANNTFOVQWLHAFLEKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFOK 300
QY 301 GYLLRVQASDGNNTSFWESEIKFDTLQAFLLPVPFNIRSLDSFHIYIGAPKOSGNTP 360
DB 301 GYLLRVQASDGNNTSFWESEIKFDTLQAFLLPVPFNIRSLDSFHIYIGAPKOSGNTP 360
QY 361 VIQDPLIYEITFWENTSNAERKIIIEKTDVTPNLPKLTYYCVKARAHNTDEKLNKSSV 420
DB 361 VIQDPLIYEITFWENTSNAERKIIIEKTDVTPNLPKLTYYCVKARAHNTDEKLNKSSV 420

OY 421 FSDAVCEKTPGNTSK 436
DB 421 FSDAVCEKTPGNTSK 436

RESULT 5

US-08-471-453-2

Sequence 2, Application US/08471453

Patent No. 5886153

GENERAL INFORMATION:

APPLICANT: MOGENSEN, Knud E.

APPLICANT: UZE, Gilles

APPLICANT: LUTFALLA, Georges

APPLICANT: GRESSER, Ion

TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR

TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYTE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,453

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/900,642

FILING DATE: 15-JUN-1992

APPLICATION NUMBER: FR 89/13770

FILING DATE: 20-OCT-1989

ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205

REFERENCE/DOCKET NUMBER: 960-7

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

TELEX: 200797 NIXN UR

INFORMATION FOR SEO ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 557 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-471-453-2

Query Match 100.0%; Score 2313; DB 2; Length 557;

Best Local Similarity 100.0%; Pred. No. 2.7e-230;

Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MMVVLGATTVLVAVGVWVLSAAGGNKLSPOKVEVDIIDNFIILWNSDESQVNT 60
DB 1 MMVVLGATTVLVAVGVWVLSAAGGNKLSPOKVEVDIIDNFIILWNSDESQVNT 60
OY 61 FSDYQKTMGNWIKLSQONTSTKCNFSSILKLVNVEEIKLIRAEKENTSSWYEVDSF 120
DB 61 FSDYQKTMGNWIKLSQONTSTKCNFSSILKLVNVEEIKLIRAEKENTSSWYEVDSF 120
OY 121 TPFRAAIGPPEVHLAEADKAIVIHISPTKDSVWMAIDGSLFTYSLLIMKNSGVEERI 180
DB 121 TPFRAAIGPPEVHLAEADKAIVIHISPTKDSVWMAIDGSLFTYSLLIMKNSGVEERI 180

OY 181 ENIYSRHKIYKLSPTTYCLKVKAAALITSMKIGVSPVHCITKYVENELPPENIEVSQ 240
DB 181 ENIYSRHKIYKLSPTTYCLKVKAAALITSMKIGVSPVHCITKYVENELPPENIEVSQ 240
OY 241 NONVYLMKDYTYANMTFOVWMLAEFLKRNPNHLYKWKQIPDCENVKTTQCVFQNVFQK 300
DB 241 NONVYLMKDYTYANMTFOVWMLAEFLKRNPNHLYKWKQIPDCENVKTTQCVFQNVFQK 300
OY 301 GYLLRVQASDGNNTSFMSEEEKFTDTQAFLLPVPFNIRLSDSFHIYIGAPKOSGNTP 360
DB 301 GYLLRVQASDGNNTSFMSEEEKFTDTQAFLLPVPFNIRLSDSFHIYIGAPKOSGNTP 360
OY 361 VIQDYPPLIYEIIFFMENTSNAERKIIKKTDVTPNLPKPLTYCVKARAHMDEKLNKSSV 420
DB 361 VIQDYPPLIYEIIFFMENTSNAERKIIKKTDVTPNLPKPLTYCVKARAHMDEKLNKSSV 420
OY 421 FSDAVCEKTPGNTSK 436
DB 421 FSDAVCEKTPGNTSK 436

RESULT 6

US-08-307-588-4

Sequence 4, Application US/08307588

Patent No. 5919453

GENERAL INFORMATION:

APPLICANT: BENOIT, Patrick

APPLICANT: MEYER, Francois

APPLICANT: MAGUIRE, Deborah

APPLICANT: PLAVEC, Ivan

APPLICANT: TOVEY, Michael G.

TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON

TITLE OF INVENTION: RECEPTOR WITH NEUTRALIZING ACTIVITY AGAINST TYPE I

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

ZIP: 20007

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/307,588

FILING DATE: 05-DEC-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/00770

FILING DATE: 30-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 92400902.0

FILING DATE: 31-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: SAXE, Bernhard D.

REGISTRATION NUMBER: 28,665

REFERENCE/DOCKET NUMBER: 17283/117/GUPL

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

INFORMATION FOR SEO ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 557 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-307-588-4

Query Match 100.0%; Score 2313; DB 2; Length 557;

Best Local Similarity 100.0%; Pred. No. 2.7e-230;

Matches	436: Conservative	0: Mismatches	0: Indels	0: Gaps					
QY	1	MMVLLGATTLVLA	VAGFWVL	LSAAAGKNNK	SPQREVEYDI	DDNFILRNN	SDSEYGVNT	60	
Db	1	MMVLLGATTLVLA	VAGFWVL	LSAAAGKNNK	SPQREVEYDI	DDNFILRNN	SDSEYGVNT	60	
QY	61	FSPDYOKTGMNM	IKLSCCONIT	STKCNFSS	KLNVYEIK	KIRIRAEK	ENTSSWYEVDSF	120	
Db	61	FSPDYOKTGMNM	IKLSCCONIT	STKCNFSS	KLNVYEIK	KIRIRAEK	ENTSSWYEVDSF	120	
QY	121	TPFRKAQIGPEV	HLAEADKA	IVIHIS	PQTKDSVM	ALDGLSFT	YSLLIMKSSGVEERI	180	
Db	121	TPFRKAQIGPEV	HLAEADKA	IVIHIS	PQTKDSVM	ALDGLSFT	YSLLIMKSSGVEERI	180	
QY	181	ENIYSRHKIKY	LSPETTYCL	KYKAAAL	LSWKIGVY	SPVHC	IKTYVENELP	PEENIEVSQ	240
Db	181	ENIYSRHKIKY	LSPETTYCL	KYKAAAL	LSWKIGVY	SPVHC	IKTYVENELP	PEENIEVSQ	240
QY	241	NONVYLKMDY	IYANTFOV	QWHLAL	KRPGHNL	KKHKI	IPDCEAKTKT	QCVPQVFXK	300
Db	241	NONVYLKMDY	IYANTFOV	QWHLAL	KRPGHNL	KKHKI	IPDCEAKTKT	QCVPQVFXK	300
QY	301	GYILLRVAO	SDNNNTSE	FWSEEEK	IFPDEIOA	FLLPVFN	IRSLSDSFH	YIGAPKSGNTP	360
Db	301	GYILLRVAO	SDNNNTSE	FWSEEEK	IFPDEIOA	FLLPVFN	IRSLSDSFH	YIGAPKSGNTP	360
QY	361	VIODYPLI	YEIFWENTS	NAERKII	EKKTDV	YVNLK	PLTVYCV	KARAHTMDEKLNKSSV	420
Db	361	VIODYPLI	YEIFWENTS	NAERKII	EKKTDV	YVNLK	PLTVYCV	KARAHTMDEKLNKSSV	420
QY	421	FSDAVCEK	TKPGNTSK	436					
Db	421	FSDAVCEK	TKPGNTSK	436					

RESULT 7

US-08-328-256-11

Sequence 11, Application US/08328256

Patent No. 5643749

GENERAL INFORMATION:

APPLICANT: REVEL, Michel

APPLICANT: ABRAMOVICH, Carolina

APPLICANT: RAYOVITSKI, Edward

TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS

TITLE OF INVENTION: PREPARATION AND USE

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROMDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/328,256

FILING DATE: 24-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 107378

FILING DATE: 24-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: BROMDY, Roger L.

REGISTRATION NUMBER: REVEL-13

REFERENCE/DOCKET NUMBER: 25,618

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 11:

```

SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-328-256-11

Query Match          97.9%; Score 2265; DB 1; Length 434;
Best Local Similarity 100.0%; Prid. No. 1,6e-225;
Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0

      1 MMVYLGGTTVLVAVGFWVLAAAGGKLNKSPQVEVDIIDDNFLIRNRSDSEGVNT 60
      |||||||
      1 MMVYLGGTTVLVAVGFWVLAAAGGKLNKSPQVEVDIIDDNFLIRNRSDSEGVNT 60
      61 FSPDQKGMNDWIKLSGCONITSTKCNFSSLKLNVYEIKLRIRAEKENTSSWYEVDSF 120
      61 FSPDQKGMNDWIKLSGCONITSTKCNFSSLKLNVYEIKLRIRAEKENTSSWYEVDSF 120
      121 TPFKRAQIGPEPEVHLEADKAIVIHISPTKDSVMALDGLSFTYSLLIMKNSSGVEERI 180
      121 TPFKRAQIGPEPEVHLEADKAIVIHISPTKDSVMALDGLSFTYSLLIMKNSSGVEERI 180
      161 ENIYSRKHITKLSPTETCYCLKYKALLNLSWKIGVYSPVACITTYENELPPENIVSVQ 240
      161 ENIYSRKHITKLSPTETCYCLKYKALLNLSWKIGVYSPVACITTYENELPPENIVSVQ 240
      181 ENIYSRKHITKLSPTETCYCLKYKALLNLSWKIGVYSPVACITTYENELPPENIVSVQ 240
      181 ENIYSRKHITKLSPTETCYCLKYKALLNLSWKIGVYSPVACITTYENELPPENIVSVQ 240
      241 NONVYLKMDYTANNTFOYQMLHFLKRNPGNHLKYMKQIPDCENKTTQCVFQNVFOK 300
      241 NONVYLKMDYTANNTFOYQMLHFLKRNPGNHLKYMKQIPDCENKTTQCVFQNVFOK 300
      301 GYLLRVQASDGNNTSFMSEEEKFDEIQAFLLPVFNIRSLSDSFHYIYGAPKSGNTP 360
      301 GYLLRVQASDGNNTSFMSEEEKFDEIQAFLLPVFNIRSLSDSFHYIYGAPKSGNTP 360
      361 VIQDPLLYEIIFFMENTSNAEKRIEKKIDYVYVNLKPLTYCVKRAHMDKLNKSSV 420
      361 VIQDPLLYEIIFFMENTSNAEKRIEKKIDYVYVNLKPLTYCVKRAHMDKLNKSSV 420
      421 FSDAVCE 427
      421 FSDAVCE 427
      421 FSDAVCE 427
      421 FSDAVCE 427

RESULT
      8
US-08-328-256-12
; Sequence 12, Application US/08328256
; Patent No. 5643749
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: ABRAMOVICH, Carolina
; APPLICANT: RATOVIETSKI, Edward
; TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,256
; FILING DATE: 24-OCT-1994
; PRIORITY APPLICATION DATA:

```

APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: REVEL-13
REFERENCE/DOCKET NUMBER: 25,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-328-256-12

Query Match 95.7%; Score 2213; DB 1; Length 496;
Best Local Similarity 98.1%; Pred. No. 4,7e-220;
Matches 419; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

OY 1 MMVVLGATTLVAVGPPVLSAAGKRLKSPQVEVDIIDNFI LRNRSDESGVNT 60
DB 1 MMVVLGATTLVAVGPPVLSAAGKRLKSPQVEVDIIDNFI LRNRSDESGVNT 60
OY 61 FSEFDYQKGMNMKILSGCONITSTKCNFSSKLNVYEIKRIRAEKENTSSWYEVDSF 120
DB 61 FSEFDYQKGMNMKILSGCONITSTKCNFSSKLNVYEIKRIRAEKENTSSWYEVDSF 120
OY 121 TPFKAQIGPPEVHLAEADKAIVIHISPTKDSVMALDGLSTYSLIMKNSGVEERI 180
DB 121 TPFKAQIGPPEVHLAEADKAIVIHISPTKDSVMALDGLSTYSLIMKNSGVEERI 180
OY 181 ENISRHKIYKLSPTTCLVKAKALLTSWKIGVSPVHCITTYENELPPENIEVSQ 240
DB 181 ENISRHKIYKLSPTTCLVKAKALLTSWKIGVSPVHCITTYENELPPENIEVSQ 240
OY 241 NQNTVLMKDYTYANTFQVQWHLAFKRNPNHLYKRAQIDCEVKTQCVFQONVQK 300
DB 241 NQNTVLMKDYTYANTFQVQWHLAFKRNPNHLYKRAQIDCEVKTQCVFQONVQK 300
OY 301 GIVLLRQASDGNNTSFSEIEIKFDTETQAFLLPVENIRSLDSFHIYIGAPKQSGNTP 360
DB 301 GIVLLRQASDGNNTSFSEIEIKFDTETQAFLLPVENIRSLDSFHIYIGAPKQSGNTP 360
OY 361 VIQDYPLIYEIIFEMTSMERKIIIEKTDVTPNKLPLYCYKARAHMDEKLNKSSV 420
DB 361 VIQDYPLIYEIIFEMTSMERKIIIEKTDVTPNKLPLYCYKARAHMDEKLNKSSV 420
OY 421 FSDAVCE 427
DB 421 FSDAVCE 419

RESULT 9
PCT-US94-14277-3
Sequence 3, Application PC/TUS9414277
GENERAL INFORMATION:
APPLICANT: Aguet, Michel
APPLICANT: Bohnl, Ruth
APPLICANT: Hemml, Silvio
TITLE OF INVENTION: Receptor Subunit Polypeptides
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14277
FILING DATE: 07-DEC-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/164596
FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 866PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 202 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US94-14277-3

Query Match 21.2%; Score 490.5; DB 4; Length 202;
Best Local Similarity 48.5%; Pred. No. 7.4e-43;
Matches 98; Conservative 34; Mismatches 69; Indels 1; Gaps 1;

OY 28 KNLKSPQVEVDIIDNFI LRNRSDESGVNTFSEFDYQKGMNMKILSGCONITSTK 87
DB 1 ENLPLDNTNXYIKTQFRRAEGNSTSSWNEVDPIFFYTAHMSPPVEHLEREDKALVHI 60
OY 88 NFSCLKNVYEIKRIRAEKEN-TSSWYEVDSFTPFKAQIGPPEVHLAEADKAIVIH 146
DB 61 EFSLLDNTNXYIKTQFRRAEGNSTSSWNEVDPIFFYTAHMSPPVEHLEREDKALVHI 120
OY 147 SPQKDSVMALDGLSTYSLIMKNSGVEERIENISRHKIYKLSPTTCLVKAKAL 206
DB 121 SPQKDSVMALDGLSTYSLIMKNSGVEERIENISRHKIYKLSPTTCLVKAKAL 206
OY 207 LTSWKIGVSPVHCITTYENE 228
DB 181 PSLKHSNYSXOCISTVANK 202

RESULT 10
PCT-US94-14277-4
Sequence 4, Application PC/TUS9414277
GENERAL INFORMATION:
APPLICANT: Aguet, Michel
APPLICANT: Bohnl, Ruth
APPLICANT: Hemml, Silvio
TITLE OF INVENTION: Receptor Subunit Polypeptides
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14277
FILING DATE: 07-DEC-1994

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/164596
FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 866PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US94-14277-4

Query Match 20.2%; Score 466.5; DB 4; Length 200;
Best Local Similarity 44.7%; Pred. No. 2.2e-40;
Matches 93; Conservative 37; Mismatches 69; Indels 9; Gaps 3;

QY 229 LPPEENIVSVQNONVYLKMDY-ITYANTFOYQMLHAFLEKRNPNHLYKKQIPDCEVAK 287
DB 1 MPVGNLQVDAQGSYVYLKMDYIASADYLFRAQWLPYKSSSGSHSDKMPDPICANVQ 60
QY 288 TTCQCFPNVPOKGIYILRQVADSGNNTSFNSEELKPDLEIQALFPPVFNIRSLDSF 347
DB 61 TTHCFVSDTYTGTGFFLHVQASGNTSFSSEKFTDSQKHILPPPIVITVTAASDYL 120
QY 348 IYIGAPKSGNTPIVQIDYPIEYIFWNTSNAERKIIETKIDYVTPNLKPLTYCVAKR 407
DB 121 VYXNQDSTCD-----GLNVEIIFWNTSNTKISMEDGDEFLKLNQPLTYVCQAR 173
QY 408 AHTMDEKLNKSSVSDAVCEKTPGNTS 435
DB 174 V-LFRALNKTSNFSEKLCETKTPGNTS 200

RESULT 11
US-08-683-743-4
Sequence 4, Application US/08683743
Patent No. 5843697
GENERAL INFORMATION:
APPLICANT: Pestka, Sidney
APPLICANT: Kotenko, Serguei
TITLE OF INVENTION: CYTOKINE RECEPTOR SIGNAL TRANSDUCTION
TITLE OF INVENTION: CHAIN
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,743
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601-1-050
TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE:
US-08-683-743-4

Query Match 9.9%; Score 228.5; DB 2; Length 325;
Best Local Similarity 29.9%; Pred. No. 1.8e-15;
Matches 67; Conservative 42; Mismatches 96; Indels 19; Gaps 8;

QY 19 WYLSAAGCKNLS-----POKVEYDIIDNFIKRNKSDSVGNVTSFDYQKGM 71
DB 3 WSLGSLWGLGLVSLAMVPPENVRNYSVFNKILQWESPAPKGNLTITAOY---LS 58
QY 72 NWIKSGCQNTSTKCNFSSSLKLNVEIKLRIRAE-KENTSSWYEVDSFTPERKAOIGP 130
DB 59 YRIPODCAMTTLTECPSS--LSKYGDTLVRVAEFADSHDQVNI-TCPVDITLIGP 115
QY 131 PEVLEA-EDKAIYHISPGTKDSV-NWALDGL--STYSLILWKNSSGVEERIENTYSR 186
DB 116 PGMQVEVLADSLHFRFLAPKRIENEYETWTKMKNYSWTYVQYKKNCTDEKFOITPOYDF 175
QY 187 HKIKLSPETTYCLKYNKALLTSKIGVYSVPHCIKTIVNELP 230
DB 176 EVLNLEPWTYTCVVRGFLPDRNKAGEWSEPCVOTTHDETVP 219

RESULT 12
PCT-US94-14277-2
Sequence 2, Application PC/TUS9414277
GENERAL INFORMATION:
APPLICANT: Aguet, Michel
APPLICANT: Bohnl, Ruth
APPLICANT: Hemml, Silvio
TITLE OF INVENTION: Receptor Subunit Polypeptides
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14277
FILING DATE: 07-DEC-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/164596
FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 866PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 332 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US94-14277-2

Query Match 8.8%; Score 203; DB 4; Length 332;
Best Local Similarity 30.1%; Pred. No. 8e-13;
Matches 69; Conservative 38; Mismatches 86; Indels 36; Gaps 13;

21 LSAAGG-----KNLKSPOKVEVDIIDNFIILNRNSDES-----VGNTFSEFDYOKGM.70
16 LQAASSPSPFSOLAAPLPLRLHLINDEQILTWBSPSPNDPRPVYQVEYSF-----I.69
71 D-NWIKL--SGCONITSTKCNFS--LKLNTYE-EIKLRIRAKEN-TSSVYEVDSFTP.122
70 DCSWRLLEPNCITDITETCDLTGGGRLLKLPFTVFLRAKAGNLSKRWGLPFOH.129
123 FKAQIGPPE-VHLEAEKAIYIHISPGTKDSVMALDGLSFTYSLLIKRNSGVEERIE.181
130 YENVTVPKPNISVTPGKSLVIHFSPPD-----VFHGATFOYLVIHWKSESTQOEQVE.184
182 NIYSRHKIY--KLSPTTYCLKVAAL-LTSMKI--GVYSPHCKT.224
185 GPFKNSIYGLNKLKPRVYCIQTEQOLIKKKIRPHGLLSNVSCHETT.233

RESULT 13

US-08-943-087-2

Sequence 2, Application US/08943087
Patent No. 5945511

GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Kho, Choon J.
APPLICANT: Jelmeberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: Protein
FRAGMENT TYPE: Internal
US-08-943-087-2

Query Match 8.6%; Score 198; DB 2; Length 553;
Best Local Similarity 21.0%; Pred. No. 6e-12;
Matches 91; Conservative 79; Mismatches 173; Indels 90; Gaps 17;

11 LVLVAVGW--VLSAAGGNLKSPOKVEVDIIDNFIILNRNSDES--VNTFSEFDYOK.67
18 LLLIAPWGRAVPCVSGG--LPRANITFLSINNKNVLOMTPEGLQGVKVTYQYFI.75
68 TGMNWKILSGCONITSTKCNFSSLKINVEEILRIRA-EKENTSSWYEVDSFTPRKA.126
76 YGOKRWLNSKCRNINNTYCDLSAETSDEHQQYAKAKAIGTKCSKMASSGREYPLET.135
127 QIGPEVHLEAEKAIYIHISPGTK-----DSVMALDGLSFTYSLLIKRNSGVE.177
136 QIGPEVALTTDEKISIVLTAPEKMKRNPEDLPSMOQIYSLNLYNVSLNLTNSNTWS.195
178 ERINITSRAKTIY--LSPETTYCLKVAAL-LTSMKIGVYSPVHCITVENE-----229
196 QCVTN---HTVLVLTWLEPMTLYCVHVESFVPCPPRAQPSKQACARTLKDQSEFRAKI.251
229 -----LPPENIEVSYONNVVLKMDTYANMTFOV-QMLHAPLKNPGRNHLKMKQIPD.282
252 IFWYVLP---ISITV-----FLFSVMGISITRYIHGVEKKHPAULI-----290
283 CENVKTCQVFPONVFOKGIYLLRVQASDCNNTSFWSEEEKFPDEI---QAFLLPVENI.339
290 -----LTYGNEFPKREFV---PAEKIVINFILNISDSKISHOMSLGKSSDV.336
340 RSLDSFHIYIGAPKQGNTPVIQDPLIYEI-----IFWENTSNARKIIEKKTDV.391
337 SSLND-----PQPSGNLRPQEEVEVKHLGYASHLMEIFDSEBNTGTSFTQOEST.388
392 --TWPNLKLTVY.402
389 SRTIPDKTIVLEY.401

RESULT 14

US-08-943-087-14

Sequence 14, Application US/08943087
Patent No. 5945511

GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Kho, Choon J.
APPLICANT: Jelmeberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305

FILING DATE: 20-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Lunn, Paul G
 REGISTRATION NUMBER: 37,743
 REFERENCE/DOCKET NUMBER: 96-24C
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-442-6627
 TELEFAX: 206-442-6668
 TELEX:
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 553 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 OS-08-943-087-14

Query Match	8.6%	Score 198;	DB 2;	Length 553;
Best Local Similarity	21.0%;	Pred. No. 6e-12;		
Matches 91;	Conservative 79;	Mismatches 173;	Indels 90;	Gaps 17;

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OY 11 LVAAGPM--VLSAAGKMLKSPKVEVDIIDDNFLRNSDESVC--NYEFPDYOK 67
Db 18 LLLLLAAPMGAVPCVSG--LPKPANITFLSINKKVNLOMTPEGLQGVYTYOYFI 75
OY 68 TGMDNWIKLSGQONITSTKCNFSSLLKINVEIKLRIR--EKENTSMYEVDSTPEPKA 126
Db 76 YGOKMLWKSECRNINRTYCDLSAETSDYEHQYAKKALMGTKCSKMAESGRYPLET 135
OY 127 QIGPPEVHLEADNAIVHISPGK-----DSYMALDGLSIFYLLINKNSGVE 177
Db 136 QIGPEVALTTDEKSIYVLAPBKMKNRPEDLPVSQOQIYSNKLKYNVSLNKTSTWTS 195
OY 178 ERIENIYSRHKIYK--LSPETTYCLKVAALITSMKIGVSPVHCIRTYENE----- 229
Db 196 QCVYN---HLVLTLWLEPNLLYCVHNESFPGPBPRAQBPSEKCATLNDQSEFPAKI 251
OY 229 -----LPPENIEVSVONQNTVLKMDITYANMTQV--OMLHAFIKRPNGHLYKWOIPD 262
Db 252 IFWYVLP---ISITV-----FLFSVMGSIYRIYHVGKXHPANLI----- 280
OY 283 CENKTTQCVPPONVFOKGIYLLRQASDGNNTSFMSSEIKFDEI---QAFLLPVENI 339
Db 290 -----LIYGNEDFKRFV---PAEKIVINFITLINISDDBSKISHQMSLLGKSSDV 336
OY 340 RSLDSFHIIYGAPKSGNTFVIODYPLIYEI-----LEWNTSNAERKILIEKTDV 391
Db 337 SSLND-----PQSGNLBPQDEEYVKHLYGASHLMETFCDSSEENTEGTSPTQOESL 388
OY 392 ---TVPNKLPLVY 402
Db 389 SRTIIPDKTVLEY 401

```

RESULT 15
 US-08-943-087-16
 : Sequence 16, Application US/08943087
 : Patent No. 5945511
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Lok, SI
 :
 : APPLICANT: Kho, Choon J.
 :
 : APPLICANT: Jeimberg, Anna C.
 :
 : APPLICANT: Adams, Robyn L.
 :
 : APPLICANT: Whitmore, Theodore E.
 :
 : APPLICANT: Farrah, Theresa M.
 :
 : TITLE OF INVENTION: CYTOKINE RECEPTOR
 :
 : NUMBER OF SEQUENCES: 60
 :
 : CORRESPONDENCE ADDRESS:
 :
 : ADDRESSEE: Zymogenetics, Inc.
 :
 : STREET: 1201 Eastlake Avenue East
 :

CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98102
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Discrete
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/943,087
 FILING DATE:
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/803,305
 FILING DATE: 20-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Lunn, Paul G
 REGISTRATION NUMBER: 32,743
 REFERENCE/DOCKET NUMBER: 96-24C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-442-6627
 TELEFAX: 206-442-6678
 TELEX:
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 553 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-08-943-087-16

Query Match	8.6%;	Score 198;	DB 2;	Length 553;
Best Local Similarity	21.0%;	Pred. No. 6e-12;		
Matches	91;	Conservative	79;	Mismatches 173;
			Indels	90;
			Gaps	17;

```

0Y 11 LVAVGPW--VLSAAGGNKLSPOKVEVDIIDDNNILMNRNSDSVG--NTFSPDYOK 67
0Y 18 LLLLLAAAGRAVPCVSGG--LKPANITELSIMKNVLOMTPEGLQGVITYOYFI 75
0Y 68 TGMDMWIKLSCGQONITSTKCNFSSLLKNYEELKIRAR--EKENTSSWYEVDSFTPRKA 126
0Y 76 YGOKKWLKNSCRNINRTYCDLSAETSDYEHQYAKKALMGTKCSMAESGRFPELET 135
0Y 127 QIGPPEVLEHEDKAIYHISPRK-----DSYMAALDGLSFYSLLIMKNSGVE 177
0Y 136 QIGPEVALITDEKISIVLTLAPBKRMRNPEDLPVSMQOIIYSNLKYVAVSLNTRKSNPTWS 195
0Y 178 ERIEITYSRHKIYK--LSPETTYCLNKAALLTSMKIGVYSPVHCITRYENE----- 229
0Y 196 QCVYN-----HLVLTWLEPNLPCVHNESFPGGPRRAQOSEKOCATLNDQOSEPKAKI 251
0Y 229 -----LPPENIEVSVONQNTVLMWDYTNMTFQV--QWLHAFILKRNPNHLLYKMOIPD 282
0Y 252 IFWYLP-----ISITV-----FLFSWGSYIRXIHVGKEXKHPANLI----- 290
0Y 283 CENVATTOCVFPONVFOKGIYLLRVAOSDGNSTFSWSEIKRDEI--CAFLLPVFN 339
0Y 290 -----LIYGHEDKRFYV---PRAKVIYVIFTLNISDSKISHODMSLLGKSDV 336
0Y 340 RSLDSFHIYIGAPROSGNTFVIDYPLIYEI-----IFWNTSNAERKILIEKTDV 391
0Y 337 RSLND-----PQPSNLNLPQDEEVKHLGVAASHLMELFCDSSENTGTSFTQOESL 388
0Y 392 -----TVPNLKPLVY 402
0Y 389 SRTIIPDKVTLEY 401

```

Mon Jun 5 12:54:26 2000

us-09-240-675-2.modif.ra1

Page 10

Search completed: June 1, 2000, 05:52:41
Job time: 4640 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 1, 2000, 04:36:46 ; Search time 16.46 Seconds

(Without alignments)
1553.011 Million cell updates/sec

Title: US-09-240-675-2

Perfect score: 2313
Sequence: 1 MMVVLGATTLLVAVGPMV.....KSSVFDVCEKTRKPGNTSK 436Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR_63:*

1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2313	100.0	557	2 A32694	Interferon alpha/b
2	1507	65.2	560	2 S27387	Interferon alpha r
3	1069	46.2	590	2 A45283	Interferon alpha/b
4	233.5	10.1	273	2 G01418	Cytokine receptor
5	228.5	9.9	325	2 A47003	Cytokine receptor
6	221.5	9.6	349	2 UC6311	Interferon recepto
7	203	8.8	332	2 A49947	Interferon gamma r
8	155.5	6.7	337	2 I38500	Interferon gamma r
9	129	5.6	1375	2 T13822	Interferon gene prot
10	129	5.6	1375	2 T13822	Interferon gene prot
11	127.5	5.5	1443	2 I50600	frizzled gene prot
12	123.5	5.3	1451	2 S42167	neogenin - chicken
13	119	5.1	1383	2 A36080	190K protein - hum
14	118	5.1	489	2 A31555	insulin receptor p
15	118	5.1	981	2 S51604	Interferon gamma r
16	118	5.1	1005	2 S49015	receptor-like tyro
17	117.5	5.1	575	2 A49667	interleukin-10 rec
18	117.5	5.1	1427	2 I51669	tumor suppressor -
19	117.5	5.1	1585	2 T19121	probable protein-t
20	117	5.1	817	2 A48721	titin, muscle - ch
21	116	5.0	1912	2 A56178	protein-tyrosine-p
22	115.5	5.0	658	2 T16040	hypothetical prote
23	115	5.0	1450	2 A44027	165K myofibrillar
24	115	5.0	26826	1 I38344	titin, cardiac mus
25	113.5	4.9	880	1 JC4166	protein-tyrosine k
26	113	4.9	1615	2 B49502	protein-tyrosine-p
27	113	4.9	1767	2 A49502	protein-tyrosine-p
28	113	4.9	1898	2 S46216	leukocyte antigen-
29	113	4.9	6831	2 T27934	hypothetical prote
30	113	4.9	6839	2 S57242	twilchin - Caenorh

31	113	4.9	7160	2 T27935	hypothetical prote
32	111.5	4.8	1896	2 T08851	Down syndrome cell
33	109	4.7	416	2 T25036	hypothetical prote
34	109	4.7	1372	2 A34157	insulin receptor p
35	108.5	4.7	1028	2 T58164	BIG-1 protein - ra
36	108.5	4.7	2033	2 T09123	hybrid receptor So
37	108.5	4.7	2215	2 T00348	LtR1 protein - mou
38	108	4.7	991	2 T78843	receptor protein-t
39	106.5	4.6	878	2 S47489	receptor tyrosine
40	105.5	4.6	898	1 A40091	interleukin-3 rece
41	105.5	4.6	893	2 S51603	receptor-like tyro
42	105.5	4.6	1825	2 T32828	hypothetical prote
43	105	4.5	36	2 S41602	interferon alpha r
44	105	4.5	13055	2 T16580	hypothetical prote
45	104.5	4.5	662	2 I37892	IL12 receptor comp

ALIGNMENTS

RESULT 1

A32694

Interferon alpha/beta receptor precursor - human

C:Species: Homo sapiens (man)

C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 22-Oct-1999

C:Accession: A32694; S17112

R:Uze, G.; Lutfalla, G.; Gresser, I.

Cell 60, 225-234, 1990

A:Title: Genetic transfer of a functional human Interferon alpha receptor into mo

A:Reference number: A32694; MUID:90124632

A:Accession: A32694

A:Molecule type: mRNA

A:Residues: 1-557 <UZE>

A:Cross-references: GB:J03171; NID:g184645; PIDN:AAA52730.1; PID:g306914

R:Lutfalla, G.

submitted to the EMBL Data Library, July 1991

A:Description: The structure of the human Interferon alpha/beta receptor gene.

A:Reference number: S17112

A:Accession: S17112

A:Molecule type: DNA

A:Residues: 1-16, 'A', 18-329, 'V', 343-557 <LUT>

A:Cross-references: EMBL:X60459; NID:g32671

C:Genetics:

A:Gene: GDB:IFNAR1; IFNAR; IFRC

A:Cross-references: GDB:120078; OMIM:107450

A:Map position: 21q22.1-21q22.1

A:Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3

C:Keywords: cytokine receptor; glycoprotein; transmembrane protein

F1-21/Domain: transmembrane #status predicted <TRN1>

F1-437-455/Domain: transmembrane #status predicted <TRN2>

F150,58,81,88,110,172,254,313,314,376,416,433,507,518,537/Binding site: carbohydr.

Query Match 100.0%; Score 2313; DB 2; Length 557;
Best Local Similarity 100.0%; Pred. No. 3.2e-165;

Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	1	MMVVLGATTLLVAVGPMVLSAAAGKRLSPKVEVDIIDNFIIRNNSDESGVNT	60
DB	1	MMVVLGATTLLVAVGPMVLSAAAGKRLSPKVEVDIIDNFIIRNNSDESGVNT	60
OY	61	FSFDYQTKGMNWKLSGCONITSTKCNFSSILKLVYEIKLRIRAEKENTSSWEVD	120
DB	61	FSFDYQTKGMNWKLSGCONITSTKCNFSSILKLVYEIKLRIRAEKENTSSWEVD	120
OY	121	TPFRQAQGPPEVHLAEADKAIVHISPGTDSVVMALDGLSFTYSLILNNSGVEERI	180
DB	121	TPFRQAQGPPEVHLAEADKAIVHISPGTDSVVMALDGLSFTYSLILNNSGVEERI	180
OY	181	ENIYRHRHRYKLSPEPTTCLVYKAALLTSMKIGVSPVHCITVTENELPPENIEVSQ	240
DB	181	ENIYRHRHRYKLSPEPTTCLVYKAALLTSMKIGVSPVHCITVTENELPPENIEVSQ	240

QY	241	NONTYKMDYTAANNMFOVQWMLHAFLEKRNPGNHLXYMKOIPDCEANKTTOQCVPOANFQK	300
Db	241	NONTYKMDYTAANNMFOVQWMLHAFLEKRNPGNHLXYMKOIPDCEANKTTOQCVPOANFQK	300
QY	301	GIYLLRVOASDGNNTSEFWSEIEIKFDEIOAFLLPVPFNIRSLSDSFHIIYGAPKQSGNTP	360
Db	301	GIYLLRVOASDGNNTSEFWSEIEIKFDEIOAFLLPVPFNIRSLSDSFHIIYGAPKQSGNTP	360
QY	361	VIQDYPLIYEIIFFMENTSNAERKIIIEKKTDTVYPNLKLPLTVYCVKARAHTMDEKLNKSSV	420
Db	361	VIQDYPLIYEIIFFMENTSNAERKIIIEKKTDTVYPNLKLPLTVYCVKARAHTMDEKLNKSSV	420
QY	421	FSDAVCEKTKPGNTSK	436
Db	421	FSDAVCEKTKPGNTSK	436

RESULT 2
S27387
Interferon alpha receptor type 1 precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 13-Jan-1995 #sequence_taurus
C:Accession: S27387; S33770
R:Mouchel-Vielh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G.
FEBS Lett. 313, 255-259, 1992
A>Title: Specific antiviral activities of the human alpha interferons are determined at
A:Reference number: S27387; MUID:93076908
A:Accession: S27387
A:Status: Preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-560 <MOU>
A:Cross-references: EMBL:X68443; NID:9431; PIDN:CAA48484.1; PID:9432
A:Experimental source: MDBK cells
R:Lim, J.K.; Langer, J.A.
Biochim. Biophys. Acta 1173, 314-319, 1993
A>Title: Cloning and characterization of a bovine alpha interferon receptor.
A:Reference number: S33770; MUID:93305725
A:Accession: S33770
A:Status: Preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-421, 'V', 423-560 <LIM>
A:Cross-references: EMBL:L06629; NID:g163187; PIDN:AAA02571.1; PID:g163188
A:Experimental source: lung
C:Keywords: antiviral; cytokine receptor; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:23-560/Product: Interferon alpha receptor type 1 #status predicted <MAT>

[illegible]

```

Db      289   :|||:||||:|||||:|||||:~::~:~::|:::~::|:::~::|:::~::|:::~::|
Oy      358   NTPVIQDYPLLIYEIIFFMENTSNARKTIEKKTIDVTENLPLTYVCYKAARHTMDELNK 417
Db      359   NMSVQLQPLLYEIVFEMENTSNAERKYLEKRTNIFDLPLTYVCYKABALLIENDBRNK 418
Oy      418   SSVSFDAYCEKTKPGNTSK 436
          | ||| ||||| |||||
Db      419   GSSFSDYCEKTKPGNTSK 437

```

RESULT 3

interferon alpha/beta receptor - mouse

A:Accession: A45283

C:Species: Mus musculus (house mouse)

C:Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #ext_change 05-Nov-1999

A:Accession: A45283; #sequence_revision 18-Nov-1994 #ext_change 05-Nov-1999

R:Uze, G.; Rutfalia, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E.

A:Title: Behavior of a cloned murine interferon alpha/beta receptor expressed in h

A:Reference number: A45283; MUID:92262522

A:Accession: A45283

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-590 <UZE>

A:Cross-references: GB:889641; NID:9194111; PIDN:AAA37890.1; PID:9194112

A>Note: sequence extracted from NCBI backbone (NCBIN:102554, NCBIP:102357)

R:Rutfalia, G.; Uze, G.

A:Title: Structure of the murine interferon alpha/beta receptor-encoding gene: high

A:Reference number: I48423; MUID:95047447

A:Accession: I48423

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 118-125 <RES>

A:Cross-references: EMBL:U06237; NID:g497103; PIDN:AAA65003.1; PID:g755810

A:Accession: I48424

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 127-224 <RE2>

A:Cross-references: EMBL:U06238; NID:g497104; PIDN:AAC01749.1; PID:g755811

A:Accession: I48425

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 243-264 <RE3>

A:Cross-references: EMBL:U06239; NID:g497106; PIDN:AAA65004.1; PID:g510261

A:Accession: I48426

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 265-375 <RE4>

A:Cross-references: EMBL:U06240; NID:g497108; PIDN:AAA65005.1; PID:g510262

A:Accession: I48427

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 397-424 <RE5>

A:Cross-references: EMBL:U06241; NID:g497110; PIDN:AAA65006.1; PID:g755812

A:Accession: I48428

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 426-445 <RE6>

A:Cross-references: EMBL:U06242; NID:g497112; PIDN:AAA65007.1; PID:g755813

A:Accession: I48429

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 473-590 <RE7>

A:Cross-references: EMBL:U06244; NID:g497114; PIDN:AAA65008.1; PID:g510265

C:Genetics:

A:Gene: IFNAR

A:Introns: 177/3; 331/1

Keywords: cytokine receptor; transmembrane protein

```

Query Match 46.2%; Score 1069; DB 2; Length 590;
Best Local Similarity 48.6%; Pred. No. 2,9e-72;
Matches 212; Conservative 77; Mismatches 137; Indels 10; Gaps
4

OY 2 MWVLGATTVLVAVGPPWVLSAAGGKNLKSPOKVEVDIIDDNFILRNRSDESVCNVT 61
Db 1 MLAVGAAALVLVAGAPWVLPSPAGGENLKPPENIDVYIIDNNYTLKMSHESMSYTF 60
OY 62 SFDIOGTGMNNIKILSGCONITSTYCNSSSLKLNYYEIKLRIRAKEN-TSSWYEVDSF 120
Db 61 SAEYRTKDEAKWLKPECOHTTTTTCFSLDNTNYIKTQFVRAEGNSTSSMNEVDF 120
OY 121 TPFRRQAIGPPVHLAEDEKALVHISPECTKSYMAALDGLSFTYSLLTKMNSSGVEER 180
Db 121 IPEYTAHNSPPVRLAEAEKALVHISPGQGGNNMALKRPFSTYIRKMQSSSDKK 180
OY 181 ENIYSRHKIYKSPETTYCLKAKAALLTSMKIGVSPVICITTYENELRPPENIEVSQ 240
Db 181 NSTYVEKIPPELLPETTYCLEYKALHPSLKKSINSTYOCISTYANKKRPVGNLQVND 240
OY 241 NONVYLVKNDY-TYANTFOVQMLHAFLEKKNPGNHLYKMKQIPDCENVKTTQCVFQNV 299
Db 241 GKSIVLKMDYIASADVLFRQAQMLPGXKSSGSSHSDKMKRPIPCANVQTHCVFSQDTV 300
OY 300 KGIYLRVQASGNNSTSPSEIEKEDTEQLAFLPPVYFNRISDSFHYITGAPKOSGT 359
Db 301 TGTFPLHVAOSGNNHSTSPSEIEKEDTQKHIIIPRPVYITVAMSDLLVYVNCODSTCD 360
OY 360 PVIOQYPLVEIIFEMENSTNAERKIETKTDVTPVLKPLTYCVKARAHTDEKLNKSS 419
Db 360 -----GLNYEILFEMENSTNKSMEKDEPFTLKNLQPLTYICVQARY-LFRALLNKTS 412
OY 420 VFSDAVCETKTPGNTS 435
Db 413 NSEKLCERTKRGSSFS 428

RESULT 4
G01418
cytokine receptor family II, member 4 - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
C:Accession: G01418
R:Luftalla, G.
submitted to the EMBL Data Library, April 1994
A:Reference number: G06935
A:Accession: G01418
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-273 <LUT>
A:Cross-references: EMBL:U08988; NID:g571295; PID:g571296
C:Genetics:
A:Gene: GDB:CRFB4; CRF2-4
A:Cross-references: GDB:138168; OMIM:123889
A:Map position: 21q22.1-21q22.2
A:Introns: 17/1; 58/2; 111/1; 166/3; 216/1

Query Match 10.1%; Score 233.5; DB 2; Length 273;
Best Local Similarity 29.9%; Pred. No. 2,6e-10;
Matches 67; Conservative 44; Mismatches 94; Indels 19; Gaps
8

OY 19 WVLISAAGGKNLKS-----POKVEVDIIDDNFILRNRSDESVCNVTSPFDYQKTGMD 71
Db 3 WELSGWLGCLLVASLGMPPPENYVMSVNFKNIIQWESPAFAKGNLTTRAY-----LS 58
OY 72 NMIKLSGCONITSTYCNSSSLKLNYYEIKLRIRAE-KENTSSWYEVDSFTPFRAQIG 130
Db 59 YRIFQDKCNTLTLECDSS--LSKYGDHTLVRBAFEADBSDMVNI-FFCPVDOTIIG 115
OY 131 PEVHLAEDEKALVH-ISGCTDSV-MMALDGL-SFTYSLTKMNSSGVEEIKENIYSR 186
Db 116 PMQVEVDLDSLMRLAKRIENEYETWTKKNYNSWTYNSVQYKNGGTDEKFIQIDYDF 175

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```

Oy 167 HKIYKLSPEYTYCLVKVKAALLTSWKIGVSPHCITKTEYNELP 230
      | | | | | | | | | | | | | | | | | | | | | | | |
Db 176 EYLRNLPEWYTYCYOVRGFLPDRNKAAGESEPCQETHTDEIVP 219

RESULT 5
A47003
Cytokine receptor family class II protein CRF2-4 precursor - human
C:Species: Homo sapiens (man)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 10-Sep-1997
C:Accession: A47003
R:Rutafalla, G.; Gardiner, K.; Uze, G.
Genomes 16, 366-373, 1993
A:Title: A new member of the cytokine receptor gene family maps on chromosome 21
A:Reference number: A47003; MUID:93300510
A:Accession: A47003
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-325 <LNU>
A:Cross-references: GB:217227; NID:g393378; PID:g393379
C:Keywords: transmembrane protein

Query Match 9.9%; Score 228.5; DB 2; Length 325;
Best Local Similarity 29.9%; Pred. No. 7.8e-10;
Matches 67; Conservative 42; Mismatches 96; Indels 19; Gaps 8;

Oy 19 WVLSPAAGGKNLKS-----POKYEVDIIDNFIILRNRSDESQGVNTFSPDYQRTGMD 71
      | | | | | | | | | | | | | | | | | | | | | | | |
Db 3 WSLGSMLGCLLVSLGWPPEPVNRMNSVNFKNILQWESPAFAKNLFTTAQY----LS 58

Oy 72 WKIKISGCONITSTYCNFSSSLKLVNYEEIKLIRAE-KENTSMYEVDSFTPPRKAQIGP 130
      | | | | | | | | | | | | | | | | | | | | | | | |
Db 59 YRIFODKCMNTLTLECDFFS--LSKYGDHTLVRAFAEDHSDWNI-TFCPPDDITIGP 115

Oy 131 PEVHLEA-EDKRIYVHISGTRKDSV-MMALDGL-SFTSLIIMKSSGVEERIENIYSR 186
      | | | | | | | | | | | | | | | | | | | | | | | |
Db 116 PMQVEVLADSLHMFRLAKINIESEYETWTKMYNNTVNOQYMKNGIDKEFOITQYDF 175

Oy 187 HKIYKLSPEYTYCLVKVKAALLTSWKIGVSPHCITKTEYNELP 230
      | | | | | | | | | | | | | | | | | | | | | | | |
Db 176 EYLRNLPEWYTYCYOVRGFLPDRNKAAGESEPCQETHTDEIVP 219

RESULT 6
JC6311
Interferon receptor class II cytokine receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: JC6311
R:Gibbs, V.C.; Pennica, D.
Article 186, 97-101, 1997
A:Title: CRF2-4: isolation of cDNA clones encoding the human and mouse proteins.
A:Reference number: JC6311
A:Accession: JC6311
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-349 <GIB>
A:Cross-references: GB:U53696

Query Match 9.6%; Score 221.5; DB 2; Length 349;
Best Local Similarity 28.1%; Pred. No. 2.9e-09;
Matches 64; Conservative 49; Mismatches 86; Indels 29; Gaps 10;

Oy 16 VGPWVLSAAGGKNLKSPOKYEVDIIDNFIILRNNSDESQGVNTFSPDYQ--KTGMDNW 73
      | | | | | | | | | | | | | | | | | | | | | | | |
Db 9 LGGFLLVPLALG--MIPPEPKVAMNSGVNFKNILQWEPAPRPNKTLFTTAQYESYRSQDH- 66

Oy 74 IRLSGCONITSTYCNFSSSLKLVNYEEIKLIRAE-KENTSMYEVDSFTPPRKAQIGPPE 132

```

Db 66 -----CKRSTACDSES--HLKSKGYTVRRAELADEHESEWNV--TFCEVEDTITGPPE 117
 Oy 133 VHEADEKAIYIHIS-----PGTKDSVMALDGL--SFTYSLILTKNKGVEERENT 183
 Db 118 MQIESLAESLELRSAPQIENEPET-----WTAKNIYSVAAYVQVQKNTNEKFGVYSP 172
 Oy 184 YSRHKIKYKSPETTYCLKVAALITSMKIGVSPVHCIRKIVENELPP 231
 Db 173 YDSEVLRLNLEPMTTTCYQVGFLLDQNRGEMSEPIC-ERTGDELTIP 219

RESULT 7
 A:Accession: A49947
 Interferon gamma receptor beta subunit - mouse
 N:Alternate names: IFN-gamma R beta chain; IFN-gamma R species-specific cofactor; type I C:Species: Mus musculus (house mouse)
 C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
 R:Hemml, S.; Bohml, R.; Stark, G.; Di Marco, F.; Aguet, M.
 A:Title: A novel member of the interferon receptor family complements functionality of A:Reference number: A49947; MID:94170381
 A:Accession: A49947
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-332 <HEM>
 A:Cross-references: GB:S69336; NID:9545841; PIDN:AA830165.1; PID:9545842
 A:Experimental source: early B-cell line Y16
 A:Note: sequence extracted from NCBI backbone (NCBIN:145654, NCBIPI:145656)
 C:Keywords: cytokine receptor

Query Match 8.8%; Score 203; DB 2; Length 332;
 Best Local Similarity 30.1%; Pred. No. 6.5e-08;
 Matches 69; Conservative 38; Mismatches 86; Indels 36; Gaps 13;
 Oy 21 LSAAGC-----KNLKSPOKVEVDIIDNFIIRNRSDES-----VGNVTFSEFDYQKGM 70
 Db 16 LGAASPSDFSQLAAPLNRHLHYNEQILTEPSSSDPRPVYQVEYSF-----I 69
 Oy 71 D-NWIKI--SGCONITSTKCNFSS---LKNVTE-EIKLRIRAKEN-TSSWEYVDSFTP 122
 Db 70 DGSNHRLEPNCTDITETKCDLITGGGRLKLPFPFTVFLVRAKRGNTLSKMGLEPFOH 129
 Oy 123 FRAAQIGPPE-VHLEADKAIYHISPGTKDSVMALDGLSFTYSLILTKNKGVEERTE 181
 Db 130 YENVTGPPKNISVTPEKGSLVTHFSPPD-----VFHGATFQYLVHYWKSSETQOEYVE 184
 Oy 182 NISYRHKIY--KLSPEYTYCLKVAAL-LTSWKI---GVSPVHCIRKT 224
 Db 185 GPKRSNIVAGNLKPYRVYCLQTEAQLILKNKIRPHGLSLNVSCHETT 233

RESULT 8
 A:Accession: I38500
 Interferon gamma receptor accessory factor-1 precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 05-Nov-1999
 R:Soth, J.; Donnelly, R.J.; Kolenko, S.; Mariano, T.M.; Cook, J.R.; Wang, N.; Emanuel, S.
 A:Title: Identification and sequence of an accessory factor regulated for activation of A:Reference number: A49946; MID:94170380
 A:Accession: I38500
 A:Molecule type: mRNA
 A:Residues: 1-337 <RES>
 A:Cross-references: EMBL:U05875; NID:9463549; PIDN:AAA16955.1; PID:9463550
 A:Experimental source: clone PSK1
 A:Accession: I38501
 A:Molecule type: mRNA
 A:Residues: 1-63; 'Q', 65-337 <RE2>
 A:Cross-references: EMBL:U05877; NID:9463551; PIDN:AAA16956.1; PID:9463552

A:Experimental source: clone pJS3
 C:Genetics:
 A:Map position: 21
 C:Keywords: cytokine receptor

Query Match 6.7%; Score 155.5; DB 2; Length 337;
 Best Local Similarity 22.3%; Pred. No. 0.00023;
 Matches 67; Conservative 54; Mismatches 112; Indels 67; Gaps 14;
 Oy 12 VLVAVGPVYLSAAGC-----KNLKSPOKVEVDIIDNFIIRW-----NRSDESQNVTF 62
 Db 9 LILLGVFAAAAPDPDLSQLPAPQPKIRLYNAEQVLSMEPVALSSTRPVYRVQFK 68
 Oy 63 FVYQTKGDMNFKLS-----GCONITSTKCNFSS-----LKNVTEEKLRIRAK 108
 Db 69 YDYSK-----WTDADINSIGNCQTITATEDFTAASAGPMDFN---TLRLREL 119
 Oy 109 ENT-SWEYVDSFTPFRAQIGPEVHLE---AEDKAIYHISPGTKDSVMALDGLSFT 164
 Db 120 GALHSAWYTMFQHYRNVTVGPPE-NIEVTPGEGSLIRSSPDIDTSTAF----FC 174
 Oy 165 YSLILKNKSSGVEERENIYSRHKIY--KLSPEYTYCLKVAALITSS---WKIGVSPV 218
 Db 175 YVHYWE--KGIQCKGPPFRSNSISLDNLRSVYCLQVOAQLMKNKSNIFRVCHLSNI 232
 Oy 219 HKIKTVENELPPENIEVSV-----QNONVYLRKDYTYANMTPVO 260
 Db 233 SCYETMAADSTELQOVLIVSGTFSLSVLGACFVLKRYGLIKYFHTPPSIPLOIE 292

RESULT 9
 A:Accession: T13822
 Frazzled gene protein - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 R:Kolodziej, P.A.; Tluppe, L.; Mitchell, K.J.; Goodman, C.S.; Fried, S.; Jan, L.Y.;
 A:Title: Frazzled encodes a Drosophila member of the DCC immunoglobulin subfamily 2
 A:Reference number: 217780
 A:Accession: T13822
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1375 <KOL>
 A:Cross-references: EMBL:U71001; NID:91621114; PID:91621115; PIDN:AA647314.1
 C:Genetics:
 A:Gene: frazzled
 A:Map position: 2
 C:Function:
 A:Description: may function in vivo as a receptor or component of a receptor mediat

Query Match 5.6%; Score 129; DB 2; Length 1375;
 Best Local Similarity 16.4%; Pred. No. 0.15;
 Matches 102; Conservative 68; Mismatches 184; Indels 268; Gaps 22;
 Oy 26 GGNLKS-----PKRVEVDIIDNFI-LRW-----NRSDES 56
 Db 447 GKKPLDSGLQARLPSPQPDVLAQIVKSRFTVLSVPEPLQNGDVVYVYKMNNSEREQ 506
 Oy 57 GNVTFSEFDYQKGMNFKLSGCONITSTKCNFSS-----LKNVTEEKLRIRAK 104
 Db 507 KMYTSHDDQCVNIOSILPGRYQVRVANNINFGGASASALEVSTQPEVAINIAGPRAFE 566
 Oy 104 --IRAENKTSWE-----V 117
 Db 567 GYARSHKEIYVWEPTVNGEILKRYVYSENDGADLYHDSALAEVLTLPAPHTDY 626
 Oy 118 DSFTPEKKAQIG-----PPEVHLE-AEDKAIYHISPGTKDSVMAL 158
 Db 627 ISVVPFRNKGMDSSAEIRVKTFSSTPSEPPNNVTLEVTSSSITVHWEPAEDDRNGOI 686

QY 159 DLSFTFYSLILKNSGVEERIENTYSRKIKYKLPETTYCLKVKAALL-----TSWKI 212
| : : : : :
Db 687 TGYKIRYRK--FKDAPOVKSTPANI--RYFELSLNDRNAEYQVIAAMTVNGSGPTEWNR 743
QY 213 GYSPVHCICKTVENELP-----PENIEVSQONQNTYVK 247
| : : : : :
Db 744 A-----NTLENDLETOVPCKPIWISHPGANNIALHMGPPQHPHEIKI--RNYVLG 792
QY 248 W-----DY-----251
| : : : : :
Db 793 WGRGIPDENTIELKETERHYHILKNLESMDVYSLRARNVKGDDPPYIDNIKTDEEVD 852
QY 251 -----TYANMFOVOMLHAFKRN-----PGNHLKWKQIP 281
| : : : : :
Db 853 APTPLEVPGVGLRAITMSSSIYVYWMIDTMLKNQHYDNRHYTVSYGTGSRNRYR----- 909
QY 281 DCENKKTQCVFPONVFOKGIYLLRVOASDGNNTSFWSEIKFDEIOAFLLPVPVENIRS 341
| : : : : :
Db 909 --HNTDNLNCMI--NDLRPNTQYEFPAVKVYKGRRESSMSVLSNSTYQNVPTPP----- 960
QY 342 LSDSFHYIGAPKOSGNTPIODYP-----LIYEIIFEMNTSNAER-----KIIKK 388
| : : : : :
Db 960 ----REVYVRLEDMNPPTVYQWIPPKHTLGQITGYNITYTDTTKRDRDMSVEAFAGEE 1015
QY 389 TDVTVPNLKPLTVYCVKARAHT 410
| : : : : :
Db 1016 TMLMLPNLKPYTTYFKVQART 1037

RESULT 10
113823
frazzled gene protein, log isoform - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T13823
R:Kolodziej, P.A.; Timpé, L.; Mitchell, K.J.; Goodman, C.S.; Fried, S.; Jan, L.Y.; Jan, C. Cell 87, 197-204, 1996
A:Title: Frazzled encodes a Drosophila member of the DCC immunoglobulin subfamily and is A:Reference number: 217780
A:Accession: T13823
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1526 <KOL>
A:Cross-References: EMBL:U071002; NID:g1621116; PID:g1621117; PIDN:AAC47315.1
C:Genetics:
A:Gene: frazzled
A:Map position: 2

Query Match 5.6%; Score 129; DB 2; Length 1526;
Best Local Similarity 16.4%; Pred. No. 0.18;
Matches 102; Conservative 68; Mismatches 184; Indels 268; Gaps 22;
QY 26 GGNLKS-----PQAYVDIIDNFI-LRW-----NRDESY 56
| : : : : :
Db 598 GGPPLDSGLQARLPSPRLVAQIVKSRFTLSWEPLOAGDVYVYTYKKNNSEBQ 657
QY 57 GNTYFSDYOKTGMNMKILSGCNTSTKCNFS-----LKLNYEEIKLR----- 104
| : : : : :
Db 658 KMTYKHHDOQVNIQSLRGRTQYFVEANTNNGSASAPLEVSQPEVINIGPPRNE 717
QY 104 --TRAENKTSWYE-----V 117
| : : : : :
Db 718 GYARSHKEIYVKEEPTVNGELIKYRVYSENDGADLYHDSALEAVTELPRHTDV 777
QY 118 DSTPRKAOIG-----PREVHLE-ADKAIIVHISGCTDSVMAL 158
| : : : : :
Db 778 ISVVPNRNGMGSSAEIRKVTSSPPSEPPNNVTLEVYSSSITVHMEPPADEDRNGOI 837
QY 159 DGLSFTYSLILKNSGVEERIENTYSRKIKYKLPETTYCLKVKAALL-----TSWKI 212
| : : : : :
Db 838 TGYKIRYRK--FKDAPOVKSTPANI--RYFELSLNDRNAEYQVIAAMTVNGSGPTEWNR 894

QY 213 GYSPVHCICKTVENELP-----PENIEVSQONQNTYVK 247
| : : : : :
Db 895 A-----NTLENDLETOVPCKPIWISHPGANNIALHMGPPQHPHEIKI--RNYVLG 943
QY 248 W-----DY-----251
| : : : : :
Db 944 WGRGIPDENTIELKETERHYHILKNLESMDVYSLRARNVKGDDPPYIDNIKTDEEVD 1003
QY 251 -----TYANMFOVOMLHAFKRN-----PGNHLKWKQIP 281
| : : : : :
Db 1004 APTPLEVPGVGLRAITMSSSIYVYWMIDTMLKNQHYDNRHYTVSYGTGSRNRYR----- 1060
QY 282 DCENKKTQCVFPONVFOKGIYLLRVOASDGNNTSFWSEIKFDEIOAFLLPVPVENIRS 341
| : : : : :
Db 1060 --HNTDNLNCMI--NDLRPNTQYEFPAVKVYKGRRESSMSVLSNSTYQNVPTPP----- 1111
QY 342 LSDSFHYIGAPKOSGNTPIODYP-----LIYEIIFEMNTSNAER-----KIIKK 388
| : : : : :
Db 1111 ----REVYVRLEDMNPPTVYQWIPPKHTLGQITGYNITYTDTTKRDRDMSVEAFAGEE 1166
QY 389 TDVTVPNLKPLTVYCVKARAHT 410
| : : : : :
Db 1167 TMLMLPNLKPYTTYFKVQART 1188

RESULT 11
150600
neogenin - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Sep-1996
C:Accession: U06000
R:Vielmetter, J.; Kayem, J.F.; Roman, J.M.; Dreyer, W.J.
J. Cell Biol. 127, 2009-2020, 1994
A:Title: Neogenin, an avian cell surface protein expressed during terminal neuron A:Reference number: A55193; MUID:95105243
A:Accession: U06000
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1443 <VIE>
A:Cross-References: EMBL:U07644; NID:g641965; PID:g641966

Query Match 5.5%; Score 127.5; DB 2; Length 1443;
Best Local Similarity 22.2%; Pred. No. 0.21;
Matches 92; Conservative 61; Mismatches 201; Indels 61; Gaps 19;
QY 21 LSAAGKNKLSPOKVEVDIIDNFI-LRMNR--SDSVGNTEFSDYOKTGMNMWIKLS 77
| : : : : :
Db 416 LAPATGPLTPAPRDVAVATLVSTRIFRLTWRTPVSDPOGDMLTISITKRG-----IURE 471
QY 78 GCONITSTKCNSSIKLVNVEEIKLRIRAEKENTSSAYEVDSTFPRRAQIGPREVHLEA 137
| : : : : :
Db 472 RVEN-TSRPGETQVMIQNLMPETVYFVRVVAQNKKGHE--SNAPLKVAT--QREVQLRG 526
QY 138 EDKAIIVHISPGTKDSVMAL---DGLSFTYSLILKNSGVEERIENTYSRKIKYLS 193
| : : : : :
Db 527 PAPNIRAYAGSEPTSVTWETPPLSGNGEIOYKLEYMKGODEDDVAVAGLSYITGLK 586
QY 194 PETTYCLKVKAALLSMKIGVSPVHCICKTVENELPPEPNEVSQONQNTYVK 252
| : : : : :
Db 587 KYTESYFRVA--YKHKPGVSTODVVVRLTSDVPSAAPQNTLELRKSSKIMLWQPP 644
QY 253 ANMTFOVOMLHAFKRNNGNL-----YKMKOIPDCENVKKTQCVFPONVFO--KGI--- 303
| : : : : :
Db 645 A-----GTHSGQITGKIRKRYKSRKSDVTESVGGTQLGLIEGLRG 687
QY 303 --YLLRVOASDGNNT---SFWSEIKFDEIOAFLLPV---FNIRSLDSFHYIGAPK 354
| : : : : :
Db 688 TEYNFRIRAAVTNGTGPATDWASAEFTESDDESVPEVPSLAHRAPLVTSI--VVSATPP 746
QY 355 QSGNTPVYODPLIYEIIFEMNTSNAER-KIIKKTDVTPVRLKLYYCVKARA 408
| : : : : :
Db 747 ENONI--VVRGIALIGIGI---GSPHAQITKDYKORYTTIENDLDPSSHYITLKA 796

RESULT 12

S42167

190K protein - human

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999

C:Accession: S42167

R:Vinkemeier, U.; Obermann, W.; Weber, K.; Fuerst, D.O.

J:Cell Sci. 106, 319-330, 1993

A:Title: The globular head domain of titin extends into the center of the sarcomeric M line

A:Reference number: S42166; MOID:94095665

A:Accession: S42167

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1451 <VIN>

A:Cross-references: EMBL:X69090; NID:g407098; PIDN:CAA4883.1; PID:g407099

C:Superfamily: skelamin

Query Match

Best Local Similarity 5.3%; Score 123.5; DB 2; Length 1451;

Matches 91; Conservative 67; Mismatches 181; Indels 121; Gaps 21;

QY 43 DNFILMNRSDSEVGN--VFSEFDYOKTGMDNMIKLSGCONITSTKCNFSLKLNVEEI 100
 DB 388 DITISMKQAVDGGSPILGIFDKCEVGTDSM-----SQCNDTPVKFARPPVT 436
 QY 101 KL-----RIRAKENTSSW-----YEVDSFTPFKKAIGPPEVHLAEADKAIYIHS 147
 DB 437 GLIEGRSYIFRVAVNMGIGFSPRSEAVAAALDPAEKARLKSP--LSTLDWTVIYTEE 493
 QY 148 PGKIDVMMALDLSFT-----YSLIWK-----NSGVEERLENIYS----- 186
 DB 494 EPEEGVPGPPTDLSVTEATRSYVLSMKPPGORGHEGIMYFEKCEAGTGNMQRVNTL 553
 QY 186 -----BHKIKYKSPETTYCLKRAALTSWIKIGYVSPHCIXKTV-----ENELP 230
 DB 554 PVKSPRALDLAEKSGYCRVRC-----SNSAGVGESEKTEVTYVGDKIDIRAKPKII 609
 QY 231 PPENIEVYVONQNYVLKMD-----YTYANMTFOVQMLHAFLEKRN--GNHLKKWK 278
 DB 610 PSRNTDTSV-----VVSMEESKDAKELGYIIEANVAGSKWEPCC--NNNPVKTHRP-- 660
 QY 279 QIDCEVNVKTQCVFPQNVKQGIYLLRQASDGNNTSFSEELKFTDEIQALPLP-- 336
 DB 660 ---TCGGLVTGQS-----YIFRVAVNAAAGLSEYSQDSE-AIEYKAAIAPSPSP 704
 QY 336 --VFNIIRSLSDSFHIYIGAPKQSGNTPVIDYPLIYEII-----FWENTSNAERKIIIEK 388
 DB 705 CDITCLESPRDSWVLGKQKQDKGAKGAEITGYVNYNREVIGVPGKMR---EAVVKAVREE 761
 QY 389 TDVTVPNLKPLTYCYVKARAHYTDKINKSSVFSDAVCEK 428
 DB 762 A-YKISNLKENMYQFOVAAAMNAGLGAPSAVSECFKCEE 800

RESULT 13

A36080

Insulin receptor precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 18-Jun-1999

C:Accession: A36080

R:Goldstein, B.J.; Dudley, A.L.

Mol. Endocrinol. 4, 235-244, 1990

A:Title: The rat insulin receptor: primary structure and conservation of tissue-specific

A:Reference number: A36080; MOID:9021337

A:Accession: A36080

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1183 <GQK>

A:Cross-references: GB:M29014; NID:g204953; PIDN:AAA1441.1; PID:g204954

C:Superfamily: Insulin receptor; protein kinase homology

C:Keywords: ATP; autophosphorylation; hormone receptor; phosphoprotein; transmembr
 F:1023-1298/Domain: protein kinase homology <KIN>
 F:1030-1038/Region: protein kinase ATP-binding motif

Query Match

Best Local Similarity 5.1%; Score 119; DB 2; Length 1383;

Matches 89; Conservative 52; Mismatches 151; Indels 172; Gaps 20;

QY 43 DNFILMNRSDSEVGNVFSEFDYOKTGMDN-----WIKLSGCON 81
 DB 481 NDIALKTNDQASCENELKFSIRTSFDKILLRWEPPYPPDFRDLGLMFLYKAPYON 540
 QY 82 IT-----STKCNFSLKLNVEIKLRIRAKENTSSWYVDSFTPFKKAIGPPEVHLA 137
 DB 541 VTIEFDGQDNC-----GNSWYVD-----IDPPQ-----RS 566
 QY 138 EDKAIYIHSPTGKDSVMMALDLSFTSYLLIMKSSGVEERLENIYSRHKIKYKSPETT 197
 DB 567 NDPKSGTSPHPC-----WLMRG-----LKPWTQ 589
 QY 198 YCLKAKAALLTSWK--ICVYSPVHCITTVENELPPPENIEVYVONQNYVLKMD--DYT 251
 DB 590 YAIYFVKTLYTFSDERTYGAKSIIYQTDATNPSPVPLDPISSVSSSQIILKMRPPSDP 649
 QY 252 YANMTFOVQMLHAFLEKRNPNHLYK--KOIPCEVNVKTQCVFPQNVFQKGIYL----- 305
 DB 650 NGNIT-----HYLYWEROAEDSELEFDLYL-----KGKLKLSRWTS 687
 QY 305 --LRVQASDGNNTSFSEELI-----KFTDEIQALPLPVENIRSLDSFHIYIGAPKO 355
 DB 688 PPFESDSDGKHNSQSEYDSDASCCGPKTDSOILKLELESSPR-KTFEDYLLNIVFVPRK 746
 QY 356 --SGN-----TPYIODYPLIYEITFWENTSNAERKIIIEK--- 388
 DB 747 TSSGNAEDTRPSRRRSLSEEVGNVYATPTPLDPDFNISTSI--APTSHHEHRPREKVVN 804
 QY 388 KTDVTVPNLKPLTYCYVKARAHYTDKINKSSVFSDAVCEKTP 431
 DB 805 KESLYVSGLRHFTGYRIELQACNDSPEERSGV-AAIYSARIMP 847

RESULT 14

A31555

Interferon gamma receptor precursor - human

C:Species: Homo sapiens (man)

C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 23-Jul-1999

C:Accession: A31555

R:Agnet, M.; Dembic, Z.; Merlino, G.

Cell 55, 273-280, 1988

A:Title: Molecular cloning and expression of the human interferon-gamma receptor.

A:Reference number: A31555; MOID:89003065

A:Accession: A31555

A:Molecule type: mRNA

A:Residues: 1-489 <AGQ>

A:Cross-references: GB:J03143; NID:g184650; PIDN:AAA52731.1; PID:g306915

C:Genetics:

A:Gene: GDB:11FNGRL; IFNGR

A:Cross-references: GDB:120688; OMIM:107470

A:Map position: 6q23-q24

C:Superfamily: Interferon gamma receptor

C:Keywords: cytokine receptor; transmembrane protein

Query Match

Best Local Similarity 5.1%; Score 118; DB 2; Length 489;

Matches 50; Conservative 39; Mismatches 102; Indels 34; Gaps 10;

QY 227 NELPPENIEVYVONQNYVLKMDYTYANM--TFQVOMLHAFLEKRNPNHLYKMDIPDCE 284
 DB 27 SSVPPTNTTISYNNPPLYWYEQIMQVPFYTE-----YKNYGVKNSNM--IDACI 78
 QY 285 NVKTCQCFPQNVFQKGIYL-LRVQASDGNNTSFSEELKFTDEIQALPLPVENIRSL-- 342

Job time: 4582 sec

```
Db 79 NISHHYCNISDHWGDPNSLWVRKAVGOKESAVAKSEEFAYACRGDKGIPPLDIRKEE 138
Oy 342 ---LSDSFH--IYIGAPKOSGN-TPIODYPLIYEIIFMENTSAERKIIKKTD----- 391
Db 139 KOIMIDIFHPSPVFNDEDEVDYDPTTCIRYNNYVYRMNGSEIYKILITOKEDDCDEI 198
Oy 391 ---VTVPNLKPPLTVYCVKARA--HTNDEKLKNS----SVFSDAV 425
Db 199 OCOLAIPVSSLSNOCYCSAECVLRHWGVTEKEKEVCITIFNSSI 243
```

RESULT 15

```
SS1604
receptor-like tyrosine kinase Eph-1 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 29-May-1998
C:Accession: S51604
R:Malsonpierre, P.C.; Barrezaeta, N.X.; Yancopoulos, G.D.
Oncogene 8, 3277-3288, 1993
A:Title: Eph-1 and Eph-2: two novel members of the Eph receptor-like tyrosine kinase fam
A:Reference number: S49015; MUID:9406777
A:Accession: S51604
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-981 <MAIL>
A:Cross-references: EMBL:568029
A>Note: The authors translated the codon GAC for residue 170 as Glu
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C:Keywords: ATP; transmembrane protein
F:651-911/Domain: protein kinase ATP-binding motif
F:659-667/Region: protein kinase ATP-binding motif
```

Query Match 5.1%; Score 118; DB 2; Length 981;

Best Local Similarity 20.1%; Pred. No. 0.64; Mismatches 165; Indels 150; Gaps 21;

```
Matches 92; Conservative 51;
Oy 27 GKNLKSPQYVEDII--DNNF-----ILRNRSDESVCNT---FSFDYQKGMNM 73
Db 165 GRNINKNOYIKIDTIADESEFTELDGDRVMKINTEVRDYGPLSKGFYLAQDVG---- 221
Oy 74 IKLSGCONITST----KCNFSSIKLNVYEILRLRAEKENTSSWTEVDSTPRKQAQI 128
Db 221 ---ACIALVSVRVYKKPCPSVVRHLAVFPD-----TITGADSSQLLEVSGCVNHSVTD 271
Oy 129 GPPEVHLEADKAIIVHISGTDKDSVMALDGLSTYSLLINKNSGVEERIENI--YSRH 187
Db 272 DPPRMHCSAGEWLV---PIGKMC-----KAGYEKNGTCQVCRP 309
Oy 188 KIKKLSPEPTYCKVKALLTSWKIGVSPVH-----CIKTVENELPP----- 232
Db 310 GFFKASHSOTCSKCP-----HSTHEASTSCYCEKDYFRRESDPPTMACTRP 359
Oy 232 ---PENIEVSQONQNTVLYKM-----DYIYANTFOYQWLHAFLEKRNPGNHLKWK 278
Db 360 PSAPRNALISVNETSVLEWIPPADTGGKDVSYIILCKKN--SHAGVCEECGHVR--- 416
Oy 279 QIPDCENVKTTQCVFPQNVQKGIYILRVASGNNNTSFWSEELKFDTEIQAFLLPPVN 338
Db 416 -----YLPQOIGLKNTSYMADPLAHTNTF-----ELEA-----VNG 448
Oy 339 IRSLSDSFHIYIG---APKOSGNTPVIO-----DYP---LIVEIIF 373
Db 449 VSDLSPECTROYVSNVTTNQAPSPTNVKKGKIAKNSISLSMQEPDRPNCIILEYEIKY 508
Oy 374 WENTSNAEKRIIE-KTQDVTPNKLPLTVYCVKARAHT 410
Db 509 FEKDOETSYTIKSKETFTIAGELKPAASYVVFQIRART 546
```

Search completed: June 1, 2000, 05:53:08

KM Receptor: Transmembrane; Glycoprotein; Signal: Polymorphism;
Phosphorylation.
FT SIGNAL 1 27
FT CHAIN 28 557
FT DOMAIN 28 436
FT TRANSMEM 437 457
FT DOMAIN 458 557
FT DISULFID 79 87
FT DISULFID 199 220
FT MOD_RES 466 466
FT MOD_RES 481 481
FT CARBOHYD 50 50
FT CARBOHYD 58 58
FT CARBOHYD 81 81
FT CARBOHYD 88 88
FT CARBOHYD 110 110
FT CARBOHYD 172 172
FT CARBOHYD 254 254
FT CARBOHYD 313 313
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FT CARBOHYD 376 376
FT CARBOHYD 416 416
FT CARBOHYD 433 433
FT VARIANT 168 168
FT CONFLICT 17 17
FT SEQUENCE 557 AA: 63525 MW: 0F6744C8A1ADB273 CRC64;
/FTID-VAR.002717.
G->A (IN REF.2).
-1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- FUNCTION: RECEPTOR FOR INTERFERON ALPHA AND BETA. BINDING TO TYPE I I FENS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-SUBUNITS THEMSELVES.
-1- CLONING AND CHARACTERIZATION OF A BOVINE ALPHA INTERFERON RECEPTOR.
-1- BLOCHM. BIOPHY. Acta 1173:314-319(1993).
-1- FUNCTION: RECEPTOR FOR INTERFERON ALPHA AND BETA. BINDING TO TYPE I I FENS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-SUBUNITS THEMSELVES.
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- SIMILARITY: CONTRAINS 2 FIBROBLAST TYPE III-LIKE DOMAINS.
-1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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EMBL: X68443; CAA48484.1; -
DR EMBL: 106320; AAO2571.1; -
DR PIR: S33770; S33770.
DR PIR: S27387; S27387.
DR PIR: PF00041; fn3; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 560
FT DOMAIN 25 437
FT TRANSMEM 438 458
FT DOMAIN 459 560
FT DISULFID 76 84
FT DISULFID 199 220
FT CARBOHYD 47 47
FT CARBOHYD 55 55
FT CARBOHYD 85 85
FT CARBOHYD 109 109
FT CARBOHYD 172 172
FT CARBOHYD 254 254
FT CARBOHYD 313 313
FT CARBOHYD 377 377
FT CARBOHYD 434 434
FT CONFLICT 422 422
FT SEQUENCE 560 AA: 63818 MW: 66D76B72861E1D11 CRC64;

Query Match 100.0%; Score 2313; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 4.4e-166;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MMYVLLGATTLVLAAGPWLAAAGGKNIKSPQKVEVDIIDDNFILRNKSDSEVGNT 60
DB 1 MMYVLLGATTLVLAAGPWLAAAGGKNIKSPQKVEVDIIDDNFILRNKSDSEVGNT 60
OY 61 SFSDYQKTGMNDWIKLSGCONITSTKCNFSLKNVYEIKLRRAKENTSSWYEDSF 120
DB 61 SFSDYQKTGMNDWIKLSGCONITSTKCNFSLKNVYEIKLRRAKENTSSWYEDSF 120
OY 121 TPFKRAOIGPPEVLEAEKAIYHISPGTKDSVMALDGLSFYSLLIMKNSGVEERI 180
DB 121 TPFKRAOIGPPEVLEAEKAIYHISPGTKDSVMALDGLSFYSLLIMKNSGVEERI 180
OY 181 ENISRRIKYLSPETTYCLVKAAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240
DB 181 ENISRRIKYLSPETTYCLVKAAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240
OY 241 NONVVLKMDTYANMTFOYOMLHAFILKRNPGNHLKKKQIPDCENVKTTQCVFQNTFOK 300
DB 241 NONVVLKMDTYANMTFOYOMLHAFILKRNPGNHLKKKQIPDCENVKTTQCVFQNTFOK 300
OY 301 GIVLLRVAQSDGNTTSMSEIEIKFDTETIOALFLPPVFNIRSLDSFHIYIGAPKQSGNTP 360
DB 301 GIVLLRVAQSDGNTTSMSEIEIKFDTETIOALFLPPVFNIRSLDSFHIYIGAPKQSGNTP 360
OY 361 VIQDYPLLEYELIIFWENTSNARKIIEKKTDTVTNKLPLIYCYKAAHNTDEKLNSSV 420
DB 361 VIQDYPLLEYELIIFWENTSNARKIIEKKTDTVTNKLPLIYCYKAAHNTDEKLNSSV 420
OY 421 FSDAVCEKTKPGNTSK 436
DB 421 FSDAVCEKTKPGNTSK 436

RESULT 2
INRL_BOVIN STANDARD: PRT: 560 AA.
AC 004790: 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
GN IFNARI OR IFNAR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RX MEDLINE: 93076908.
RA Mouchel-Viehl E., Lutfalla G., Mogensen K.E., Uge G.;
RT "Specific antiviral activities of the human alpha interferons are determined at the level of receptor (IFNAR) structure.";
RL FEBS Lett. 313:255-259(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93305725.
RA Lim J.-K., Langer J.A.;
RT Cloning and characterization of a bovine alpha interferon receptor.";
CC Blochm. Biophys. Acta 1173:314-319(1993).
CC -1- FUNCTION: RECEPTOR FOR INTERFERON ALPHA AND BETA. BINDING TO TYPE I I FENS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-SUBUNITS THEMSELVES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTRAINS 2 FIBROBLAST TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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EMBL: X68443; CAA48484.1; -
DR EMBL: 106320; AAO2571.1; -
DR PIR: S33770; S33770.
DR PIR: S27387; S27387.
DR PIR: PF00041; fn3; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 560
FT DOMAIN 25 437
FT TRANSMEM 438 458
FT DOMAIN 459 560
FT DISULFID 76 84
FT DISULFID 199 220
FT CARBOHYD 47 47
FT CARBOHYD 55 55
FT CARBOHYD 85 85
FT CARBOHYD 109 109
FT CARBOHYD 172 172
FT CARBOHYD 254 254
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FT CARBOHYD 377 377
FT CARBOHYD 434 434
FT CONFLICT 422 422
FT SEQUENCE 560 AA: 63818 MW: 66D76B72861E1D11 CRC64;
Query Match 65.2%; Score 1507; DB 1; Length 560;
Best Local Similarity 64.9%; Pred. No. 1.1e-105;
Matches 285; Conservative 65; Mismatches 83; Indels 6; Gaps 6;

OY 2 MMYVLLGATTLVLAAGPWLAAAGGKNIKSPQKVEVDIIDDNFILRNKSDSEVGNTVF 61
DB 1 MMYVLLGATTLVLAAGPWLAAAGGKNIKSPQKVEVDIIDDNFILRNKSDSEVGNTVF 61
OY 62 SFSDYQKTGMNDWIKLSGCONITSTKCNFSLKNVYEIKLRRAKENTSSWYEDSF 119

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DB 59 SADYQLGTDNMKLLSGCHITSTKCNFSSVELNFEIETIRAEENNSTWYEVP 118
OY 120 FPFRAKQIGPEVHLAEADKAIVIHIS-PGTRDSYMAALDGLSFTYSLILKNSGVEE 178
DB 119 FVPFLAQIGPPDVHLEADKAIIISISPGTRFDSIMAMADSSFRIVYIKNSSLEE 178
OY 179 RIENIYSRRKIYKLSPEITCYLKVAKAALLTSKIGYSPVHCITVENELPPENIEVS 238
DB 179 RRETYVPEDKIYKLSPEITCYLKVAKAALLTSKIGYSPVHCITVENELPPENIEVS 238
OY 239 VONONVYLVKMDYTYANMTQVOMLAFLKRNPNHLYKKKQIPDCENVTTCVPPONVF 298
DB 239 ADNQIYLVKMDYTYANMTQVOMLAFLKRNPNHLYKKKQIPDCENVTTCVPPONVF 298
OY 299 OKGIYLLRQVADGNNTSFWSEIKFDTIOAFLPPVNIISLS-DSFHIYIGAPKQSG 357
DB 299 SNGIYVVRASNGNISTSWSEKEKENTETKIIFPPVYSVSVTDLSLHVSASSEEB 358
OY 358 NTPVYIDYPLIYEIIFWENTSNAERKIEKTDVYVNLKPLTYCVKARAHMDEKLNK 417
DB 358 NNSVQVLYPLIYEIIFWENTSNAERKIEKTDVYVNLKPLTYCVKARAHMDEKLNK 418
OY 418 SSFSDAVCEKTRPGNTSK 436
DB 419 GSSFSDTVCEKTRPGNTSK 437
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RESULT 3
INRL_SHEEP STANDARD: PRT: 560 AA.
AC Q28389; Q95206;
DB 01-NOV-1997 (Rel. 35, Created)
DB 01-NOV-1997 (Rel. 35, Last sequence update)
DB 15-FEB-2000 (Rel. 39, Last annotation update)
DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC)
DE (INTERFERON ALPHA/BETA RECEPTOR-1).
GN IFNARI OR IFNAR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Caprinae; Ovis.
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE-ENDOMETRIUM.
RX MEDLINE: 97135690.
RA Kaluz S., Fisher P.A., Kaluzova M., Sheldrick E.L., Flint A.P.F.:
RT "Structure of an ovine interferon receptor and its expression in
RT endometrium."
RL J. Mol. Endocrinol. 17:207-215(1996).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE-ENDOMETRIUM.
RX MEDLINE: 98006426.
RA Han C.-S., Matulalagan N., Klemann S.W., Roberts R.M.:
RT "Molecular cloning of ovine and bovine type I interferon receptor
RT subunits from uteri, and endometrial expression of messenger
RT ribonucleic acid for ovine receptors during the estrous cycle and
RT pregnancy."
RL Endocrinology 138:4757-4767(1997).
CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
CC I LINS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
CC SUBUNITS THEMSELVES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT
CC CONCEPTUS AT DAY 15 OF PREGNANCY.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: X95978; CA65183.1; -
DR EMBL: U65978; AAB84231.1; -
DR PIR: P00041; fn3; 1.

KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 560

FT DOMAIN 25 437
FT TRANSMEM 438 458
FT DOMAIN 459 560
FT DISULFID 76 84
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FT CARBOHYD 47 47
FT CARBOHYD 55 55
FT CARBOHYD 85 85
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FT CONFLICT 522 522
SQ SEQUENCE 560 AA; 63918 MW; E7198A1905D4805C CRC64;

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SQ SEQUENCE 560 AA; 63918 MW; E7198A1905D4805C CRC64;

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FT CARBOHYD 434 434
FT CONFLICT 522 522
SQ SEQUENCE 560 AA; 63918 MW; E7198A1905D4805C CRC64;

[illegible]

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Db      181 NSTIYVEKPELLPETTYCLEAVKAIHPKLSKHSNSTVGCISPTVANKRPVGNLDQ 240
Qy      241 NONVYLKMWY-ITYANNTEPOVNLHAFLEKKNPNGNHLKMKQIPDCEVKTTCQYPONVQ 299
Db      241 GNSYVLKMWYIASADVLFFAQMPLPGYSKSSSSGSHSDKMRPIPTCANVOTTHCVFSQDTY 300
Qy      300 KGIYLLRVOASDGNMNTSEFSEIEIKFDTETIQATFLPPFNIRSLDSFHIYIGAPKOSGM 359
Db      301 TGTFFLHVQASSGNHNTSEFSEIEIKFIDSKHILPPRPVIVTAMSDLLVYVNCQDSTCD- 360
Qy      360 PVIQDIPLIYEIETIEMNTSNABEKIETKTDVTPNLKPLVYCYKARAHMDEKLNKSS 419
Db      360 -----GLNYEIIIFEMNTSNIKISMEDKDPETFLKMLPFLVYCVQARV-LFRALLNKTS 412
Qy      420 VESDAVCEKTRPGNTS 435
Db      413 NSEKLCETKTRGSPS 428

RESULT 5
CRE4_HUMAN
ID      CRE4_HUMAN          STANDARD:      PRT:      325 AA.
AC      008334:

DT      01-FEB-1995 (Rel. 31, Created)
DT      01-FEB-1995 (Rel. 31, Last sequence update)
DT      01-OCT-1996 (Rel. 34, Last annotation update)
DE      CYTOKINE RECEPTOR CLASS-II CRP2-4 PRECURSOR.
GN      CREB4.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
        Ducteria; Primates; Catarrhini; Homiidae; Homo.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE-FETAL BRAIN;
RX      MEDLINE: 93300510.
RA      Iutafalla G., Gardiner K., Uze G.:
RT      "A new member of the cytokine receptor gene family maps on chromosome
RT      21 at less than 35 kb from IFNAR."
RL      Genomics 16:366-373(1993).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE: 96054036.
RA      Iutafalla G., McInnis M.G., Antonarakis S.E., Uze G.:
RT      "Structure of the human CREB4 gene: comparison with its IFNAR
RT      neighbor."
RL      J. Mol. Evol. 41:338-344(1995).
CC      -1- FUNCTION: IS PROBABLY INVOLVED IN THE INTERFERON SYSTEM.
CC      -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC      -1- SIMILARITY: CONTAINS 2 FIBROBLAST TYPE II-LIKE DOMAINS.
CC      -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC      -----
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CC      entities requires a license agreement (see http://www.isb.ch/announce/
CC      or send an email to license@isb.slb.ch).
CC      -----
DR      EMBL: 211727; CAI8933.1;
DR      EMBL: 008988; AAA86872.1;
DR      PIR: A47003; A47003.
DR      HSSP: P13726; IDAN.
DR      MIM: 123869;
KM      Receptor; Transmembrane; Glycoprotein; Signal.
FT      SIGNAL          1          19
FT      CHAIN           20          325
FT      DOMAIN          20          220
FT      TRANSMEM       221          249
FT      DOMAIN          250          325
FT      DISULFID        66          74
FT      DISULFID        188          209
FT      BY SIMILARITY.

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FT CARBOHYD 49 49 POTENTIAL.
FT CARBOHYD 68 68 POTENTIAL.
FT CHAIN 102 102 POTENTIAL.
FT CARBOHYD 161 161 POTENTIAL.
FT TRANSMEM 124 124 A -> D (IN REF. 2).
FT CONFLICT 269 273 FLGHP -> VGRME (IN REF. 2).
FT CONFLICT 274 325 MISSING (IN REF. 2).
SQ SEQUENCE 325 AA; 37011 MW; 66706C79F8514B23 CRC64;

Query Match 9.9%; Score 228.5; DB 1; Length 325;
Best Local Similarity 29.9%; Pred. No. 3.5e-10;
Matches 67; Conservative 42; Mismatches 96; Indels 19; Gaps 8;

QY 19 WLSAAGCKMLKS-----POKVEVDIIDNFIKRNRSDESGVNTFSFDYOKTGD 71
D 3 WLSGWLGGCLLYSALGVPPENVRMNSVKNILQWESPAFAGNLTFTQY----LS 58
QY 72 NWIKLSGCONITSTKCNSSSLKLNVEEIKLRPAE-KENSSWYEVDSFPPRAQIGP 130
D 59 YRIFODKCMNTLTTECDSS--LSKYGDHTLRVRAEFADHSDMVNI-TFCFVDDTIIGP 115
QY 131 PEVHLEA-EDKAIVIHISPGTKDSV-MMALDGL--SFYSLIKKNSGVEERIENTYS 186
D 116 PEMQVEVLADSLHMFPLAPKLENEYETMKNNVNSWYVKNNGTDEKFOITPQIDF 175
QY 187 HKIYLSPEPTYCLKVKAAALLTSKIGVSPVHCITVENELP 230
D 176 EVLRLEPWTTCVGRGFLPDNRKAGEMSEVPCQTHDETVP 219

RESULT 6
INGS_HUMAN STANDARD: PRT: 337 AA.
AC P38484:
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (INTERFERON-GAMMA RECEPTOR ACCESSORY FACTOR-1) (AF-1) (INTERFERON-GAMMA TRANSUCER-1).
GN IFNGR2 OR IFNGT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP TISSUE=LUNG FIBROBLAST;
RX MEDLINE: 94170380.
RA Son J., Donnelly R.J., Kotenko S., Mariano T.M., Cook J.R., Wang N., Emanuel S.L., Schwartz B., Miki T., Pestka S.;
RT "Identification and sequence of an accessory factor required for activation of the human interferon gamma receptor.";
RL Cell 76:793-802(1994).
CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERFERON GAMMA. REQUIRED FOR SIGNAL TRANSDUCTION. THIS ACCESSORY FACTOR IS AN INTEGRAL PART OF THE IFN-GAMMA SIGNAL TRANSDUCTION PATHWAY AND IS LIKELY TO INTERACT WITH GAF, JAK1, AND/OR JAK2.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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CC EMBL: U05875; AAA16955.1;
CC EMBL: U05877; AAA16956.1;
CC MIM: 1475569;
DR PFM: PF00041; fn3; 1.

KM Receptor: Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 337 INTERFERON-GAMMA RECEPTOR BETA CHAIN.
FT DOMAIN 28 247 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 248 268 POTENTIAL.
FT DOMAIN 269 337 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 56 56 POTENTIAL.
FT CARBOHYD 85 85 POTENTIAL.
FT CARBOHYD 110 110 POTENTIAL.
FT CARBOHYD 137 137 POTENTIAL.
FT CARBOHYD 219 219 POTENTIAL.
FT CARBOHYD 231 231 POTENTIAL.
FT VARIANT 64 64 R -> Q.
SQ SEQUENCE 337 AA; 37834 MW; 18C61B10AD90E509 CRC64;

Query Match 6.7%; Score 155.5; DB 1; Length 337;
Best Local Similarity 22.3%; Pred. No. 0.00011;
Matches 67; Conservative 54; Mismatches 112; Indels 67; Gaps 14;

QY 12 VLVAAGPVLAAAG--KNLSPKVEVDIIDNFIKRNRSDESGVNTFS 62
D 9 LLLILGFAAAAAAPPDPLSQLPAPQPKITLYNAEOVLSWEPYALNSSTFPVYRQFK 68
QY 63 FDYKGTGDMNKLKSGCONITSTKCNSS-----LKNVEEIKLRPAEK 108
D 69 YTDK-----WETADIMSIGVNCQTATATEDFPAASPSAGFPMDFNV---TLRLAEL 119
QY 109 ENT-SSWTEVDSEFPFRQAQIGPPEVHLE--AEDKAIVIHISPGTKDSVMMALDGLSFT 164
D 120 GALHSAMWTMPFQHYRVTVGPPE-NIEVTPGGSILIRPSSPDIAIDISTAR---FC 174
QY 165 YSLIKKNSGVEERIENTYSRHKTY-KLSPEPTYCLKVKAAALLTS--WKIGVSPV 218
D 175 YVYHWE--KGIQVQKGFPSNSISLDNLKPSRYVCLQVQAOLLMKNSIFRRGHSNI 232
QY 219 HCITVENELPPENIEVSV-----QONVYLVKWDYTYANMTPQVO 260
D 223 SCVETMADASTELQOVILISVGFSLSLVLAGCFVLVKYRGILKYVHFTHPPSPIDIE 292

RESULT 7
MYM1_HUMAN STANDARD: PRT: 1451 AA.
AC P52179:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE MYOMESIN 1 (190 KD TITIN-ASSOCIATED PROTEIN) (190 KD CONNECTIN-ASSOCIATED PROTEIN).
GN MYO1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP TISSUE=SKELETAL MUSCLE;
RX MEDLINE: 94095655.
RA Vinkemeier U., Obermann W., Weber K., Fuerst D.O.;
RT "The globular head domain of titin extends into the center of the sarcomeric M band. cDNA cloning, epitope mapping and immunoelection microscopy of two titin-associated proteins.";
RL J. Cell Sci. 106:319-330(1993).
CC -1- FUNCTION: MAJOR COMPONENT OF THE VERTEBRATE MYOFIBRILLAR M BAND. BINDS MYOSIN, TITIN, AND LIGHT MEROMYOSIN. THIS BINDING IS DOSE DEPENDENT.
CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 7 FIBRONECTIN TYPE III-LIKE DOMAINS.
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EMBL: X69090; CAA48833.1; -
 DR MIM: 603508; -
 DR PFAM: PF00041; f03; 5.
 DR PFAM: PF00047; f03; 3.
 DR PRINTS: PR00014; FNTYPEIII.
 KW Immunoglobulin domain; Muscle protein; Thick filament; Repeat.
 FT DOMAIN 46 81
 FT REPEAT 46 81
 FT REPEAT 52 57
 FT REPEAT 58 63
 FT REPEAT 64 69
 FT REPEAT 70 75
 FT REPEAT 76 81
 FT DOMAIN 156 289
 FT DOMAIN 290 384
 FT DOMAIN 385 511
 FT DOMAIN 512 612
 FT DOMAIN 613 711
 FT DOMAIN 712 816
 FT DOMAIN 817 917
 FT DOMAIN 918 1023
 FT DOMAIN 1024 1137
 FT DOMAIN 1138 1239
 FT DOMAIN 1240 1352
 FT DOMAIN 1353 1451
 FT SEQUENCE 1451 AA: 162452 MW: 35293FE6C5FEFFD10 CRC64;

Query Match 5.3%; Score 123.5; DB 1; Length 1451;
 Best Local Similarity 19.8%; Pred. No. 0.19; Indels 121; Gaps 21;
 Matches 91; Conservative 67; Mismatches 181;

QY 43 DNFILMNRNSDSVGN-VTFSEFYOKTGMWIKLSCGCONITSTKCNFSKLNYEEI 100
 DB 388 DVIISMKPADVGGSPILIGFIDKCEVGTDSW-----SCCNTPYKFAFPPT 436
 QY 101 KL-----RIAKEKNTSSW-----YEVDSFTPRKQIGPPEVHLAEDEKAIYHIS 147
 DB 437 GIEGRSYIFRYAVAKMKIGFPRVSEVAALDPAEKARKLSP--LSTLDMTVIVTEE 493
 QY 148 PGKDSVMMALDGLSFT-----YSLILMK-----NSSGVEERIENTYS----- 186
 DB 494 EPESEGIYPPPTDLSTYETATRYVLSMRPPGORGHEGIMYVEKCEAGTENMQRVNTL 553
 QY 186 ----RHKIYKLSPEITTYCLKYKAAALTSKIGVSPVHCIRKTV-----ENELP 230
 DB 554 PKSPFALFDLAEGKSYCFVRRC-----SNSAGVGEPSATETVYVGDKLDIPKAPKII 609
 QY 231 PRENIEVSQNONVYLKMD-----YYANKTFVOYOLHAFKRNPGNHLKYWK 278
 DB 610 PARNDFISV-----VVSWEESDKAKELVYVEANVAGSKWPC--NNNPVKTRHF-- 660
 QY 279 QIPDENVTQOCVPPQNFQKGIYLLRYQASDGNNTSMSEIKFDEIOAFLPP-- 336
 DB 660 ----TCHGLVITGOS-----YIFRRAYNAAGLSYSDSE--AIYVKAIAIAPSPFP 704
 QY 336 --VFNIKLSDSFHYIGAPKOSGNTPTIADYPLIYEI-----FWENTSNAERIIKK 388
 DB 705 CDITCESEFRSDMVLGWMKPPDKGTGAEITGYVNVREIDVGPQKWR--EANNKAVRDE 761
 QY 389 TDVTVPNLKPLTVYCYKAKAHMDEKLKSSVFSDAVCKK 428
 DB 762 A-YKISLNKENNYIOFOVAAMNAGIGADSAVSECFCKEE 800

RESULT 8
 INSR_RAT
 ID INSR_RAT STANDARD; PRT: 1383 AA.

AC P15127; P97681;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE INSULIN RECEPTOR PRECURSOR (EC 2.7.1.12) (IR).
 GN INSR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 90231337.
 RA Goldstein B.J., Dudley A.L.;
 RT "The rat insulin receptor: primary structure and conservation of
 RL tissue-specific alternative messenger RNA splicing.";
 RL Mol. Endocrinol. 4:235-244(1990).
 RN [2]
 RP PARTIAL SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY;
 RA Liu Y., Tam J.M.O.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THIS RECEPTOR BINDS INSULIN AND HAS A TYROSINE-PROTEIN
 CC KINASE ACTIVITY.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
 CC -1- ENZYME REGULATION: AUTOPHOSPHORYLATION ACTIVATES THE KINASE
 CC ACTIVITY.
 CC -1- SUBUNIT: TETRAMER OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE
 CC BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LIGAND-
 CC BINDING DOMAIN, WHILE THE BETA CHAIN CARRY THE KINASE DOMAIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC
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DR EMBL: M29014; AAA41441.1; -
 DR EMBL: AF005776; AAB61414.1; -
 DR EMBL: AF005777; AAB61415.1; -
 DR EMBL: U80633; AAB38746.1; -
 DR EMBL: U80632; AAB38968.1; -
 DR EMBL: U80631; AAB38968.1; JOINED.
 DR EMBL: U80630; AAB38967.1; -
 DR EMBL: U80629; AAB38967.1; JOINED.
 DR PTR: A36080; A36080.
 DR HSPF; P06213; IIRK.
 DR PRINTS: PR00014; FNTYPEIII.
 DR PROSITE: PR00107; TYRKINASE.
 DR PROSITE: PS00109; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PFAM: PF00041; f03; 1.
 DR PFAM: PF00069; pkinase; 1.
 DR PFAM: PF00757; Furin-like; 1.
 DR PFAM: PF01030; Recep_L_domain; 1.
 KW Transmembrane; Tyrosine-protein kinase; Receptor; Transmembrane;
 KW Glycoprotein; ATP-binding; Phosphorylation; Signal; Repeat.
 FT SIGNAL 1 26
 FT CHAIN 27 760
 FT PROPEP 761 763
 FT CHAIN 764 1383
 FT DOMAIN 764 957
 FT TRANSMEM 958 978
 FT DOMAIN 979 1383
 FT DOMAIN 619 848
 FT DOMAIN
 FT FIBRONECTIN TYPE-III.

FT DOMAIN 849 949 FIBRONECTIN TYPE-III.
 FT NP_BIND 1024 1299 PROTEIN KINASE.
 FT BINDING 1030 1038 ATP (BY SIMILARITY).
 FT ACT_SITE 1058 1058 ATP.
 FT MOD_RES 1190 1190 PHOSPHORYLATION (AUTO-).
 FT ACT_SITE 1000 1000 IMPORTANT FOR BIOLOGICAL ACTIVITY.
 FT DISULFID 461 494 BY SIMILARITY.
 FT DISULFID 550 550 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 42 42 POTENTIAL.
 FT CARBOHYD 51 51 POTENTIAL.
 FT CARBOHYD 104 104 POTENTIAL.
 FT CARBOHYD 137 137 POTENTIAL.
 FT CARBOHYD 241 241 POTENTIAL.
 FT CARBOHYD 281 281 POTENTIAL.
 FT CARBOHYD 321 321 POTENTIAL.
 FT CARBOHYD 363 363 POTENTIAL.
 FT CARBOHYD 423 423 POTENTIAL.
 FT CARBOHYD 444 444 POTENTIAL.
 FT CARBOHYD 540 540 POTENTIAL.
 FT CARBOHYD 634 634 POTENTIAL.
 FT CARBOHYD 652 652 POTENTIAL.
 FT CARBOHYD 699 699 POTENTIAL.
 FT CARBOHYD 770 770 POTENTIAL.
 FT CARBOHYD 783 783 POTENTIAL.
 FT CARBOHYD 921 921 POTENTIAL.
 FT CARBOHYD 934 934 POTENTIAL.
 FT CONFLICT 1119 1119 L -> M (IN REF. 2).
 SO SEQUENCE 1383 AA; 156756 MW; 4891956902A944A CRC64;

Query Match 5.1%; Score 119; DB 1; Length 1383;
 Best Local Similarity 19.2%; Pred. No. 0.38;
 Matches 89; Conservative 52; Mismatches 151; Indels 172; Gaps 20;

QY 43 DNFIKMRSDSGVNTFSFYOKTGMDN-----WIKLSGCON 81
 DB 481 NDIAKLTNGDAQSCNELKFSFIRSEKILLRMEPPWPDPFRLGFMFLKAPYON 540
 QY 82 IT-----STKCNFSSIKLNYEIEIKLIRAEKENTSSWVEFTFPRKAQIGPPEVHLEA 137
 DB 541 VTEFGGODAC-----GNSMTYVD-----IDPPQ---RS 566
 QY 138 EDKAIIVHISPTKDSVMWALDGLFTYSLLIMKNSGVEERIEINYSRHKIYKLSPEET 197
 DB 567 NDPKSGTSPHG-----WLMRG-----LKPWTQ 589
 QY 198 YELAKYKALLITSMK---IGVYSPVHCITTVENELPPPENIEVSQONQYVLK---DYT 251
 DB 590 YAIFFKTLVTFSDERTYGAKSDIIVYQDATNPVSVPDIPISVNSSSQIILKMKPPSPDP 649
 QY 252 YANMTFOYQWHLAFLKRNPNGLYKW-KQIPCCENVKTCQVFPQVFGKGYL-----305
 DB 650 NGNIT-----HLYVYWEKQAESELEFELDYCL-----KGLKLSRWS 687
 QY 305 --LRVQASDGNTSFWSSEI-----KEDTEIOAFLPPVENIRSLSDSFHYIGAPKO 355
 DB 688 PFESDDSKQHNQSEYDSDASCCSCPKTDSQILKELESSSR-KTFEEDYLNWVFPVRK 746
 QY 356 --SGN-----TPVIODYPLIYEITFEWNTSNAEKIIEK---388
 DB 747 TSSGGAEDTPSRKRKRSLEEVGNVATATPLTPDEPNISSTI--APTSHHEHRPEFEKYVN 804
 QY 388 KTDVTVPNLKPLTVYCVKRAHTMDKLNKSSVFSDAVCEKTKP 431
 DB 805 KESLVIISGLRHFTGTRIELQACNODSPERSGV-AAVYSARWIP 847

RESULT 9
 INGR_HUMAN STANDARD: PRT: 489 AA.
 AC P15260;
 DT 01-APR-1990 (rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119).
 GN IFNGRL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NC [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 89003065.
 RA Aguet M., Dombic Z., Merlin G.;
 RT "Molecular cloning and expression of the human Interferon-gamma
 RT receptor.";
 RL Cell 55:273-280(1988).
 RN [2]
 RP DISULFIDE BONDS, PARTIAL SEQUENCE, AND MUTAGENESIS.
 RX MEDLINE: 93183911.
 RA Stueder D., Friedlehn A., Pountoulakis M., Lahn H.-W., Garotta G.;
 RT "Alignment of disulfide bonds of the extracellular domain of the
 RT Interferon gamma receptor and investigation of their role in
 RT biological activity.";
 RL Biochemistry 32:2423-2430(1993).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 26-248.
 RX MEDLINE: 95342235.
 RA Walter M.R., Windsor W.T., Nagabhushan T.L., Lundell D.J., Lunn C.A.,
 RA Zaudow P.J., Narula S.K.;
 RT "Crystal structure of a complex between interferon-gamma and its
 RT soluble high-affinity receptor.";
 RL Nature 376:230-235(1995).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 28-122 COMPLEX WITH ANTIBODY.
 RX MEDLINE: 98035727.
 RA Sogabe S., Stuart F., Henke C., Bridges A., Williams G., Birch A.,
 RA Winkler F.K., Robinson J.A.;
 RT "Neutralizing epitopes on the extracellular interferon gamma receptor
 RT (IRNGamma) alpha-chain characterized by homolog scanning mutagenesis
 RT and X-ray crystal structure of the A6 fab-IRNGammaR1-108 complex.";
 RL J. Mol. Biol. 273:882-897(1997).
 CC -1- FUNCTION: RECEPTOR FOR INTERFERON GAMMA. TWO RECEPTORS BIND ONE
 CC INTERFERON-GAMMA DIMER.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- PTM: PHOSPHORYLATED AT SER/THR RESIDUES.
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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 CC
 CC EMBL: J03143; AAAS2731.1; -
 CC PIR: A31555; A31555.
 DR PDB: 1JRH; 25-MAR-98.
 DR MIM: 107470; -
 DR MIM: 209950; -
 KW Receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation;
 KW Immunoglobulin domain; 3D-structure.
 FT SIGNAL 1 17
 FT CHAIN 18 489
 FT DOMAIN 18 245 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.
 FT TRANSMEM 246 266 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 267 489 POTENTIAL.
 FT DISULFID 77 85 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 122 167
 FT DISULFID 195 200
 FT DISULFID 214 235
 FT CARBOHYD 34 34 POTENTIAL.


```

Db 310 GFFVASHSQSCSKRP-----HSTYHEASTSCVCKDFRRESDDPPIACGRP 359
Oy 232 ---DENIEVSQONONYLWK-----DYTANMTFOVOMLHAFIKRNPNGHLKWK 278
Db 360 PSARFANNAISNENETSVFLEWIPADTGCGKDVSYILCKKN-SHAGVCECGGHR--- 416
Oy 279 QIPDCENKTKOCVFPQVFOKGIILLKVAOSDGNNTSFNSEEITFDIEIQAFLLPYFN 338
Db 416 -----XLPQIGLKNTSVKMAADPLAHTNTF-----EIDA---VNG 448
Oy 339 IRSLSDFSHIYG---AKOSGNFPIVQ-----DYP-----LTYEITF 373
Db 449 VSDSPGTRQVYSVAVTNOAAPSPYTVYKKGKIKAKNSISLSMOEPPDNPNGIILEYEIKY 508
Oy 374 WENTSNAERKIE-KRTDVTYPNLKLPTLYCVKARHT 410
Db 509 FEKDETSYTIILKSKETITITAGLKPAVYVQIARHT 546

RESULT 11
ID 110R.MOUSE STANDARD: PRF: 575 AA.
AC 061727:
AD 15-JUL-1998 (Rel. 36, Created)
AD 15-JUL-1998 (Rel. 36, Last sequence update)
AD 15-DEC-1998 (Rel. 37, Last annotation update)
DE INTERLEUKIN-10 RECEPTOR PRECURSOR (IL-10R).
GN IL10RA OR IL10R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6 X AJ F1; TISSUE-HEMATOPOIETIC;
RX MEDLINE: 94068595.
RA Ho A.S.-Y., Liu Y., Khan T.A., Hsu D.-H., Bazan J.F., Moore K.W.;
RT "A receptor for interleukin 10 is related to interferon receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:11267-11271(1993).
CC -1- FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC or send an email to license@isb-sdb.ch).
CC -----
DR EMBL, L12120; AAA16156.1; -.
KW MGD; MGI:96538; IL10RA.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 575 INTERLEUKIN-10 RECEPTOR.
FT DOMAIN 17 241 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 242 262 POTENTIAL.
FT DOMAIN 263 575 CYTOPLASMIC (POTENTIAL).
FT DISULFID 204 225 POTENTIAL.
FT CARBOHYD 50 50 POTENTIAL.
FT CARBOHYD 66 66 POTENTIAL.
FT CARBOHYD 113 113 POTENTIAL.
FT CARBOHYD 182 182 POTENTIAL.
FT CARBOHYD 238 238 POTENTIAL.
SQ SEQUENCE 575 AA: 64248 MW: 820B96CD576F66B7 CRC64;

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Db      9  LVITISLSLEFLIAGTELPSPSYVWEARFQHILMHKKPIPNQSESPYEEVAL----KQY 64
QY      69  GMDNWIKLSCQNTSTKCNFSLSKLNVYEE---IKIRIRA-EKENTSSYEVDS-FTPF 123
Db      65  GNSWMDNIHICRKAQALSCLOTFTLDTLYHSRGYGRARAVANQSOYSNNMTTETRET-- 123
QY      124  RKAQIGPEVHLEEDKAIYIHISPGKSDV-KMALDGLSFYLSLWKSSGVEEHLEN 182
Db      123  -----VDEVIL-----TVDSVTLKAMDGIYGTIHPRPITTPAGDEYEQ 162
QY      183  IYSRHKITYKLS-----DET-----TYCLKVKKALLTSWKIGVSP 217
Db      163  VFKRLRYRKIKISIRKFSSELKNAKTRKVRDEFTLIVPIGVKRFQCVKVLPRLSRIKNAEMSE 222
QY      218  VHCIKTVENELPPENIEVSVONQNVYLKMDTYTANMFOY-----QWL 262
Db      223  EQCLLTTEQY-----FVYTNLSLIVISMLLFCGLVCLVLM-- 261
QY      263  HAFIKRPNGNHLYKKQIDPCENKTKTCQCFPN-----VFQKGYTLR 306
Db      261  --YIRHNG-----KLPTLVYKRRKHDFEPANPLCPETPDAGIHIVDELFVKVSDLR 310
QY      307  VQASDGNNTS-FWSEIKFDEIQAFLRP 334
Db      311  DSVLHGSTDGSGGSKPSLOTESQFLRP 339

RESULT 12
PTPD_HUMAN
ID      1  PTPD_HUMAN      STANDARD;      PRT;      1912 AA.
AC      232468;
DT      01-NOV-1991 (Rel. 20, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      01-NOV-1997 (Rel. 35, Last annotation update)
DE      PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (EC 3.1.3.48) (R-PTP-
DE      DELTA).
GN      PTPRD.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC      Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE; 95204468.
RA      Pulido R., Krueger N.X., Serra-Pages C., Saito H., Streuli M.;
RT      "Molecular characterization of the human transmembrane
RT      protein-tyrosine phosphatase delta. Evidence for tissue-specific
RT      expression of alternative human transmembrane protein-tyrosine
RT      phosphatase delta isoforms."
RL      J. Biol. Chem. 270:6722-6728(1995).
RL      [2]
RP      SEQUENCE OF 390-1912 FROM N.A.
RC      TISSUE-PLACENTA;
RX      MEDLINE; 91006018.
RA      Krueger N.X., Streuli M., Saito H.;
RT      "Structural diversity and evolution of human receptor-like protein
RT      tyrosine phosphatases."
RL      EMBO J. 9:3241-3252(1990).
CC      -1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O =
CC      PROTEIN TYROSINE + ORTHOPHOSPHATE.
CC      -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC      -1- ALTERNATIVE PRODUCTS: DIFFERENT ISOFORMS ARE FOUND IN DIFFERENT
CC      TISSUES DUE TO ALTERNATIVE SPLICING.
CC      -1- PTM: A CLEAVAGE OCCURS THAT SEPARATES THE EXTRACELLULAR DOMAIN
CC      FROM THE TRANSMEMBRANE SEGMENT.
CC      -1- SIMILARITY: EXTRACELLULAR REGION TYPIC OF A CAM FAMILY (3 IG-
CC      LIKE DOMAINS FOLLOWED BY 8 FIBRONECTIN TYPE III-LIKE DOMAINS),
CC      AND A CYTOPLASMIC REGION COMPOSED OF TWO PTPASE DOMAINS.
CC      -----
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CC EMBL: L38929; AAC1749.1; -
DR EMBL: X54133; CAA38068.1; -
DR PIR: S12052; S12052.
DR HSSP: P18052; 1YFO.
DR MIM: 601598; -
DR PRINTS: PRO0014; ENTPPE11.
DR PRINTS: PRO0700; PRTYPHPTASE.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE: PS00056; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
DR PFAM: PF00041; fn3; 8.
DR PFAM: PF00047; 1q; 3.
DR PFAM: PF00102; Y.phosphatase; 2.
DR Hydrolase, Receptor, Glycoprotein, Signal, Transmembrane, Duplication;
KW Immunoglobulin domain; Alternative splicing.
FT SIGNAL 1 20
FT CHAIN 21 1912
FT DOMAIN 21 1265
FT TRANSMEM 1266 1290
FT DOMAIN 1291 1912
FT DOMAIN 23 115
FT DOMAIN 118 225
FT DOMAIN 232 318
FT DOMAIN 320 414
FT DOMAIN 417 513
FT DOMAIN 516 606
FT DOMAIN 609 708
FT DOMAIN 711 822
FT DOMAIN 825 916
FT DOMAIN 918 1017
FT DOMAIN 1020 1137
FT DOMAIN 1137 1618
FT DOMAIN 1619 1912
FT ACT_SITE 1533 1553
FT ACT_SITE 1844 1844
FT SITE 1175 1178
FT CARBOHYD 254 254
FT CARBOHYD 289 289
FT CARBOHYD 724 724
FT CARBOHYD 832 832
FT VARSPLIC 181 189
FT VARSPLIC 226 229
FT VARSPLIC 775 783
FT VARSPLIC 609 1137
FT MUTAGEN 1178 1178
SQ SEQUENCE 1912 AA; 214759 MW; 3AE8CBDC32182E26 CRC64;

Query Match 5.0%; Score 116; DB 1; Length 1912;
Best Local Similarity 21.8%; Pred. No. 0.97; Indels 40; Gaps 11;
Matches 62; Conservative 47; Mismatches 136; Indels 40; Gaps 11;

QY 171 KNSGVEERIENI-YSRHKYRLSPETTYCLVKAKALLTSKMGVSPHYCIKTVEENEL 229
DB 361 KNSSELYKREIDGAVTRYSVAGLSPEYDFRVAVN---NIGRPSSEPLVLTQTSSEA 416
QY 230 P--PENIVSVQNONYVL-KMDYTYANTFOYOMLHAFLKRNPGHLYKKQIPDCENV 286
DB 417 PSSAPPDVQARMLSTTILVQWKEP-EEPDGQIOGQRYVYITMDPOHVNMMK---HNV 471
QY 287 KTKQCFQNFQKGIYLLRVOASDGNNTSFWSEIKFTEIOAFLPVEFNIRLSDSF 346
DB 472 ASDQITITGNLVPOKTYISKVLAFTSIGDPLSSDQVITQGVGQPLNFAAPESETS 531
QY 347 HIYICAKOSGNTPVLYQDPLIYEITWENTSNAERKI-IEKTDVYVNLKPLTVY--- 403
DB 532 ILLSTWPPRS-----DTIANVELYKXDEGEORITIEPGTSYRLQGLKPNLSLYPR 584
QY 403 -----CVKRAHTMDKLNKSSVFSDAVCEKRPKPTS 435

DB 585 LAARSPQIGASTAISAARTQSK--PSAPPDISC--TSPESTS 625

RESULT 13
ID MPSE_CHICK STANDARD; PRT; 1450 AA.
AC 002173;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE M-PROTEIN, STRIATED MUSCLE.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-EMBRYONIC PECTORALIS MUSCLE;
RX MEDLINE; 93015907.
RA Noguchi J., Yanagisawa M., Imamura M., Kasuya Y., Sakurai T.,
RA Tanaka T., Masaki T.;
RT "Complete primary structure and tissue expression of chicken
RT pectoralis M-protein".
RL J. Biol. Chem. 267:20302-20310(1992).
CC -1- FUNCTION: IS A STRUCTURAL CONSTITUENT OF MYOFIBRILLAR M-BAND IN
CC -1- TISSUE SPECIFICITY: IS EXPRESSED IN PECTORALIS AND CARDIAC MUSCLE.
CC -1- DEVELOPMENTAL STAGE: CAN BE DETECTED BY DAY 10-13 IN OVO. THE
CC CONTENT IS GRADUALLY INCREASED THROUGHOUT THE OVO DEVELOPMENT AND
CC REACHED ITS PEAK AFTER HATCHING.
CC -1- SIMILARITY: CONTAINS 7 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC EMBL: D11774; BAA02033.1; -
DR PIR: A44027; A44027.
DR HSSP: P56276; 1TLK.
DR PFAM: PF00041; fn3; 5.
DR PFAM: PF00047; 1q; 3.
DR PRINTS: PRO0014; ENTPPE11.
KW Muscle protein; Repeat; Immunoglobulin domain.
FT DOMAIN 142 238
FT DOMAIN 266 364
FT DOMAIN 368 464
FT DOMAIN 466 592
FT DOMAIN 597 693
FT DOMAIN 696 794
FT DOMAIN 797 898
FT DOMAIN 899 990
FT DOMAIN 1002 1095
FT DOMAIN 1126 1205
FT DOMAIN 1225 1312
FT DOMAIN 1333 1427
SQ SEQUENCE 1450 AA; 163400 MW; E313CD39E6AC7 CRC64;

Query Match 5.0%; Score 115; DB 1; Length 1450;
Best Local Similarity 21.6%; Pred. No. 0.8; Indels 136; Gaps 26;
Matches 92; Conservative 63; Mismatches 134; Indels 136; Gaps 26;

QY 21 LSAAGKNLKSPQKVEV-DIIDNFIKRNSESYGN--VTSPDYOKTGMNWKLS 77
DB 366 LIAGAPG---APMDVCHDANRDYVITWKPPTTSQNPVIGFVQKCEVGLNWMV--- 419
QY 78 GCQNTSTKCNFSSSLKLVNVEIKL-----RIAREKENTSSWYEDSTPPRKAQIG 129
DB 419 -----QCNDAPVKICKIPVTGLYEGRSYIFRVRA-----VNSAGISRPSPRV 460

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OY 130 PPEVHLEMD--KAIVIHISPC-----TKDSYMMALDG-----LSFTYSL 167
DB 461 EFWALDLPDLERTQTQVHDEGRKIYSKDD-----LEGDIQIPGPTNVHASEISKTYV 516
OY 168 LTKN-----SSGVERENIYS-----RKIKYLSSETTYCKLVKA 205
DB 517 LSWDPVPVPRGPRPLTYFEIKSVAGSGSMORVNAOVAKSPRAVVDLAGKRPVFRV--- 574
OY 206 LITSMKIGVSPVHCIKTVENEL---PPENIEVSVOV---ONYVLKMD----- 250
DB 574 -LSAKKHGSDSEITEPIQODIYVVPSPGRVATRTKTSVYQMKPKHEENTLYG 632
OY 250 YTYANNTQVQWLAFLKRNPGNHLKWKQIPDCENVKTQCVFQNVFQKQ-ITYLRYQ 308
DB 633 YIDYSVVGSNOM-----EPANH-----KPI-----NYNR-----FVHGLETGEQYIFRYK 673
OY 309 ASDG---NNTSFMSSEIKFTDEIQAFLEPVPF--NIRSL-DSFHLYIG--APKOSGNP 360
DB 674 AVNAVGFSENSESESAIK---VQALTCPSYPHGITLLNCGHSMTLGMAKPKYSGGSP 729
OY 361 VIODY 365
DB 730 ILGY 734

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RESULT 14

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TYO3_RAT
ID TYO3_RAT STANDARD: PRT: 880 AA.
AC P55146:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN
DE KINASE SKY).
GN TYRO3 OR SKY.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RN RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN:
RX MEDLINE: 96104999.
RA Ohashi K., Honda S., Ichinomiya N., Nakamura T., Mizuno K.;
RT "Molecular cloning and in situ localization in the brain of rat sky
RT receptor tyrosine kinase."
RL J. Biochem. 117:1267-1275(1995).
CC -1- FUNCTION: MAY BE INVOLVED IN CELL ADHESION PROCESSES, PARTICULARLY
CC IN THE CENTRAL NERVOUS SYSTEM.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: ABUNDANT IN THE BRAIN AND LOWER LEVELS IN
CC OTHER TISSUES.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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CC -----
DB EMBL: D37880; BA07119.1; -.
DB HSSP: P11362; IFGI.
DB PROSITE: P500107; PROTEIN_KINASE_ATP; 1.
DB PROSITE: P500109; PROTEIN_KINASE_TYR; 1.
DB PROSITE: P50011; PROTEIN_KINASE_DOM; 1.
DB PFAM: PF00041; fn3; 2.
DB PFAM: PF00047; fn2; 2.
DB PFAM: PF00069; pkinase; 1.

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KW Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;
KW Transferase; Phosphorylation; Transmembrane; Signal; Repeat;
KW Immunoglobulin domain.
FT SIGNAL 1
FT CHAIN 31
FT DOMAIN 31
FT TRANSMEM 420
FT DOMAIN 441
FT DOMAIN 441
FT DOMAIN 131
FT DOMAIN 131
FT DOMAIN 214
FT DOMAIN 305
FT DOMAIN 305
FT NP_BIND 514
FT BINDING 540
FT ACT_SITE 645
FT MOD_RES 676
FT CARBOHYD 53
FT CARBOHYD 75
FT CARBOHYD 181
FT CARBOHYD 220
FT CARBOHYD 230
FT CARBOHYD 283
FT CARBOHYD 356
FT CARBOHYD 370
SQ SEQUENCE 880 AA; 95918 MW; C3751E86A85FA5B CRC64;

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Query Match 4.9%; Score 113.5; DB 1; Length 880;
 Best Local Similarity 22.3%; Pred. No. 0.54; Indels 91; Gaps 17;
 Matches 79; Conservative 53; Mismatches 132;

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OY 3 VLLGATLLVYAVGPWVLSAAGKLNKSPQK-----EVDIIDNFIKRW 50
DB 15 LLLAASLLLPG-----SAAAGLKMGAIPKVMVSGQPKVLCNSVEGMDPDI-HM 67
OY 51 RSDSEVGN---VTSEFDYQKGMNWKLSGQNTSTKCNFSSKLNVYEIKIRIAE 107
DB 68 KDGAIVQNAOSVSISSBQ-----NMIGLLSIKSAERSDAGLYWCQVKGDETKI- 118
OY 108 KENTSMWEVDS---FTFPRKAQIGPPEVHLEAEKKAIVIHISPTKSNVM-ALD 159
DB 118 --SQSVWLTVESVPFTPEPDLAIVPVPOLSCA---VGPEPVYITFMKGPITYG 171
OY 160 GLSEFYLLIMKNSGVEREINYSRKIKYKLSPEYTYCKLVKALITSMKIGVSPVH 219
DB 172 GRASSPSVL---NTGVAQRTFEFSCSEAHNINGLARSRAIRLQA----- 214
OY 220 CIKTTVENELDP--PENIEV-SVONQNYVLK---DYTYANMTQVOMLAFLKRNPGN 272
DB 214 -----PPAEPFNITVTITSSNSASVAVMPGADLALLHSCTYGVANA-----PG- 258
OY 273 HLYKKQIPDCENVKTQCVFQNVFQKGIYLLRYQASDGNNTSWSSEIKFTDE 327
DB 258 ---EWEALAVVVPVPPFTCLL-RNLAPATNLSLRVCANALGPSYGDWVPQTK 308

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RESULT 15

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DCC_MOUSE
ID DCC_MOUSE STANDARD: PRT: 1447 AA.
AC P70211:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR.
GN DCC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RN RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-BRAIN;
RX MEDLINE: 96112625.

```

RA Cooper H.M., Armes P., Britto J., Gad J., Wilks A.F.;
 RT Cloning of the mouse homologue of the deleted in colorectal cancer
 RL gene (MCC) and its expression in the developing mouse embryo.";
 RN Oncogene 11:2243-2254(1995).
 RP REVISIONS.
 RC STRAIN-BALB/C; TISSUE-BRAIN;
 RA Cooper H.M.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: IMPLICATED AS A TUMOR SUPPRESSOR GENE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: TWO FORMS OF THE PROTEIN ARE PRODUCED FROM
 CC THE SAME GENE BY THE USE OF ALTERNATIVE INITIATION SITES. A THIRD
 CC FORM WHICH IS EXPRESSED ONLY IN THE EMBRYO IS PRODUCED BY
 CC ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: IN THE EMBRYO, EXPRESSED AT HIGH LEVELS IN THE
 CC DEVELOPING BRAIN AND NEURAL TUBE. IN ADULT, HIGHLY EXPRESSED IN
 CC BRAIN WITH VERY LOW LEVELS FOUND IN TESTIS, HEART AND THYMUS.
 CC -1- DEVELOPMENTAL STAGE: LOW LEVELS IN EARLY GESTATION. HIGHEST LEVELS
 CC EXPRESSED DURING MID GESTATION. LEVELS DECREASE IN LATE GESTATION
 CC AND REMAIN AT THIS LEVEL IN THE ADULT.
 CC -1- SIMILARITY: CONTAINS 4 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 6 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC
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 CC
 DR EMBL: X85788; CAA59786.1; -
 DR HSSP: P56276; ITLK.
 DR MGD: MGI:94869; DCC.
 DR PRAM: PF00047; fn3.6.
 DR PRAM: PF00047; 19.4.
 DR PRINTS: PR00014; FNTYPEIII.
 KW Glycoprotein; Immunoglobulin domain; Transmembrane; Signal;
 KW Anti-oncogene; Alternative Initiation; Alternative splicing.
 FT SIGNAL 1 25
 FT CHAIN 26 1447
 FT CHAIN 85 1447
 FT DOMAIN 26 1097
 FT TRANSMEM 1098 1122
 FT DOMAIN 1123 1447
 FT DOMAIN 54 124
 FT DOMAIN 154 219
 FT DOMAIN 254 317
 FT DOMAIN 345 407
 FT DOMAIN 426 522
 FT DOMAIN 525 618
 FT DOMAIN 619 716
 FT DOMAIN 722 816
 FT DOMAIN 840 940
 FT DOMAIN 941 1042
 FT DISULFID 61 117
 FT DISULFID 161 212
 FT DISULFID 261 310
 FT DISULFID 352 400
 FT CARBOHYD 60 60
 FT CARBOHYD 94 94
 FT CARBOHYD 299 299
 FT CARBOHYD 318 318
 FT CARBOHYD 478 478
 FT CARBOHYD 628 628
 FT CARBOHYD 702 702
 FT VARSPLIC 819 838
 SO SEQUENCE 1447 AA; 158298 MW; 0D1F1097C22D5B9F CRC64;

Query Match 4.8%; Score 111.5; DB 1; Length 1447;
 Best Local Similarity 21.4%; Pred. No. 1.5;

Matches 106; Conservative 63; Mismatches 174; Indels 153; Gaps 29;
 QY 32 SPQKVVVDIIDNFI-LRNRNRSDESGNV-TSPFYQKGMNWKLSGCCQNTITSKNF 89
 DB 431 APRDVLPIVSSREYVLSRRPPEAKGNIGTTFVPSREGDNRERALNTOP----- 483
 QY 90 SSLKL---NVEEIKLRIRAEKENTSSWEVDSFTPFKRA-----QIGPEVHLAEADKA 141
 DB 483 GSIQLVGNLKRKEAMTFEYVAVN--EMGPGSSQPIKVAQPELOVPGPVENLHA---- 537
 QY 142 YIHISPGKDSVMAA---LDGLSTYSLLIMKSSGVEEIEINYSRHKTYKLSPEPT 197
 DB 537 --VSTSP-TSIIITPEPPAYANGPVQGYRLFCTEYSTGKEQNIIEVDGLSKLEGKETE 593
 QY 198 YCLKVAALLTSMKIGVSPVHCITVTVENELPPENIEVSQN-----Q 242
 DB 594 YIIRFLA--YNRGCGVSTIDITVTLSDVPAPPNISLEVVNSRSIKVSLPPSGTQ 651
 QY 243 N---YVLK-----WDYTYANN-----TFQV-----QW 261
 DB 652 NGFITGKIRHKKTRRGEMETLEPNNLN-YLTGLEKSGQSPQVSAATVNGTGPSPW 710
 QY 262 LNAFLKRNQNLKWKQIPDCEV---KTQCVPPO-----NFKGIYLLRQAS 310
 DB 711 ---YTAETPNDLDE-SQVPDQPSLHVRPQTCIIMSTPPLNPNIVRG-YIIGYGVG 765
 QY 311 DGNNSFWSEELKPFDEIQAFLPPVFNRSLSDSFHII-----GAP-KQSGT 359
 DB 766 ----SPIAEYRVDSKQ-----YSTERLESSHYISLKAENNGEGVPLYESATT 814
 QY 360 PYIOD-----YPLYEIIEMWNTSMAEKIIEKTDVTPNLPPLFYCV-----XAR 407
 DB 815 RSITDPTDVPDYPPILDDF---PTSG-----PDVSTMLPDPVGOVALHENV 861
 QY 408 AHFMDEKLKSSVFS 423
 DB 862 VSMADNSVPKQKTS 877

Search completed: June 1, 2000, 10:24:04
 Job time: 20622 sec

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OY 238 SVONQNVYVKMDYTY-ANMFOYQWLHAFKRNPGNHLKWKQIIPDCENKTKTQC----- 292
DB 246 FALNMKFYLLMDNHNHEHYTYTYOYLTKNLIDYSSKWKQVSCENTSKMNLSSV 305
OY 292 VEPONVFOKGIYLLRVOASDGNNTSFMSEIKFDEIOAFLLPVPNINSLSSPFIYIG 351
DB 306 IKRTS---ASYFRVOQANNEYSKSLSDKVEYDPVTEIGPDPVKVDSVLYLHKIT 361
OY 352 APRQSGNTFVIDIPLYEIIEMFMENTSNAERKIEKTD---VTVPNLKPLVYCVKARA 408
DB 362 PPGGPKNKIMSIDLYDFSYOILYWKNSDNEEYKMKETKOTIATVSDLAPOSTLYCVKVOA 421
OY 409 HTMDEKLKSSVSDAVCEKTRPG 432
DB 422 ---FSEAYNKSSDFSPREECIGTAGG 443

RESULT 2
061190 PRELIMINARY: PRT: 349 AA.
AC 061190:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE CYTOKINE RECEPTOR FAMILY 2, MEMBER 4 (CLASS II CYTOKINE RECEPTOR 4).
GN IL10RB OR CRF4 OR CRF2-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97199375.
RA GIBBS V.C., PENNICA D.;
RT "CR2-4: Isolation of cDNA clones encoding the human and mouse
RT proteins."
RL Gene 186:97-101(1997).
DR EMBL: U53696; AAC53062.1;
DR MGD: MGI:109380; Il10rb.
DR PFAM: PF00041; fn3; 1.07654;
SQ SEQUENCE 349 AA; 39774 MW; 4AC1802A CRC32;

Query Match 9.6%; Score 222.5; DB 11; Length 349;
Best Local Similarity 26.2%; Pred. No. 3.9e-10;
Matches 56; Conservative 47; Mismatches 82; Indels 29; Gaps 9;

OY 229 LPPENIEVSVONQNVYVKMD---YTYANMFOVQWLHAFKRNPGNHLKWKQIIPD-CE 284
DB 21 IPPPEKVRMNSVFNKNILOMEVPAFPKTNLTFTAQY-----ESYRSFQDHCK 67
OY 285 NVKTTQCVFPONVFOKGIYLLRVOASDGNNTSFMSEIKFDEIOAFLLPVPNINSLSD 344
DB 68 RTASTQCDP-SHLSKYGDTVRRAELADEHSEM-VNVTFCPEYEDTIIISPENQIESLAE 125
OY 345 SFHIYICAPKQSGNTFVIDIPLYE-----IIFMENTSNAERKIEKTDVTPNLKPL 399
DB 126 SLHLRSAP-QIENEPEETMLKNIYOSMAVRYQWKNGINEKQVSPIDSEVLRNLEPM 184
OY 400 TYVCVARRAHTMDEKLKSSVSDAVCEKTRPGN 433
DB 185 TTYCIOVOGFLDDQ--NRIGEMSEPICERT--GN 214

RESULT 3
063953 PRELIMINARY: PRT: 332 AA.
AC 063953:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE INTERFERON GAMMA RECEPTOR 2 (INTERFERON GAMMA RECEPTOR BETA SUBUNIT).
GN IFNGR2.

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94170381.
RA HEMMI S., BOINI R., STARK G., DI MARCO F., AGUET M.;
RT "A novel member of the interferon receptor family complements
RT functionality of the murine interferon gamma receptor in human
RT cells."
RL Cell 76:803-810(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-128SV/J;
RX MEDLINE: 97128072.
RA EBENSPERGER C., RHEE S., MUTHUKUMARAN G., LEMBO D., DONNELLY R.,
RA PESTKA S., DEMBIC Z.;
RT "Genomic organization and promoter analysis of the gene Ifng2
RT encoding the second chain of the mouse interferon-gamma receptor."
RL Scand. J. Immunol. 44:599-606(1996).
DR EMBL: U69599; AAC52938.1; JOINED.
DR EMBL: U69594; AAC52938.1; JOINED.
DR EMBL: U69595; AAC52938.1; JOINED.
DR EMBL: U69596; AAC52938.1; JOINED.
DR EMBL: U69597; AAC52938.1; JOINED.
DR EMBL: U69598; AAC52938.1; JOINED.
DR EMBL: S69386; AAB30165.1;
DR MGD: MGI:107654; Ifng2.
DR PFAM: PF00041; fn3; 1.
SQ SEQUENCE 332 AA; 37471 MW; 0BF24E9E CRC32;

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Query Match 8.8%; Score 203; DB 11; Length 332;
Best Local Similarity 30.1%; Pred. No. 1.3e-08;
Matches 69; Conservative 38; Mismatches 86; Indels 36; Gaps 13;

OY 21 ISAAGC---KNLSPQKVEVDIDNFIIRMNNSDES-----VGNVTFSPDYQKTM 70
DB 16 LGAAASPDSPSQALAPNPRHLNDBOILTWEPSPSNDPRPVYGVESF-----I 69
OY 71 D-NWIKL--SGQNTITSKCNFS--LKLNYE-EIKLRIRAKEN-TSSWYEDSFT 122
DB 70 DGSWRLLEPNCTDITTEKCDLTGGRLKLPHPPTVFLVRARAKGNLTSKWVGLEPRQ 129
OY 123 FKKADIGPPE-VHLEADKAIYIHISPTKSYMALDGLSTYLLYWKSSGVEEIE 181
DB 130 YENVTVGPPKNISVPPGSLVIFHSPDPD-----VFHGATFOYLVIHWKSESTQOEVE 184
OY 182 NIYSRHKTY--KLSPETTYCLAKVKAL-LTGWKI---GVSPVHCIKTT 224
DB 185 GPKFNSIYLGNLKRYRYCLOTETQOLILKKKIRPHOLLSNVSCHETT 233

RESULT 4
09YGC8 PRELIMINARY: PRT: 341 AA.
AC 09YGC8:
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE INTERLEUKIN-10 RECEPTOR 2.
GN IL10R2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RA REBOUL J., GARDINER K., MONNERON D., UZE G., LUTFALLA G.;
RT "Comparative genomic analysis of the interferon/interleukin-10
RT receptor gene cluster."
RL Genome Res. 0:0-0(1999).
DR EMBL: AF082667; AAD13678.1;
DR EMBL: AF082666; AAD13671.1;

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DB 346 APSSDTSFVGHSTSSDSSSWSONPDGPEVFE-----ENEMDAFE---EKDTS 398
QY 392 TYPNKKPLT---VYCVKARAH 409
DB 399 EL--LSPLSKVNCTYSLRSRSN 418
RESULT 7
P97798
ID P97798 PRELIMINARY; PRT; 1493 AA.
AC P97798;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-NOV-1997 (TREMBLrel. 03, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE NEOGENIN (NEOGENIN PROTEIN).
GN NEOL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RP [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97407661.
RA "KEELING S.L., GAD J.M., COOPER H.M.;
RT "Mouse Neogenin, a DCC-like molecule, has four splice variants and is
RT expressed widely in the adult mouse and during embryogenesis.";
RL Oncogene 15:691-700(1997).
DR EMBL; 109535; CAA70727.1; .
DR HSSP; P02751; 1TTG.
DR MGD; MGI:1097159; Neol.
DR PFAM; PF00041; fn3; 6.
DR PFAM; PF00047; fn3; 4.
DR PRINTS; PR00014; FNTYPEIIT.
SQ SEQUENCE 1493 AA; 163159 MW; 98F26676 CRC32;

Query Match 5.6%; Score 130; DB 11; Length 1493;
Best Local Similarity 21.4%; Pred. No. 0.063;
Matches 89; Conservative 75; Mismatches 191; Indels 60; Gaps 20;

QY 21 LSAAGGKNIKSPQKVEVDIIDNFI-LRWN--RSDESGVNTFSFDYQKGMNLIKLS 77
DB 461 LAPATGPLPSAPRDVVASISVTRFIKLTWRTPASDPHGNDLTVSVFYTKEGVDR----E 516
QY 78 GCONITS-----TKCNFSLKLVYVEIKRIRAKENNTSSWYEDSTPFKKAIGCP 131
DB 517 RVENISQPGEMOYTIONLMPATYIF-----KVMAQNKHGSG---ESSAPLKEVT--OP 565
QY 132 EHVLEAEDRAIVHISPGTKDSVMAL-----DGLSFTYSLILWKNSSGVEERIENTYSRH 187
DB 566 EVQOLPPAPANIRAYATSPISITYTWETPLSGNGEIONKLYKEKTDKEDIDIVSSHSY 625
QY 188 KTYKLSPEYTYCLKVKAAALTSKIGVSPVHCITTVENELPPENIEVSON-QNYVL 246
DB 626 TINGLKRYTEYSERVYA--YKNHGPSTQDVAVRFLSDVPSAQNLSLEVRNKSIIYI 683
QY 247 KM---DYTYAN--MTFOVOMLHAFKRNPNHLYKKKQIIPDCENKTKTQCVPQVAFK 300
DB 684 HMOPTSTQNGOITGKIRYKRSKSDVTELTGTOL-----SGLI--EGLDGG 733
QY 301 GIYLLRQASDGNNT---SFWSEELKFDTEIOAFLLPV---FNIRLSDSFHIYIGAPK 354
DB 734 TENENFVALIYNGTGPALDWLSAEFEESDLDETRIVEPSSLHVAPLVTSI--VYSWTP 792
QY 355 QSGNTPVADYPLIYIETIEMWNTSNAER-KIEKKTQDVTPNKLPLTYCVKARA 408
DB 793 EMONI--VVRGVAIGYI-----GSPHAQTIKVDYKQRYTIENLDPESHVITILKA 842

RESULT 8
ID 094537 PRELIMINARY; PRT; 1375 AA.
AC 094537;

DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE FRAZZLED.
GN FRAZZLED.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RP [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97015076.
RA KOLODZIEJ P.A., TIMPE L., MITCHELL K.J., GOODMAN C.S., FRIED S.,
RA JAN L.Y., JAN Y.N.;
RT "Frazzled encodes a Drosophila member of the DCC immunoglobulin
RT subfamily and is required for CNS and motor axon guidance.";
RL Cell 87:197-204(1996).
DR EMBL; U71001; AAC47314.1; .
DR FLYBASE; FBgn0011592; fra.
DR PFAM; PF00047; fn3; 6.
DR PFAM; PF00047; fn3; 6.
DR PRINTS; PR00014; FNTYPEIIT.
SQ SEQUENCE 1375 AA; 151692 MW; 43806DBC CRC32;

Query Match 5.6%; Score 129; DB 5; Length 1375;
Best Local Similarity 16.4%; Pred. No. 0.068;
Matches 102; Conservative 68; Mismatches 184; Indels 268; Gaps 22;

QY 26 GGNKLS-----POKVEVDIIDNFI-LRW-----NRSDSV 56
DB 447 GKKPLDSGLQARLPSPQPDVLAQIKSRFVLSWEPQONAGDVYIYVYKMNSEREQ 506
QY 57 GNWTFSDYQKGMNLIKSGCONITSTKCNFSS-----LKNVYEIKLR----- 104
DB 507 KWTYKSHDDQVNIQSLPGRTRYQFRVYANNTFGSAGSABLEVSTOEVNIAQPRNFE 566
QY 104 --IRKENITSSWY-----Y 117
DB 567 GYARSHKEIYVKEEPTVYNGEILKRYVYENDSGADLYDSTALEAVLTLPHPHYV 626
QY 118 DSFTPFRAQIG-----PPEVHLE-AEDKATYVHISPGTKDSVMAL 158
DB 627 ISVVPFNNGMGDSAEIRVKTFSSTPSEPPNNNTLVETSSSITVHPEPAEDRNGOI 686
QY 159 DGLSTYSLILWKNSSGVEERIENTYSRHKYKLSPEYTYCLKVKALL-----TSWKI 212
DB 687 TGYKIRYRK--FKDAPQVSTPANI-RYFELSNDRNAEYQVKIAAMVNGSGPTEWNR 743
QY 213 GYSPVHCITTVENELP-----PPENIEVSONQNYVLK 247
DB 744 A-----NTLENDLDETQVPGKPIWISHPGANNIALHMGPPHPEIKI--RNYVLG 792
QY 248 W-----DY----- 251
DB 793 MGRGIPDENTIELEKTERHYHLINKLESMDVYSLARNVAGDPPITYDNKTRDEEYD 852
QY 251 -----TYANMFOVOMLHAFKRN-----PGNHLKKWQIP 281
DB 853 APTPLEVPGRLATIMSSSIIVYVWIDMLKNKHVTDNRHYTVSYGIGTSNRRYR---- 909
QY 282 DCENKTKTQCVPQVAFKQIYLLRQASDGNNTSFWSEELKFDTEIOAFLLPVFNIRS 341
DB 909 --HNTDLNCMI--NDLRNTQYEFRAVYVKGRRSSMSVLSNITYONVPTPP----- 960
QY 342 LSDSEHIYIGAPKQSGNTPVADY-----LIYEIEMWNTSNAER-----KIEKK 388
DB 960 ----REVTVRLDENMNPPIYIQWIPKHTLGQITGINIYITDTTKKDRDMSVAFAGEE 1015
QY 389 TDVTPNKLPLTYCVKARAHT 410
DB 1016 TMLMLPNLKPYYTYFVKVQART 1037

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RESULT 9
ID Q94538 PRELIMINARY; PRT; 1526 AA.
AC Q94538;
DT 01-FEB-1997 (Tremblrel. 02, Created)
DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE FRAZZLED.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Preygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97015076.
RA KOLODIEJ P.A., TIMPE L., MITCHELL K.J., GOODMAN C.S., FRIED S.,
RA JAN L.Y., JAN Y.N.;
RT "Irazzled encodes a Drosophila member of the DCC immunoglobulin
RT subfamily and is required for CNS and motor axon guidance."
RL Cell 87:197-204(1996).
DR EMBL; U71002; AAC47315.1;
DR FLYBASE; FBgn0011592; fra.
DR PRAM; PF00047; fn3; 6.
DR PRAM; PF00047; 19; 3.
DR PRINTS; PR00014; FNTYPEIII.
SQ SEQUENCE 1526 AA; 168787 MW; F17B1EC9 CRC32;

Query Match 5.68; Score 129; DB 5; Length 1526;
Best Local Similarity 16.48; Pred. No. 0.078;
Matches 102; Conservative 68; Mismatches 184; Indels 268; Gaps 22;

OY 26 GGNKLS-----POKVEVDIDNFI-LRW-----NRSDESV 56
DB 598 GGRPLDSGLQARLPSPQPDVLAQIYKSRFVILSWEPLOMGDVYVYVKMNSEREQ 657
OY 57 GNVTFSFDYOKTGMNWKILSGCONITSTKCNFS-----LKLNYEIKIR----- 104
DB 658 KMTKSHDDQVNIQISLLPGRTYQPRVEANTNFGSGASAPLEVSTOPEVINAGPPRNE 717
OY 104 --IRAEKENTSSWE-----Y 117
DB 718 GYARSHKEIYKWEPEPTVNGEILKYRYYSSENDGADLYHDSALAEVLELRPHDYV 777
OY 118 DSFTFERRAQLG-----PEVHLE-AEDKAIYIHLSPGTRKDSVMAL 158
DB 778 ISVVFNRNGMGDSAEIRVKTFSSTPSEPNNVTLLEVTSSTIVHMEPRAEEDRNGOI 837
OY 159 DGLSFTYSLILWKNSSGVEERIENTYSRHKIYKLSPETTYCLKVRAAL-----TSWKI 212
DB 838 TGYKLRIRYK--FKDAPOVXSTPANI-RYFELSLNDRNAEYQVIAAMTVNGSGPTEWNR 894
OY 213 GYTSYVHCKTIVENELP-----PENIEVSQNONVYK 247
DB 895 A-----NTLENDLETOVGRKPIWISHPGANNIALHWGPOHPHPIKI--RNYVLG 943
OY 248 W-----DY----- 251
DB 944 WGRGIPDENTIELKETERYHILKLNESNNDYVYSLARNVKGDGPPIYINIKTRDEEVD 1003
OY 251 -----TYANNTFOVOMLHAFLEKRN-----PGNHLKWKQIP 281
DB 1004 APTPLEVPYGLRAITFMSSSIYVYWDITMLNKNQHVTDNRHYTVSYGIGSRNRYR---- 1060
OY 282 DCENKTKTCVFPONVFOGCIYLLRYQASDGNNTSFWSSEIKFDFEIQAFLLPVPFNIS 341
DB 1060 --HNTDLCMT--NDLRPTQYEFAYKVKYGRRESSMSKSVNSTQONVPVTP----- 1111
OY 342 LSDSFIIYIGADPKOSGNTPVIOYP-----LIYEIIFMENTSNAER-----KIIKK 388
DB 1111 ----REVYRLDEMPPIYIVQWIPKHLGQITGYNITYTDTTRDRDMVSVEAFAGEE 1166
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OY 389 TDVTPRLKPLRYCYKARAH 410
DB 1167 TMLLPLKPLRYCYKARAH 1188

RESULT 10
ID Q90610 PRELIMINARY; PRT; 1443 AA.
AC Q90610;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE NEOGENIN (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-WHITE LEGHORN; TISSUE-BRAIN;
RX MEDLINE; 95105243.
RA VIELMEYER J., ROMAN J.M., DREYER W.J.;
RT "Neogenin, an avian cell surface protein expressed during terminal
RT neuronal differentiation, is closely related to the human tumor
RT suppressor molecule deleted in colorectal cancer."
RL J. Cell Biol. 127:2009-2020(1994).
DR EMBL; U07644; AAC59662.1;
DR HSSP; P80362; 1WTL.
DR PRAM; PF00041; fn3; 6.
DR PRAM; PF00047; 19; 4.
DR NON_TER 1
SQ SEQUENCE 1443 AA; 158050 MW; 270B77DC CRC32;

Query Match 5.58; Score 127.5; DB 13; Length 1443;
Best Local Similarity 22.28; Pred. No. 0.095;
Matches 92; Conservative 61; Mismatches 201; Indels 61; Gaps 19;

OY 21 LSAAGKKNLSPKVEVDIIDNFI-LRWNR--SDSEVGNVTFSFDYOKTGMNWKILS 77
DB 416 LAPATTGGLPAPDVAVATLVSTFRILRTWTPVSDPOGDVLTISITFTEG-----INRE 471
OY 78 GCONITSTKCNFSILKNVYEIKLRIRAEKENTSSWYEVDSFTFERRAQLGPEVHLEA 137
DB 472 RVEN-TSRPGTQVMIQNLMPETVYFRVYAQNKHGCE--SNAPLAVAT--QREVQLPG 526
OY 194 PETTYCLKVRAALLSMKIGYSYVHCITVENELPPEPIEVSQON-QNYVLKMDYTY 252
DB 587 KYTESFPRVVA--YKNHQPVSITODVYVRLSDVPSAAPQWLTLFARSKSIMLHWOPPP 644
OY 253 ANMTFOVOMLHAFLEKRNPNL-----YKWKQIPDCENVKTQCVFPONVFO--KGI-- 303
DB 645 A-----GTHSGQITGKIKIRKYSKSDVTESVGGQLFOLLBLELGG 687
OY 303 --YLLRQASDGNNT--SFWSSEIKFDFEIQAFLLPV--FNIRSLDSFHIYIGAPK 354
DB 688 TEYNRIAMVNGSPATDVAETFSDESRSRVPVPSLHVRLPVTSI--VVSWTPP 746
OY 355 QSGNTPVIOYDPLIYEIIFMENTSNAER-KIIKKTDVTVNKLPLATYCYKARA 408
DB 747 ENONI--VVRGYAIGYGI--GSPRAQIKVYKORYTITENLDPSHYYITLKA 796

RESULT 11
ID Q98949 PRELIMINARY; PRT; 873 AA.
AC Q98949;
DT 01-FEB-1997 (Tremblrel. 02, Created)
DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)
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DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
 DE AXL-RELATED RECEPTOR TYROSINE KINASE.
 GN REX.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
 CC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97067156.
 RA BISCARDI J.S., DENHEZ F., BUEHLER G.F., CHESNUT D.A., BARAGONA S.C.,
 O'BRYAN J.P., DER C.J., FIORALISI J.J., FUTIS D.W., MANESS P.F.;
 RT 'Re', a gene expressed in retina and brain, encodes a receptor
 RT tyrosine kinase of the Axl/Tyro3 family.*;
 RL J. Biol. Chem. 271:29049-29059(1996).
 DR EMBL: U70045; AAC60041.1; f3; 4.
 DR HSSP: P00041; f3; 2.
 DR PROSITE: P50107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: P80109; PROTEIN_KINASE_TYR; 1.
 DR PFAM: PF00041; f3; 2.
 DR PFAM: PF00069; pkinase; 1.
 DR SEQUENCE 873 AA: 96402 MW: 2918550 CRC32:

Query Match 5.3%; Score 123; DB 13; Length 873;
 Best Local Similarity 22.5%; Pred. No. 0.11;
 Matches 102; Conservative 58; Mismatches 151; Indels 142; Gaps 25;

OY 13 LVAVGPWVL-----SAAAGKMLKSPQKVEY-----DIIDNFIILNRNSDES 55
 DB 12 LLLLLMAALRDGAVAAAMKFTGSIKLKVSOGQPVKNCISLEMEDEPL-WIKD-- 68
 OY 56 VGNVTFSPD--YOKTGMNDWIKLSCGQNTSTKCNFSKLNVYEIKRIAEKENTSS 113
 DB 68 -GAVQVSDQVYIIPVDEDMW-----GFLSLK-----SVERIDS 100
 OY 114 ---WEVDSFTPFRAQ-----IGPPEVHLEAEDEKAIYIHISPTKDSVMALDGLSFT 164
 DB 101 GKWCQVENGKKEESQWLVIEGVPTVEPED---VSVPNAPFHMCAAAVGPPEP 156
 OY 165 YELLWK-----NSSGVERIENTISRAKITYLSEPTTYCLKVKAALLTS 209
 DB 157 VTIWMGDSRVGLPDISPISILNVSGINOSTFSCAHNVKGLSSSRATVQIKAMPL-- 215
 OY 210 WKIGYSPVHCIKITVENELPPENIEVSQONQVYVLMKDYAMTQVQWLAHFLKRN 269
 DB 215 -----PPLNVTVS-----QVTSNNS--VWVWPGFDGRA 241
 OY 270 P-GNHLVYMKQIPDCENKTKTQCVFPONVFQGI-----YLLRVOASDGNNTSPWSE 320
 DB 242 PLHSCTLVAAESPDCQEVSTE--VAPVPFAVYGGLKHSYVSVYVOCNSNMSSPTE 299
 OY 321 EIKETELQAFLLPVPFNIRSDSFHYIGAP-----KQSGTTP-VIDYPIITYIITW- 375
 DB 300 RYVF---QTELEAP-----SSTPONIHVIQRPGLVLEMEGAVPDLKENVLGR-LEMI 350
 OY 375 -ENTSNAERKITEKTDVTPN-LKPLTV-YCV 404
 DB 351 QDNVTOGEMIVQDTKANLTMTNPKLDLIRVCV 383

RESULT 12
 O92859 PRELIMINARY; PRT: 1461 AA.
 AC O92859;
 DT 01-FEB-1997 (Tremblrel. 02, Created)
 DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)
 DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
 DE NEOGENIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]

RP SEQUENCE FROM N.A.
 RA MEYERHARDT J.A., LOOK A.T., BIGNER S.H., FEARON E.R.;
 RL Oncogene 0:0-0(0).
 DR EMBL: U61262; AAB17263.1; -.
 DR HSSP: P02751; 1TTG.
 DR PFAM: PF00041; f3; 6.
 DR PFAM: PF00047; f3; 4.
 DR PRINTS: PR00014; FNTYPTIT.
 DR SEQUENCE 1461 AA: 159958 MW: 0AB7247E CRC32:

Query Match 5.3%; Score 122.5; DB 4; Length 1461;
 Best Local Similarity 20.7%; Pred. No. 0.24;
 Matches 87; Conservative 80; Mismatches 197; Indels 57; Gaps 20;

OY 11 LVAVGFWVLSSAAGKMLKSPQKVEVDIIDNFI-LRNW--RSDSVGNVTFSPDYOK 67
 DB 425 LILEHAP-----ATTGFLPSAPRDVVAASLVSTFFIKLTWRTPASDPHGDNLTVSYPTK 479
 OY 68 TGM--DNWIKLSCGQNTSTKCNFSKLNVYEIKRIAEKENTSSWTEVDSFTPFK 125
 DB 480 EGIAREREVNTSHPGEQVITQNLMPATYIF-----RYVAKNKHGSG---ESSAPLRY 530
 OY 126 AQGPPEVHLEAEDEKAIYIHISPTKDSVMAL-----DGLSTYSLILNRNSGVEERIE 181
 DB 531 ET--QPEVQLPGRAPNLRAYASTSTVETWETVSGNELQNKLYTMEKTDKEDVD 588
 OY 182 NIYRHKIKYKLSPEPTYCLKYKALTSWKIGYSPVHCIKITVENELPPENIEVSQON 241
 DB 589 VSSHRTINGKLYKTEYSERVVA--YKHHGVSTPPVAVRTLSDVSAAPQNSLSEVRN 646
 OY 242 -QNVYVLMKDYAMTQVQWLAHFLKRNPNHLYKMKQIPDCENKTKTQCVFP 294
 DB 647 SKSIIHNPAPPATONGQITGKIRYRKASRKSVDVETLVSQTOL-----SGLI-- 697
 OY 295 QNVFQKGIYLLRVOASDGNNT--SFWSSEIKPTELEQAFLLPV---FNIRSDSFHI 348
 DB 697 EGLDRGTEYNRVAALNTINGPATDMLSAETESDDETRVPEPSLSHRLVPTVSI-V 755
 OY 349 YIGAPKQSGNTPIQDYPLIYEIIFMENTSNAER-KIIEKTDVTPNKLPLTVYCYKAR 407
 DB 756 VSMTPPEPQNI-VYRGAIYGCI---GSPHAGIKVDYKQRYVYTIENLPSSHYVITLK 810
 OY 408 A 408
 DB 811 A 811

RESULT 13
 O00340 PRELIMINARY; PRT: 1461 AA.
 AC O00340;
 DT 01-JUL-1997 (Tremblrel. 04, Created)
 DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
 DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
 DE NEOGENIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN.
 RX MEDLINE: 97312699.
 RA VIELMEITER J., CHENG X.N., MISKEVICH F., LANE R.P., YAMAKAWA K.,
 KOENIGBERG J.R., DREYER W.J.;
 RT "Molecular characterization of human neogenin, a DCC-related protein,
 RT and the mapping of its gene (NEO1) to chromosomal position 15q22.3-
 RT q23.";
 RL Genomics 41:414-421(1997).
 DR EMBL: U72391; AAC51287.1; -.
 DR HSSP: P02751; 1TTG.
 DR PFAM: PF00041; f3; 6.
 DR PFAM: PF00047; f3; 4.

DR PRINTS: PRO0014: FNTYPEIII
SQ SEQUENCE 1461 AA; 160015 MW; 905AEIC4 CRC32;

Query Match 5.3%; Score 122.5; DB 4; Length 1461;
Best Local Similarity 20.7%; Pred. No. 0.24;
Matches 87; Conservative 80; Mismatches 197; Indels 57; Gaps 20;

OY 11 LVLVAVGPWLSAAGKLNKSPQKVEVDIIDNFI-LRNN--RSDSVGNVTFSPDYOK 67
DB 425 LILLENAP-----ATGPLPSPAPRDVVASLSTVFILKLTWRTPASDHPGDLTYSEFYTK 479
OY 68 TGM--DWIKISGCONITSTFCNSSLKLNLYEIKLRIRAKENTSSWVEVDSFTPRK 125
DB 480 EGIREREVENTSHPEGMOVTIQNLMPATVYLF-----RYMKNKHSGS---ESSAPLV 530
OY 126 AOIPPEVHLAEEDKAIYIHISPGTKDSVMAL-----DGLSFTSLIMKNSGVEERIE 181
DB 531 ET--QPEVQLPGPAPNLRAVASPTSTVETPVSNGEIQNKLYMEKGTREKQDQVD 588
OY 182 NIYSRHKIYKLSPEPTYCLKYKAAALLTSWKIGVSPVHCITTVENELPPENIEVSYON 241
DB 589 VSSHSTYINGLKXYTESFRVYA--YKNHGPVSTPDVAVRTLSVPSAQNLSLEYRN 646
OY 242 -QNYVLKD-----YTYANMT-FOYQMLHAFLRNPGNHLKMKQIPCCENVKTTQCVFP 294
DB 647 SKSIIHQPAPAFONQOIGYKIRYKASKSDVETETLVSGTOL-----SGLI-- 697
OY 295 QNVFQKGIYLRVQASDGNNT---SFWESEIKFDEIOAFVLPY---FNIRLSDSFHI 348
DB 697 EGLDRGTENFRVVALTINGCPATDMLSAETFEESDLETRVPESSLHVRPLVTST-V 755
OY 349 YIGAKQSGNTPIVDYPLIYEIIFWENTSNAER-KIIEKTDVTPNKLPLTYCVKAR 407
DB 756 VSWPEPEQNII-VVRGVAIGYGI-----GSPHMQITKVDYKQXYTIENLDPSSHYVILK 810
OY 408 A 408
DB 811 A 811

RESULT 14
OY1562 PRELIMINARY: PRT: 1427 AA.
AC OY1562;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE TUMOR SUPPRESSOR.
GN XDCCA.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae; Xenopodinae;
OC Xenopus.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE; 9511183.
RA PIERCELL W.E., REALE M.A., CANDIA A.F., WRIGHT C.V., CHO K.R.,
RA FEARON E.R.;
RT "Expression of a homologue of the deleted in colorectal cancer (DCC)
RT gene in the nervous system of developing Xenopus embryos."
RL Dev. Biol. 166:654-665(1994).
DR EMBL: U10986; AAA70168.1;
DR HSSP: P56276; TLTK.
DR PFAM: PF00041; fn3; 6.
DR PFAM: PF00047; 19; 4.
DR PRINTS: PRO0014: FNTYPEIII.
SQ SEQUENCE 1427 AA; 156533 MW; E50B7475 CRC32;

Query Match 5.1%; Score 117.5; DB 13; Length 1427;
Best Local Similarity 22.2%; Pred. No. 0.59;
Matches 93; Conservative 70; Mismatches 163; Indels 93; Gaps 22;

OY 32 SPQKVEVDIIDNFI-LRNNRSDSVGNV-TESFDYOKTGMNWKISGCONITSTKCNF 89
DB 431 APRDVPVVLVSSRFVRLSRPVESKGNITQTVYFSKQGVORRAVNTSOP1----- 484
OY 90 SSKLNV-----YEEKLRIRAKENTSSWVEVDSFTPRP-----KAQIGPEVHLAED 139
DB 484 -SLQITVGNLTPEETYNFRVAANE-----WGPESSQEVKVVYTOPLOYGPGVENLQ--- 536
OY 140 KAIYIHISPGTKDSVMALDGLSFT-----YSLIMKNSGVEEIEINISRHKIYKLS 193
DB 536 ---VSTYAP---TSVLISMDPPAYANGPVQGYRPFCAETFSGHEQNIEDVGIYRLREGLR 589
OY 194 PETTYCLKYKAAALLTSWKIGVSPVHCITTVENELPPENIEVSYONQNYVLKMDYTXA 253
DB 590 KTEYSIRVLA--YNRGPEVSSSEHTVTLSDVPSAMPQNVSEVAN----- 636
OY 254 NMTFOVQMLHAFLRNPGNHL-----YKMQIPDCENVKTT-----OCYEPQNVF----- 299
DB 636 SRGSIKVM-----LPPPGTONGFITGK-----IHRKTRRGELETLEPNMLWYFTG 685
OY 299 -QNGI-YLNRVQASDGNNTSFWESEIKFDT-----EQAFLLPPVFNIRLSDSFHIYI 350
DB 686 LEKSGQSFQVAAVTVNGTSPSSDWTYAEETPENDLDESQVDPDPSLHVRPLTTSI-IMS 744
OY 351 GAPQSGNTPIVDYPLIYEIIFWENTSNAER-KIIEKTDVTPNKLPLTYCVKARA 408
DB 745 WTPPLPNII-VVRGVIIGYGV-----GSPVETVAVDSKORYSTIENLEPSHYISLKA 798

RESULT 15
OY17859 PRELIMINARY: PRT: 1585 AA.
AC OY17859; Q20137;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE CO9D8.1 PROTEIN.
GN CO9D8.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidae; Rhabditidae; Peloderinae; Caenorhabditis.
RN (1)
RP SEQUENCE FROM N.A.
RA COLES L.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z46811; CA86842.1;
DR EMBL: Z49338; CA86842.1; JOINED.
DR EMBL: Z49338; CA90189.1;
DR EMBL: Z46811; CA90189.1; JOINED.
DR HSSP: P28827; IRPM.
DR PFAM: PF00041; fn3; 3.
SQ SEQUENCE 1585 AA; 178386 MW; EA03A8DD CRC32;

Query Match 5.1%; Score 117.5; DB 5; Length 1585;
Best Local Similarity 19.7%; Pred. No. 0.68;
Matches 86; Conservative 74; Mismatches 171; Indels 105; Gaps 24;

OY 33 PQKVEVDIIDNFI-LRNNRSDSV--GNVTFSPDYOKTGMNWKISGCONITSTKCNFS 90
DB 263 PIDVOYEMKGIYVSNRPPESEKRNQNT-SYKAILSAMQ--ATADYEDPVAPSPSS 319
OY 91 SKLNVYEIKLRIRN-----EKENTSSWVEV---D 118
DB 320 TFEVNVRAVYLFKVAALAMKIGIPYVLTINPDADILDNNEEENODPEATWGE 379
OY 119 SFTPRKAQIGPEVHLAEEDKAIYIHISPGTKDSVMALDGLSFTYSLIMKNSGVEE 178
DB 380 NNRPKRSKISTADY-----SALHHAHP-----LTHPISAAALAKAPTIGA 423
OY 179 RENIYSRHKIYKLSPEPTYCLKYKAAALLTSWKIGVSPVHCITTVENELPPENIEV- 238

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Db 424 PMBAPYTTTS-----TBSTLFFOYTLPPMTTAMN-----RVTKLETLVGPPTNVRE 470
OY 238 SYONONTVLKMDYTYANM-TEOVQWLAFLKRNPNHNL--YKMKOIP---DCENVKTQ 290
Db 471 ATSNSTAVVQMDPESOKADSFVVKYMH-----EPGNMDEKMKOLPVYSIDKENPKRFA 525
OY 291 CVPQOVFOKGIYLLRVQASDGNNTSEFSEIEKFTIEIOAFLLPVENIRSL-----SD 344
Db 526 VVSDLANHAP--YAFCVLAVKNNRQGPCSDP---PTVLES--VTPTVMQNLRLVMTKTSN 578
OY 345 SFH1---YIGAPKQSG---NTPVIOYPLIYEIIEMENTSNAE---KRIIEKTDVTPN 395
Db 579 SVQLTWEYNG-PRNVGFYVNHGKRDY--VNHLE--OECTWSIPFGQDVDEKHREYLMWTN 634
OY 396 LKPLVYCVKARAHIM 411
Db 635 LRPHMYTIIHGVRTL 650

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Search completed: June 1, 2000, 05:54:18
 Job time: 4523 sec

OM of: US-09-240-675-1 to: A_Geneseq_36:* out_format: pfs
 Date: Jun 1, 2000 5:43 PM
 About: Results were produced by the Gencore software, version 4.5,
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Command line parameters:
 -MODEL-frame: n2p.model -DEV-xlp
 -O/cgcn2.1/USPTO.spool/US09240675.r/unat.30052000.165117.2964/app_query.fasta.1
 -DB-A_Geneseq_36 -OPTM-fastan -SUFFIX-modif.reg -GAPOP-17.000
 -GAPEXT-4.000 -MINMATCH-0.100 -LOOPEXT-0.000 -LOOPEXT-0.000
 -GAPOP-6.000 -GAPEXT-7.000 -YGAPOP-10.000 -YGAPOP-10.000
 -DELOP-6.000 -DELEXT-7.000 -START-1 -MATRIX-biosum62
 -TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR SCORE-9ct
 -ALIGN-15 -MODE-LOCAL -OUTPMT-pfs -NORM-ext -MINLEN-0
 -MAXLEN-1000000 -USBR-US09240675 -NCPU-6 -ICPU-3 -NO_XLPHY -WAIT
 -THREADS-1

Search information block:
 Query: US-09-240-675-1
 Query length: 1343
 Database: A_Geneseq_36:*
 Database sequences: 18963
 Database length: 23686106
 Search time (sec): 79.530000

score_list:

Sequence	Strd Orig	ZScore	EScore	Len	Documentation
A_Geneseq_36:R14487	+ 2313.00	4111.17	3.7e-222	436	1 Soluble interferon-alpha/beta
A_Geneseq_36:R28495	+ 2313.00	4111.17	3.7e-222	436	1 Sequence of a soluble form of
A_Geneseq_36:R11958	+ 2313.00	4108.62	4.0e-222	557	1 Human alpha-interferon receptor
A_Geneseq_36:R14488	+ 2313.00	4108.62	4.0e-222	557	1 Complete interferon-alpha/beta
A_Geneseq_36:R28496	+ 2313.00	4108.62	4.0e-222	557	1 Sequence of a soluble form of
A_Geneseq_36:R24635	+ 2309.00	4108.62	4.0e-222	557	1 Human interferon receptor. Monoc
A_Geneseq_36:R75356	+ 2309.00	4101.48	1.0e-221	557	1 Human IFN receptor. Compn. of
A_Geneseq_36:R21804	+ 2308.00	4099.66	1.3e-221	557	1 Transmembrane interferon alpha
A_Geneseq_36:R171723	+ 2304.00	4095.09	1.3e-221	456	1 IFN receptor extracellular doma
A_Geneseq_36:R21805	+ 2260.00	4016.49	7.0e-217	434	1 Spliced-deleted interferon alph
A_Geneseq_36:R21806	+ 2208.00	3922.16	1.1e-211	436	1 Spliced-deleted interferon alph
A_Geneseq_36:W52296	+ 228.50	388.62	1.1e-14	335	1 CRFB4 protein. New recombinant
A_Geneseq_36:R75782	+ 203.00	342.82	3.8e-12	332	1 IFN-gamma receptor beta-subunit
A_Geneseq_36:R79159	+ 198.00	328.58	1.4e-11	553	1 Zcytor7 cytokine receptor polyd
A_Geneseq_36:R171035	+ 155.50	257.77	2.1e-07	337	1 Human IFN-gamma accessory fact
A_Geneseq_36:R75783	+ 153.50	254.19	3.3e-07	337	1 IFN-gamma receptor beta-subunit
A_Geneseq_36:W97861	+ 151.00	244.19	6.9e-07	574	1 Human cytokine receptor 11 (Zcy
A_Geneseq_36:W97861	+ 131.50	219.74	4.3e-05	211	1 Human cytokine receptor 11 (Zcy
A_Geneseq_36:R07469	+ 124.00	197.60	0.0003	489	1 Plasmid PBABLU human interfer
A_Geneseq_36:R57469	+ 122.00	194.37	0.0005	473	1 Extracellular domain of human h
A_Geneseq_36:R70113	+ 118.50	180.95	0.0014	942	1 Gamma-IFN-R-GP 130 fusion prot
A_Geneseq_36:R14642	+ 118.00	194.85	0.0010	227	1 Gamma interferon receptor. New
A_Geneseq_36:R14641	+ 118.00	194.67	0.0010	231	1 Gamma interferon receptor. New
A_Geneseq_36:R57139	+ 117.50	184.30	0.0015	575	1 Interleukin-10 receptor subunit
A_Geneseq_36:R57139	+ 117.50	184.30	0.0015	575	1 Mouse IL-10 receptor. Interleuk
A_Geneseq_36:W41803	+ 117.50	170.28	0.0024	2214	1 Human IDL receptor analogue. D
A_Geneseq_36:W41803	+ 117.50	170.28	0.0024	2214	1 Gamma interferon receptor. New
A_Geneseq_36:R14643	+ 115.00	170.80	0.0036	1370	1 Deleted in Colorectal Carcinom
A_Geneseq_36:R14643	+ 115.00	168.39	0.0038	1728	1 Deleted in Colorectal Carcinom
A_Geneseq_36:R13144	+ 114.50	187.80	0.0022	245	1 Soluble human interferon gamma
A_Geneseq_36:R67023	+ 112.00	167.85	0.0065	1086	1 Human neuronal calcium channel
A_Geneseq_36:R70103	+ 112.00	167.85	0.0065	1086	1 Human calcium channel alpha-2c
A_Geneseq_36:W42087	+ 111.50	163.12	0.0083	1571	1 Human Down syndrome-cell adhes
A_Geneseq_36:W42086	+ 111.00	161.09	0.0089	1910	1 Human Down syndrome-cell adhes
A_Geneseq_36:W26356	+ 110.50	156.88	0.0131	2213	1 Rabbit LDL receptor analogue.
A_Geneseq_36:R14403	+ 109.50	163.91	0.0124	948	1 Extracellular domain of hybrid
A_Geneseq_36:R97853	+ 108.00	163.23	0.0138	928	1 Rat REK7 eph-related tyrosine k
A_Geneseq_36:R85090	+ 108.00	161.66	0.0159	991	1 Eph-like receptor protein tyros
A_Geneseq_36:W09822	+ 107.00	168.65	0.0151	426	1 Human interleukin-12 receptor a
A_Geneseq_36:W42973	+ 107.00	168.62	0.0151	427	1 Human interleukin-13 alpha rece

A_Geneseq_36:R57138 + 107.00 165.48 0.0167 578 1 Interleukin-10 receptor s
 A_Geneseq_36:W41804 + 107.00 165.48 0.0167 578 1 Human IL-10 receptor. Int
 A_Geneseq_36:W83927 + 107.00 162.73 0.0182 753 1 Human T85 protein. New is
 A_Geneseq_36:R15049 + 107.00 160.33 0.0197 948 1 Hybrid human Insulin-IGF-

seq_name: A_Geneseq_36:R14487

seq-documentation_block:

ID R14487 standard; Protein; 436 AA.
 AC R14487:
 DT 16-JAN-1992 (first entry)
 DE Soluble interferon-alpha/beta receptor.
 KW IFN; autoimmune disease; graft rejection; histocompatibility.
 OS Homo sapiens.
 PN FR2657881-A.
 PD 09-AUG-1991.
 PF 05-FEB-1990; 001298.
 PR 05-FEB-1990; FR-001298.
 PA (EUBI-) LAB EURO BIOTECNO.
 PI Elid P. Gresser I, Lutfalla G, Meyer F, Mogensen KE;
 PI Tovey MG, Uze G;
 DR WPI: 91-319778/44.
 DR N-PSDB: Q14239.
 PT New water-soluble polypeptide(s) with affinity for IFN-alpha and
 PT beta - used to treat e.g. lupus erythematosus, Bennett's disease,
 PT aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.
 PS Claim 2; Page 45; 52pp; French.
 CC The transmembrane and cytoplasmic domains of the native IFN receptor
 CC have been deleted to obtain a soluble, circulating form of the
 CC receptor. Potentially immunogenic epitopes have thus been eliminated.
 CC Derivatives obtained by substitution or deletion of this sequence
 CC are also claimed as are hybrid molecules comprising the soluble
 CC receptor (or deriv.) and an immunoglobulin such as IgG1.
 CC See also Q14240.
 SO Sequence 436 AA;

alignment_scores:

Quality: 2313.00 Length: 436
 Ratio: 5.305 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1 x R14487 ..
 Align seg 1/1 to: R14487 from: 1 to: 436

27 ATGATGCTGCTCTCTCTGCGCCGACGACCCAGTCTGTCGCGCGG 76
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 1 MetMetValValLeuLeuValValLeuValValLeuValValVal 17
 77 CCCATGGGTGTGTCGCGCCGACGCGGAGGAGGAGGAGGAGGAGG 126
 |||||||
 17 ProTrpValValLeuSerAlaAlaAlaAlaAlaAlaAlaAlaAla 34
 127 AAAAAGTAGAGTGCATCATGATGATGATGATGATGATGATGATG 176
 |||||||
 34 IllyValAlaAlaValAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 50
 177 AGAGCGATGATGCTGTCGCGGAGTGTGATGATGATGATGATGATG 226
 |||||||
 51 ArgSerAspGluSerValGluValValValValValValValValVal 67
 227 AACTGGAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 276
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 67 ThrGlyMetAspAspThrPheLeuLeuSerLeuLeuSerLeuLeuSer 84
 277 GATCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 326
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 84 eThrIlySerAspPheSerSerLeuValValValValValValValVal 100
 327 AATTGCGGTATGAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 376
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101 LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrGluVal 117
377 TGACTCATTTACACCATTTGGCAAGCTGATGTCCTCCCAACATAC 426
117 LAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluValH 134
427 ATTPAGAGCTGAAGATAGCAATAGTATACATCATCTCCGGAACA 476
134 LsLeuGluAlaGluAspLysAlaIleValIleHisIleSerProGlyThr 150
477 AAGATAGTGTATGTGGGCTTTGGATGTTTAAAGCTTTCATATACCT 526
151 LysAspSerValMetTrpAlaLeuAspGlyLeuSerPheThrTyrSerIe 167
527 ACTATCTGGAAGAACTCTCAGCTGTAGAAGAAAGATGGAATATTT 576
167 uLeuIleTrpLysAsnSerSerGlyValGluGluArgIleGluAsnIleT 184
577 ATTCCAGACATAAAATTTATTAATCTCACAGAGACTACTATTGTCTA 626
184 YrSerArgHisLysIleTyrLysLeuSerProGluThrThrTyrCysLeu 200
627 AAAGTTAAAGCAGCAGCTACTTACTCTATGAAAATTGGTGTCTATCTC 676
201 LysValLysAlaAlaLeuLeuThrSerTrpLysIleGlyValTyrSerPr 217
677 AGTACATGTATTAAGACACAGTGTAAATGAATCACTCCACCAAGAAA 726
217 ovalHisCysIleLysThrThrValGluAsnGluLeuProProProGluA 234
727 ATATAGAAGTCAGTGTCCAAATTCAGACATATGTTCTTAATGGGATAT 776
234 snIleGluValSerValGlnAsnGlnAsnTyrValLeuLysTrpAspTyr 250
777 ACATATGCAACATGACCTTCAAGTTCAGTGGCTCCAGCGCTTTTAA 826
251 ThrTyrIleAsnMetThrPheGlnValGlnTrpLeuHisAlaPheLeuL 267
827 AAGCAATCTCGAAGAACCATTTGTATTAATGGAACAATACCTGACGTG 876
267 sArgAsnProGlyAsnHisLeuTyrLysTrpLysGlnIleProAspLysG 284
877 AAAATGTCAAACTACCCAGTGTGTCTTCTCCAAAACGTTTCCAAAA 926
284 LuAsnValLysThrThrGlnCysValPheProGlnAsnValPheGlnLys 300
927 GGAATTTACCTTCTCCGCTACAAAGCATTCGATGGAATAACACATCTTT 976
301 GlyIleTyrLeuLeuArgValGlnAlaSerAspGlyAsnAsnThrSerPh 317
977 TTGGTCTGAAGAGATAAGTTGTACTGAAATCAAGCTTCTCTACTTC 1026
317 eTrpSerGlnGluIleLysPheAsnProGluIleGlnAlaPheLeuLeuP 334
1027 CTCAGTCTTTAACATTAGATCCCTTAGTATTCATTCAATATCATATATC 1076
334 roproValPheAsnIleArgSerLeuSerAspSerPheHisIleTyrIle 350
1077 GGTGCTCCAAAACAGTCTGGAACACCGCTGTGATCCAGATTTATCCACT 1126
351 GLyAlaProLysGlnSerGlyAsnThrProValIleGlnAspTyrProLe 367
1127 GATTATGAAATTTATTTTGGGAAAAACACTCAAAATGCTGAGAGAAAA 1176
367 uIleTyrGluIleIlePheTrpGluAsnThrSerAsnAlaGluArgLysI 384
1177 TTATCGAGAAAAAACTGATGTTACAGTCTCTAATTTGAAACCACTGACT 1226
384 leIleGluLysLysThrAspValThrValProAsnLeuLysProLeuThr 400
1227 GTATATGTGTGAAGCCAGACGACACACATGATGATAAAGCTGAATAA 1276
401 ValTyrCysValLysAlaArgAlaHisThrMetAspGluLysLeuAsnL 417

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1277 AAGCACTGTTTATGACGCTGTATGTGAGAAAACAAACACGGAATA 1326
417 sSerSerValPheSerAspAlaValAlcysGluLysThrLysProGlyAsnT 434
1327 CCTCTAAA 1334
434 hSerLys 436

seq_name: A_Geneseq_36:R28495

seq_documentation_block:
ID R28495 standard; Protein; 436 AA.
AC R28495:
DE 31-MAR-1993 (first entry)
DE Sequence of a soluble form of the interferon (IFN) receptor
DE with a high affinity for IFN-alpha and -beta.
KM Interferon receptor; alpha-interferon; beta-interferon.
OS Synthetic.
PN MO9218626-A.
PD 29-OCT-1992.
PF 17-APR-1991; F00318.
PR 17-APR-1991; WO-F00318.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
PI Eld P, Gresser I, Luftalla G, Meyer F, Mogenssen KE,
PI Toyev M, Uze G;
DR WPI: 97-382110/46.
DR N-PSDB: Q30532.
PT Water soluble polypeptide(s) strongly bind interferon(s) alpha
PT and beta - useful as immunosuppressants, for treating auto-immune
PT diseases and transplant rejection
PS Claim 2; Fig 1; 58pp; English.
CC DNA encoding the water-soluble polypeptide with a high affinity for
CC IFN-alpha and -beta is isolated by PCR, using appropriate
CC oligonucleotides as primers and cloned cDNA as template. For example,
CC bacteriophage lambda ZAP, containing the entire coding sequence of
CC the IFN-alpha and -beta receptor (Q30533), was incubated with oligos
CC Q30534 and Q30535. R28496 represents the complete receptor. R28495
CC lacks the transmembrane and cytoplasmic domains. Both forms bind
CC IFN in the same way as antibodies so are immunosuppressants e.g. for
CC treating autoimmune diseases and graft rejection. They lack the
CC toxic side-effects of known immunosuppressants such as steroids.
SQ Sequence 436 AA;

alignment_scores:
Quality: 2313.00 Length: 436
Ratio: 5.305 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-240-675-1 x R28495 ..

Align seg 1/1 to: R28495 from: 1 to: 436

27 ATGATGATGCTCTCTCTGGGCGGAGACCTAGTGTGTCGCGCGGAG 76
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1 MetMetValValLeuLeuGlnLysAlaThrThrLeuValIleValAlaGln 17
34 InLysValGluValAspIleIleAspAspAsnPheIleLeuArgTyrPasn 50
127 AAAAGTAAAGTCGACATCATAGTACAACTTTATCTCTGAGGTGAAC 176
|||||
17 yProTrpValLeuSerAlaAlaGlyLysLysAsnLeuLysSerProG 34
77 CCCAGGTGGTGTGTCGCGAGCGGAGGTGGAATAAATCTAAATCTCTC 126
|||||
34 InLysValGluValAspIleIleAspAspAsnPheIleLeuArgTyrPasn 50
177 AGGAGGATGACTGTGCGGAATGTGACTTTTTCATTGATTCATCAAAA 226
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLys 67
227 AACTGGAGTGAATAATGGATAAATTTGTCTGGGTGTCAGAAATATTA 276
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177 AGGACGATGAGCTGTGGGAAATGGAATTTTCATTGATGATATCAAA 226
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51 ArgSerAspGluSerValGlnValAlaThrPheSerPheAspTyrGln 67
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227 AACTGGATGGAATAATGGATTTCTGGGTGTGAGATATATCTACTA 276
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67 sthrlGluMetAspAsnTrpIleTyrLeuSerGlyCysGlnAsnIleTrs 84
|||||
277 GTACCAATATGCACTTTCTTCTACCAAGCTGAATGTTATGACAAAT 326
|||||
84 ertHrLysCysAsnPheserSerLeuLysLeuAsnValTyrGlnGlu 100
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337 AAATGCGTATAGAGAGAAAAAGAAAACCTTTCATGATGATAGAGT 376
|||||
101 LysLeuAlaGlnLeuAlaGlnLysGlnAsnThrSerTyrTrpGlnVal 117
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377 TGACTCATTTACACCATTTCCCAAGCTCAGATTGGTCTCCAGAAATG 426
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117 LAspSerPheThrProPheArgGlyAlaGlnIleGlyProProGlnVal 134
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427 ATTTAGAGCTGAGATTAAGCAATAGTATACATCTCTCCGGAACA 476
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134 lslGluAlaGlnLysPylsAlaIleValIleHisIleSerProGlyThr 150
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537 ACTATATCGAATAAACTCTGAGGTGTGAGAAAGATGAAATATATT 576
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167 uleuIleTrpLysAsnSerSerGlyValGlnGlnArgIleGlnAsnIle 184
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577 ATTCAGACATATAATTTATAAATCTCTACAGAGAGACTATATTGTTA 626
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184 YrSerArgHisLysIleTyrLysLeuSerProGlnThrThrTyrCysLeu 200
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627 AAAGTTAAGCAGCAGCTACTACGTCATGAGAAATGGTGTATAGACC 676
|||||
201 LysValLysAlaIleLeuLeuThrSerTrpLysIleGlyValTyrSerP 217
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677 AGTACATTTGATTAAGACAGCAGTGTGAAATGAATACCTCCAGCA 726
|||||
217 oValHisCysIleLysThrThrValGlnAsnGlnLeuProProGlnUA 234
|||||
727 ATATAGAGTCAGTGTCCAAATCAGAACTATGTTCTTAATGGATTA 776
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234 snlIleGlnValSerValGlnAsnGlnAsnTyrValLeuLysTrpAsp 250
|||||
777 ACATATGCAAAACATGACCTTCAAGTTCAAGTGGTCCAGGCTTTTAA 826
|||||
251 ThrTyrAlaAsnMetThrPheGlnValGlnTrpLeuHisAlaPheLeu 267
|||||
827 AAGGAATCTTGGAACCATTTGTATTAATGGAACCAATACCTGACTG 876
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267 sarGAsnProGlyAsnHisLeuTyrLysTrpLysGlnIleProAsp 284
|||||
877 AAAATGCAAAACATGACCTGTGTCTTCTCCAAAGCTTTTCCAAA 926
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284 lAsnValLysThrThrGlnCysValIleProGlnAsnValPheGlnLys 300
|||||
927 GGAATTTACCTTCTCCGCTACAAGCATCTGATGAAATAACATCATCT 976
|||||
301 GlyIleTyrLeuLeuArgValGlnAlaSerAspGlyAsnAsnThrSer 317
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977 TTGGCTGAGAGATTAAGTTGATCTGAAATACAAAGCTTCTCTACT 1026
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317 etrpSerGlnGlnIleLysPheAspThrGlnIleGlnAlaPheLeu 334
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1077 GGTGCTCCAAACAGTGTGAAACAGCGCTGTGATCCAGGATTAATCA 1126
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367 uIleTyrGlnIleIlePheTrpGlnAsnThrSerAsnAlaGlnArgLys 384
|||||
1177 TTATCGAGAAAAAACTGATGTACAGTTCTCAATTTGAAACCACTGAC 1226
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384 lIleGlnLysLysThrAspValThrValProAsnLeuLysProLeuThr 400
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1227 GTATATGTGTGAAAGCAGACAGCACACCATGATGAGAAAGCTGAATA 1276
|||||
401 ValTyrCysValLysAlaArgAlaHisThrMetAspGlnLysLeuAsn 417
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1277 AAGCAGTGTTTAGTACGCTGTATGTGGAACCAAAACAGGAATA 1326
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417 sSerSerValPheSerAspAlaValCysGlnLysThrLysProGlyAsn 434
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434 hrSerLys 436
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seq_name: A_Geneseq_36:R14488
seq_documentation_block:
ID R14488 standard; Protein: 557 AA.
AC R14488;
DT 16-JAN-1992 (first entry)
DE Complete interferon-alpha/beta receptor.
KW IFN; autoimmune disease; graft rejection; histocompatibility.
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 437..457
FT domain 458..557
FT domain /label= cytoplasmic
PN FR2657881-A.
PD 09-AUG-1991.
PF 05-FEB-1990; 001298.
PR 05-FEB-1990; FR-001298.
PA (EUBI-) LAB EURO BIOTECHNO.
PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE.
PI Tovey MG, Uze G.
DR N-PSDB; Q14240.
DR N-PSDB; Q14240.
PT New water-soluble polypeptide(s) with affinity for IFN-alpha and
PT beta - used to treat e.g. lupus erythematosus, Behcet's disease,
PT aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.
PS Discloure; Page 47; 52pp; French.
CC The invention covers derivatives of the interferon-alpha and/or beta
CC receptor obtained by deleting the transmembrane and cytoplasmic domains
CC of the native receptor or by substitution. Potentially immunogenic
CC epitopes are eliminated and the deriv. can be secreted from
CC transformed cells. Soluble deriv.s block the activity of IFN alpha/beta
CC and can be used to treat autoimmune diseases or to inhibit graft
CC rejection. See also Q14239.
SQ Sequence 557 AA;

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alignment_scores:
Quality: 2313.00 Length: 436
Ratio: 5.305 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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alignment_block:
US-09-240-675-1 x R14488 ..

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Align seg 1/1 to: R14488 from: 1 to: 557
27 ATGATGTCGTCCTCTGGCGCGAGACCACTAGTGCCTGTCGCGGTGG 76
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1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
77 CCCATGGGTGTTCGCCAGCCGACGGTGAAGAAAAATCTAAATCTCTC 126
17 yProripValLeuSerAlaAlaGlyLysAsnLeuLysSerProG 34
127 AAAAGTAGAGTCGACATCATAGATGACAACTTTATCCTGAGGTGAAC 176
34 LnlsvAlaGluValAspIleIleAspAspAsnPhelleLeuArgTrpAsn 50
177 AAGAGCGATAGTCGTGGGAATGATGATTTTTCATTCGATTAATCAAAA 226
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTrpGlnIly 67
227 AACTGGATGATTAATGATTAATTAATGCTGTGGGTGTCAGAAATATCTA 276
67 sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS 84
277 GTACCAATATGCAACTTTTCTTCACCTGACGTGAATGTTATGAAGAAAT 326
84 eThrLysCysAsnPheserSerLeuLysAsnValTyrgIuGluIle 100
327 AAATTCGATATAGACGAGAAAAGAAACACTTCTTCATGATGATGAGGT 376
101 LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrgIuVal 117
377 TGACATCTTACACCATTTTCGCAAAAGCTGATGGTCTCCAGAGATAC 426
117 LAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluValH 134
427 ATTTAGAGCTGAAGATTAAGCAATAGTGATACATCTCTCTGGAACA 476
134 LsIeuGluAlaGluAspLysAlaIleValIleHisIleSerProGlyThr 150
477 AAGATAGTGTATAGGCTTGGAGTGGATGTTAAGCTTTCATATAGCTT 526
151 LysAspSerValMetTrpAlaLeuAspGlyLeuSerPheThrTyrgSerIle 167
527 ACTTATCTGGAAAACTCTTCAGGTGAGAGAAAGATTAATATTT 576
167 uLeuIleTrpLysAsnSerSerGlyValGluGluArgIleGluAsnIleT 184
577 ATTCGACACATAAATTATTAACCTCTCACAGACTACTTATGTCTA 626
184 ySerArgHisLysIleTyrgLysLeuSerProGluThrTyrgCysLeu 200
627 AAAGTTAAACGACACTACTTACTGATCGAAATGGTGTCTATATCC 676
201 LysValLysAlaAlaLeuLeuThrSerTrpLysIleGlyValTyrgSerP 217
677 AGTACATGTATTAAGACACAGTGTGAAGAACTACTCTCCACAGAAA 726
217 oValHisCysIleLysThrThrValGluAsnGluLeuProProGluVal 234
727 ATATAGAAGTCAGTGTCCAAATGAGACTATGTTCTTAATGGGATTAAT 776
234 snIleGluValSerValGlnAsnGlnAsnTyrgValLeuLysTrpAspTy 250
777 ACATATGCAAAACATGACCTTTCAAGTCAAGGTCTCCACGCCCTTTTAAA 826
251 ThrTyrgLysAsnMetThrPheGlnValGlnTrpLeuHisAlaPheLeuL 267
827 AAGGAATCTGGAACCATTTGTATTAATGAAGAAACAAATACCTACTGTG 876
267 sArgAsnProGlyAsnHisLeuTyrgLysTrpLysGlnIleProAspGly 284
877 AAAATGTCAAAACTACCAAGTGTCTTCTTCAAAAAGTTTTCAAAAA 926
284 LAsnValLysThrThrGlnCysValPheProGlnAsnValPheGlnLys 300
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301 GlyIleTyrgLeuLeuArgValGlnAlaSerAspLysAsnAsnThrSerPh 317

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1027 CTCGAGCTCTTAACATTTAGATCCCTTAGTGTGATTCATTCATATCATATC 1076
334 rOProValPheAsnIleArgSerLeuSerAspSerPheHisIleTyrgIle 350
1077 GGTGCTCCAAAACAGTCTGGAACACGCGCTGTGATCCAGATTAATCCACT 1126
351 GlyAlaProLysGlnSerGlyAsnThrProValIleGlnAspTyrgProLe 367
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367 uLleTyrgIuIleIlePheThrTyrgLysAsnThrSerAsnAlaIuArgLys 384
1177 TTATGAGAAAAAAACGATGATGATCAGTTCCTTAATTTGAAACCACTGACT 1226
384 LeIleGluLysLysThrAspValThrValProAsnLeuLysProLeuThr 400
1227 GTATATTGTGTGAAGCCAGACACACACATGATGAAGAAAGCTGAATAA 1276
401 ValTyrgCysValLysAlaArgAlaHisThrMetAspGluLysLeuAsnL 417
1277 AAGCAGTGTTTTACTGACGCTGTATGTGAGAAAAACAAACCGAGAAATA 1326
417 sSerSerValPheSerAspAlaValCysGluLysThrLysProGlyAsnT 434
1327 CCTCTAAA 1334
434 hrSerLys 436

seq_name: A_Geneseq_36: R28496

seq_documentation_block:
ID R28496 standard; Protein; 557 AA.
AC R28496;
DT 31-MAR-1993 (first entry)
DE Sequence of a soluble form of the interferon (IFN) receptor
with a high affinity for IFN-alpha and -beta.
KW Interferon receptor; alpha-interferon; beta-interferon.
OS Synthetic.
PN WO9218626-A.
PD 29-OCT-1992.
PE 17-APR-1991; F00318.
PR 17-APR-1991; WO-F00318.
RA (EUBI-) LAB EURO BIOTECHNOLOGIE.
PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,
PI Tovey M, Uze G;
DR N-PSDB; Q30533.
PT Water soluble polypeptide(s) strongly bind interferon(s) alpha
and beta - useful as immunosuppressants, for treating auto-immune
PT diseases and transplant rejection
PS Claim 3; Fig 2; 58pp. English.
CC DNA encoding the water-soluble polypeptide with a high affinity for
CC IFN-alpha and -beta is isolated by PCR, using appropriate
CC oligonucleotides as primers and cloned cDNA as template. For example,
CC bacteriophage lambda ZAP, containing the entire coding sequence of
CC the IFN-alpha and -beta receptor (Q30533), was incubated with oligos
CC Q30534 and Q30535. R28496 represents the complete receptor. R28495
CC lacks the transmembrane and cytoplasmic domains. Both forms bind
CC IFN in the same way as antibodies so are immunosuppressants e.g. for
CC treating autoimmune diseases and graft rejection. They lack the
CC toxic side-effects of known immunosuppressants such as steroids.
SQ Sequence 357 AA;

alignment_scores:
Quality: 2313.00 Length: 436
Ratio: 5.305 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1 x R28496

Align seg 1/1 to: R28496 from: 1 to: 557

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1  MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG 17
77  CCCATGGGTGTGTCCGACGCCGAGTGGAAAAATCTAAATCTCCCTC 126
    |||
17  yProTrrValLeuSerAlaAlaIleGlyLysAsnLeuLysSerProG 34
127  AAAAAGTAGAGTCGACATCATGATGACAACCTTATCCGAGCTGAGAC 176
    |||
34  InLysAlaGluValAspIleIleAspAspAsnPhenIleLeuAsnGrrPasn 50
177  AGAGCGATGAGTGTGCGGAAATGAGCTTTTCATTCGATTCATAAAA 226
    |||
51  ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTrrGlnLys 67
227  AACTGGGAGCATTAATTGATTAATAATGTCGTGTCAGATATATCTA 276
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67  sThrGlyMetAspAsnTrrPileLysLeuSerGlyCysGlnAsnIleThrS 84
277  GTACCAATGCAACTTTCTTCACCTCAGCTGAATGTTATGAGAAAT 326
    |||
84  eThrLysGlyAsnPheserSerLeuLysLeuAsnValIlyrGluGluIle 100
327  AAATTCGGTAAAGACAGCAAAAAAACAACCTTCATGATGATGAGGT 376
    |||
101  LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrrPrrGluValH 117
377  TGACATATTACACCATTTGCGAAAGCTGAGATGTCCTCCAGAGATGAC 426
    |||
117  LAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluValH 134
427  ATTAGAACCTGAAGATAAGCAATAGTATACATCTCTCCTCGAGACA 476
    |||
134  IsLeuGluValGluAspLysAlaIleValIleHisIleSerProGlyThr 150
477  AAAGATAGTGTATGTGGGCTTTGATGGTTTAAGCTTACATATAGCTT 526
    |||
151  LysAspSerValMetTrrPalaLeuAspGlyLeuSerPheThrTyrSerIle 167
527  ACTTATCTGGAATAAACTCTTCAGGTGTAGAAAGAAAGATGAAATATT 576
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167  ULeuIleTrrPlysAsnSerSerGlyValGluGluAsnIleGlyLysAsnIle 184
577  ATTCAGACATAAAATTTATAACTCTCAGCAGAGACTACTATTGTCTTA 626
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627  AAAGTTAAAGCAGCACTACTTACGTATGAAAAATGGTGTCTATAGTCC 676
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201  LysValLysAlaAlaLeuLeuThrSerTrrPlysIleGlyValTrrSerPrr 217
677  AGTACATTGTATAAGACACAGTGAATAAGTAACTACTCCACAGAGAA 726
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217  oValHisCysIleLysThrThrValGluLysGluLeuProProGluVal 234
727  ATATAGAACTAGTGTCCAAAAATCAGAACTATGTTCTTAATGGATATAT 776
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234  snIleGluValSerValGlnAsnGlnAsnTrrValLeuLysTrrAspTrr 250
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251  ThrTrrAlaAsnMetThrPheGlnValGlnTrrPheHisAlaPheLeuLys 267
827  AAGGAATCCTGGAAACATTTGTATAATGAAACAAATACTGACTGTG 876
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301  GlyIleTrrLeuLeuArgValGlnAlaSerAspGlyAsnAsnThrSerPh 317
977  TTGGTCTGAAGATAAAGTTGATACGAAATACAACTTTCCTACTTC 1026
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317  eTrrPrrGlnGluIleLysPheAspTrrGluIleGlnAlaPheLeuLys 334
1027  CTTCCAGCTTTTACATTAGATCCCTTACTGATTCATTCATATCATATC 1076
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1127  GATTATGAAATTAATTTTGGGAAAACATTCAAATCCTGAGAGAAAAA 1176
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367  uIleTrrGluIleIlePheTrrPrrGluAsnThrSerAsnAlaGluArgLysI 384
1177  TTATGAGAAAAAATCGATGTACAGTTCCTAATTGAAACCACTGACT 1226
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    |||
434  hrSerLys 436

seq_name: A_Geneseq_36:R42635
seq_documentation_block:
ID R42635 standard; Protein; 557 AA.
AC R42635;
DT 20-Apr-1994 (first entry)
DE Human interferon receptor.
KW IFN-R; extracellular domain; monoclonal antibody; viral infection;
KW cell proliferation; allograft rejection; systemic lupus erythematosus;
KW psoriasis; multiple sclerosis; Behcet's disease; aplastic anaemia;
KW immunodeficiency; measles virus; interferon alpha-beta.
OS Homo sapiens.
FH Key
FT domain
FT 1. 436
FT /label= extracellular domain
FT /note= "soluble, immunogenic form of IFN-R"
EP-563487-A.
PD 06-OCT-1993.
PF 31-MAR-1992; 400902.
PR 31-MAR-1992; EP-400902.
PA (EURI-) LAB EURO BIOTECHNOLOGIE SA.
PI Benoit P, Maguire D, Meyer F, Plavec I, Tovey MG;
DR WPI: 93-312951/40.
DR P-RSDB; R42635.
PT Monoclonal antibody to human interferon type-I receptor - having
PT neutralising activity against human type I interferon, used for
PT therapy and diagnosis
PS Disclosure; Fig 3; 21pp; English.
CC Monoclonal antibodies produced against soluble forms of the human
CC interferon alpha-beta receptor based on the full-length human IFN-R
CC sequence are claimed. The antibodies are useful for treatment and
CC prophylaxis of disorders involving cell proliferation and/or viral

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CC Infection.
50 Sequence 557 AA:

alignment_scores:
Quality: 2313.00 Length: 436
Ratio: 5.305 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-240-675-1 x R42635

Align seg 1/1 to: R42635 from: 1 to: 557

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1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValAla 17
77 CCCATGGGTGTGTCCGACGCGCAGCGTGAATAATCTATCTC 126
17 yProTrpValLeuSerAlaAlaValGlyLysAsnLeuLysSerProG 34
127 AAAAGTAGAGTCGACATCATGATGACACTTATCCTGAGGTGAG 176
34 LbLysValGluValAspLeuLeuAspAspAspPheLeuValGlyTrpAsn 50
177 AGGAGCATGAGTCTGCGGAGATGACTTTTCATTCGATTCACAA 226
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTrpGlnLys 67
227 AACTGGGATGATTAATGATAAATTTGCTGGGTCTCAGAAATATTACTA 276
67 sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS 84
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377 TGACATCATTTACACATTTGCGAAGCTCAGATTGCTCTCCAGAAAGTAC 426
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167 uLeuIleTrpLysAsnSerSerGlyValGluGluArgIleGluAsnIle 184
577 ATTCGAGACATAAATTTAATTAACCTGCACAGACAGACTACTATTGCTA 626
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627 AAGATTAAAGCAGACTACTATGATGATGAAAAATGGTGTCTATAGTCC 676
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677 AGTACATTTGATTAAGACACAGCTTGAATAATGAACTCCACGAGAAA 726
217 oValHISCYsIleLysThrThrValGluAsnGluLeuProProGluVal 234
727 ATATAGAAAGTCAGTGCAGAAATCAGAAATATGTTCTTAATGGATTA 776
234 snIleGluValSerValGlnAsnGlnAsnTrpValLeuLysTrpAspTrp 250

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267 sArgAsnProGlyAsnHisLeuTrpLysTrpLysGlnIleProAspCysG 284
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301 GlyIleTrpLeuValArgValGlnAlaSerAspGlyAsnAsnThrSerPh 317
977 TTGCTGTGAAGATGAAGTTGATACAGAAATACAACTTTCACACTTC 1026
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1027 CTCACGCTTTTACATTAGATCCCTTAGTATTCATTCATTCATATAC 1076
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367 uIleTrpGluIleIlePheTrpGluAsnThrSerAsnAlaGluValLysI 384
1177 TTATCGAGAAAAAACTGATGTATGACAGTCTCAATTTGAAACACTGACT 1226
384 lIleGluLysLysThrAspValThrValProAsnLeuLysProLeuThr 400
1227 GATATATGTTGTAAGCCAGACACACACACATGATGAAAGCTGAATA 1276
401 ValTyrcysValLysAlaArgAlaHisThrMetAspGluLysLeuAsnLys 417
1277 AAGCAGTCTTTTATGACGCTGATGTCAGAGAAACAAACAGAGAAATA 1326
417 sSerSerValPheSerAspAlaValCysGluLysThrLysProGlyAsnT 434
1327 CCTCTAAA 1334
434 hTrSerLys 436
seq_name: A_Geneseq_36:R75356
seq_documentation_block:
ID R75356 standard: Protein: 557 AA.
AC R75356:
DT 16-OCT-1995 (first entry)
DE Human IFN receptor.
KW IFN receptor; Interferon receptor; Interferon-alpha;
KW Interferon-beta; monoclonal antibody; immunomodulator; AIDS.
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 1..436
FT /label= Extracellular_domain
PN W09507716-A.
FD 23-MAR-1995.
FE 16-SEP-1994; E03114.
PR 17-SEP-1993; EP-402279.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
PI Benizri EJ, Tovey MG;
DR WPI: 95-131187/17.
DR N-PSDB: 086458.
PT Compn. of monoclonal antibodies against Interferon receptor
PT useful as immuno-modulator, eg. for treating AIDS
PS Disclosure: Fig. 3A-2B; 105pp; English.

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CC The amino acid sequence of human Interferon class I receptor is
 CC given in R75356. A recombinant soluble form of the extracellular
 CC domain of this receptor (R71723) has been used to raise
 CC immunomodulatory monoclonal antibodies.
 SQ Sequence 557 AA:

Alignment_scores:
 Quality: 2309.00 Length: 436
 Ratio: 5.296 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 99.771

alignment_block:
 US-09-240-675-1 x R75356

Align seg 1/1 to: R75356 from: 1 to: 557

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1 MetMetValValLeuLeuGlyAlaThrThrValLeuValAlaValAl 17
77 CCCATGGGTGTTCGCGGCGGAGTGGAAAAATCTAAATCTCTC 126
17 yProTrrValLeuSerAlaAlaGlyGlyLysAsnLeuLysSerProG 34
127 AAAAAGTAGAGTCGACATCATAGATGACAACATTATCTGAGGTGAAC 176
34 LnlYsValGluValAspIleIleAspAspAsnPhelIleLeuArgTrrAsn 50
177 AGGAGCATGAGTGTGCGGAATGTGACTTTTCATTGATTCATAAA 226
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTrrGln 67
227 AACTGGATGGATTAATGGATAAATGTCTGGGTGCAGAAATTTACTA 276
67 sThGlyMetCaspAsnTrrPheLysLeuSerGlyCysGlnAsnIleThrS 84
277 GTACCAAAATGCACCTTTCTTCTACTCAAGCTGAATGTTTGAAGAATT 326
84 eThrLysCysAsnPheSerSerLeuLysLeuAsnValTrrGluGlnIle 100
327 AAATGGCTTAAAGACGAAAAAACAATCTTCTTCAATGATGATGAGT 376
101 LysLeuArgIleArgAlaGlnLysGlnAsnThrSerSerTrrPrrGln 117
377 TGACTCATTTACACCATTTGCGAAAGCTGATGGTGCCTCCGGAATAC 426
117 LAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluValH 134
427 ATTAGAAGCTGAAGATAGCAATAGTATACATCTCTCTGAGACA 476
134 LsLeuGlnAlaGlnAspLysAlaIleValIleHisIleSerProGlyThr 150
477 AAAGATAGTGTATGTGGCTTGGATGGTTTAAAGCTTACATATAGCTT 526
151 LysAspSerValMetTrrPalaLeuAspGlyLeuSerPheThrTrrSerLe 167
527 ACTTATCTGAAAAAATCTCTCAGGTGAGAGAAAGATGGAATATTT 576
167 uLeuIleTrrPrrLysAsnSerSerGlyValGlnGluValGlyIleGlnAsn 184
577 ATTCAGACATAAAATTTATTAACCTCTCACAGAGACTACTATTGCTTA 626
184 YSerArgHisLysIleTrrLysLeuSerProGluTrrThrTrrTrrCysLeu 200
627 AAAGTTAAAGACACTACTACTAGTCTGAGAAAATGGTGTCTATAGTCC 676
201 LysValLysAlaIleLeuLeuThrSerTrrPrrLysIleGlyValYSerP 217
677 AGTACATTGTATTAAGACACACAGCTGAAAAATGAACACCCGCGAGA 726
217 oValHisCysIleLysThrThrValGlnAsnGlnLeuProProGlu 234

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727 ATATAGAGTCAGTGTCCAAATCAGAACTATCTTAAATGGATTAAT 776
234 snIleGluValSerValGlnAsnGlnAsnTrrValLeuLysTrrAspTrr 250
777 ACATATGCAAAACATGACCTTTCAAGTTCAGTGGCTCCAGCCCTTTTAA 826
251 ThrTrrAlaAsnMetThrPheGlnValGlnTrrPheHisAlaPhePhe 267
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267 sArgAsnProGlyAsnHisLeuTrrLysTrrPrrLysGlnIleProAspCysG 284
877 AAAATGCAAAACTACCCAGTGTCTTCTCCAAACCTTTTCCAAAA 926
284 LysnValLysTrrTrrGlnCysValPheProGlnAsnValPheGlnLys 300
927 GGAATTACCTTCTCCGCTACAGCATGTGATGAAATACACATCTTT 976
301 GlyIleTrrLeuLeuArgValGlnAlaSerAspGlyAsnAsnThrSerP 317
977 TTGGCTGAAAGATTAAGATTGATACGAAATACAGCTTCCCTACTTC 1026
317 eTrrSerGlnGlnIleLysPheAspPrrGlnIleGlnAlaPheLeuL 334
1027 CTCACGCTTTAACATTAGATCCCTAGTGAATTCATTCATATATATC 1076
334 rProValAlaPheAsnIleArgSerLeuSerAspSerPheHisIleTrr 350
1077 GGTGCTCCAAAACAGTCTGGAACACAGCCTGTGATCCAGGATTAATCACT 1126
351 GlyAlaProLysGlnSerLysAsnThrProValIleGlnAspTrrPro 367
1127 GATTTTGAAATTTATTTTGGGAAAAACACTCAATGCTGAGAGAAAA 1176
367 uIleTrrGlnIleIlePheTrrPrrLysnThrSerAsnAlaGlnArgLysI 384
1177 TTATCGAGAAAAAATGATGTATACAGTCCCAATTTGAAACACAGTACT 1226
384 IeIleGlnLysLysThrAspValThrValProAsnLeuLysProLeuThr 400
1227 GATATATGTGTGAAAGCCAGACACACACACATGATGAAAGCTGAATTA 1276
401 ValTrrCysValLysAlaArgAlaHisThrMetCaspGlnLysLeuAsn 417
1277 AAGCACTGTTTATGACGCTGTATGTGAGAAAAAACAACGAGAAATA 1326
417 sSerSerValPheSerAspPalaValCysGlnLysThrLysProGlyAsnT 434
1327 CCTCTAAA 1334
434 hrSerLys 436

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seq_name: A_Geneseq_36:W21804

seq_documentation_block:
 ID W21804 standard: Protein: 557 AA.
 AC W21804:
 DT 23-SEP-1997 (first entry)
 DE Transmembrane1 Interferon alpha-receptor.
 KW Interferon alpha-receptor; IFNAR.
 OS Homo sapiens.
 FH Key
 FT domain location/Qualifiers
 FT /label= Extracellular_domain
 FT /label= 437..457
 FT /label= Transmembrane_domain
 FT /label= 458..557
 FT /label= Intracellular_domain
 AU9475977-A.
 PD 11-MAY-1995.
 PF 20-OCT-1994: 075977.
 PR 24-OCT-1993: IL-107378.
 PA (YEDA) YEDA RES & DEV CO LTD.

PA (ABRA) ABRAMOVICH C.
 PI Abramovich C, Ratovitski E, Revel M:
 DR MPI: 95-200634/27.
 PR New mammalian soluble interferon alpha-receptor forms - used for
 inhibiting, modulating or modifying the activities of interferon(s)
 PT Disclosure; Fig 7; 46pp; English.
 CC Human transmembrane interferon alpha receptor (IFNAR) (W21804)
 CC includes a 21-amino acid transmembrane region. Novel, splice-
 CC deleted IFNAR forms 1 (W21805) and 2 (W21806) have been detected
 CC that lack this transmembrane domain. These, soluble non-membrane
 CC bound polypeptides can be expressed in host cells and used to
 CC inhibit, modulate or modify the activities of interferons alpha
 CC and beta in cells, tissues and organisms, or for diagnostic
 CC purposes.
 SO Sequence: 557 AA.

Alignment scores:

Quality: 2308.00 Length: 436
 Ratio: 5.306 Gaps: 0
 Percent Similarity: 99.771 Percent Identity: 99.771

Alignment block:

US-09-240-675-1 x W21804

Align seg 1/1 to: W21804 from: 1 to: 557

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1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGly 17
77 CCATGGGCTGTTCGCGACCGGAGGTGAAAAATCTAAATCTCTC 126
|||||
17 ProTTPValLeuSerAlaAlaAlaGlyGlyValAsnLeuSerProG 34
127 AAAAGTAGAGTGCACATCATAGATGACAACTTATCTGAGGTGAAC 176
|||||
34 InlyValGluValAspIleIleAspAspAsnPhelIleLeuArgTyrAsn 50
177 AGAGCGATAGTCTCTGGGAAATGTACTTTTCATTCGATTATCAAA 226
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGln 67
227 AACTGGATGATTAATGATTAATGATGCTGGGTGACAAATTTACTA 276
|||||
67 StrArgMetAspAsnTyrIleLeuSerGlyCysGlnAsnIleThrS 84
277 GTACCAATGCAACTTTCTTCTCACTCAAGCTGATGTTTATGAAGAATT 326
|||||
84 erThrLysCysAsnPheserSerLeuLysLeuAsnValTyrGlnGluIle 100
327 AATTGCGTATAGACGAGAAAAAGAAACACTTCTTCATGTAGTAGGT 376
|||||
101 LysLeuArgIleArgGlnGlnLysGlnAsnThrSerSerTyrPyrGln 117
377 TGACTATTACACCAATTCGCAAGCTCAGTGGTCCCTCCGAAATAC 426
|||||
117 LaspSerPheThrProPheArgLysAlaGlnIleGlyProGlnValH 134
427 ATTAGAAGCTGAGATAGGCAATAGTATACATCTCTCGAGACA 476
|||||
134 IsteGlnIleGlnIleAspLysAlaIleValIleHisIleSerProGlyThr 150
477 AAAGATAGTATTATGCGCTTGGATGTTTAACTTAACTTAACTTAACTT 526
|||||
151 LysAspSerValMetTyrPalauAspGlyLeuSerPheThrTyrSerIle 167
527 ACTTACTGGAAGAAACCTCTCAGGTGAGAGAAAGATGAAGAAATTT 576
|||||
167 uLeuIleTyrPylAsnSerSerValGlnGlnIleGlnIleGlnIleGlnIle 184
577 ATTCGACACTAAATTTATTAATCTCACAGAGACTACTTATTTGCTCA 626
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184 YrSerArgHisLysIleTyrLysLeuSerProGlnThrThrTyrCysLeu 200
627 AAAGTTAAACACACACTTACTACGTATGGAATAATGGTGTCTATAGTCC 676
|||||
201 LysValLysAlaAlaLeuLeuThrSerTyrPylGlyValTyrSerPyl 217
677 AGACATGTTGATTAAGCCCACTTGAATAAGTAACATCCACCAAGAA 726
|||||
217 OValHisCysIleLeuThrThrValGlnGlnGlnLeuProProGln 234
727 ATATGAGACAGCTGTCCAAATCAGAACTATGTTCTTAAATGAGATTAT 776
|||||
234 snIleGlnValSerValGlnAsnGlnAsnTyrValLeuLysTyrPyl 250
777 ACATATGCAAACTACACTTTCAAGTCAAGTGGCTCCAGCGCTTTTAA 826
|||||
251 ThrTyrAlaAsnMetThrPheGlnValGlnTyrPheHisIleAlaPheLeu 267
827 AAGGAATCCGTGAAACCATTTGTATAAATGGAACAAATACCTGACTGT 876
|||||
267 StrArgSerProGlyAsnHisLeuTyrLysTyrPylGlnIleProAspG 284
877 AAAATGCAAACTACCCAGTGTCTCTCCCAAAACGTTTCCAAAAA 926
|||||
284 LysnValLysThrThrGlnCysValPheProGlnAsnValPheGlnLys 300
927 GGAATTTACCTTCTCGCGTACAGCATGTGATGAAATACACATCTTT 976
|||||
301 GlyIleTyrLeuLeuArgValGlnAlaSerAspGlyAsnAsnThrSerP 317
977 TTGCTGAGAGATTAAGTTGATCTGAAATACAAAGCTTCTCTCTC 1026
|||||
317 erTPSerGlnGlnIleLysPheAspThrGlnIleGlnAlaPheLeuLeu 334
1027 CTCAGCTCTTAACTTAGATCCCTTAGTATGATTCATTCATATATATC 1076
|||||
334 roProValPheAsnIleArgSerLeuSerAspSerPheHisIleTyrIle 350
1077 GGTGCTCAAAACAGTCTGGAACAGCGCTGTATCCAGGATTAATCCACT 1126
|||||
351 GlyAlaProLysGlnSerGlyAsnThrProValIleGlnAspTyrProle 367
1127 GATTATGAATATTTTGGGAAAACTCAATAGCTGAGAGAAAAA 1176
|||||
367 uIleTyrGlnIleIlePheThrPylAsnThrSerAsnAlaGlnVal 384
1177 TTATCGAAAAAAACTGATGTACAGTTCCTTAATTTGAAACACAGTACT 1226
|||||
384 IeIleGlnLysLysThrAspValThrValProAsnLeuLysProLeuThr 400
1227 GATATGTGTGAAAGCCAGACAGACACACCATGATGAAAGCTGAATTA 1276
|||||
401 ValTyrCysValLysAlaArgAlaHisThrMetAspGlnLysLeuAsn 417
1277 AAGCACTGTTTATGAGCGCTGATGATGAGAAAAAACCAGGAAAAA 1326
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417 sSerSerValPheSerAspAlaValCysGlnLysThrLysProGlyAsn 434
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434 HiserLys 436

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seq name: A.Geneseq_36:R71723

seq documentation block:

ID R71723 standard; Protein; 436 AA.

NC R71723

DT 16-OCT-1995 (first entry)

DE IFN receptor extracellular domain.

KW IFN receptor; interferon receptor; interferon-alpha;

OS interferon-beta; monoclonal antibody; immunomodulator; AIDS.

PN MO507716-A.

PD 23-MAR-1995.
 PF 16-SEP-1994: E03114.
 PR 17-SEP-1993: EP-402279.
 PA (EUBI-), LAB EURO BIOTECHNOLOGIE SA.
 PI Benizri EJ, Tovey MG;
 DR WPI: 95-131187/17.
 DR N-PSDB: 086457.
 PT Compn. of monoclonal antibodies against interferon receptor
 PT useful as immuno-modulator, eg. for treating AIDS
 PS Disclosure: Fig. 2A-2B; 105pp; English.
 CC A recombinant soluble form of the human interferon class I receptor
 CC protein extracellular domain, given in R71723, was expressed in
 CC either E. coli or COS cell hosts. The protein was used to raise
 CC immunomodulatory monoclonal antibodies.
 SQ Sequence 436 AA;

Alignment_scores:
 Quality: 2304.00 Length: 436
 Ratio: 5.284 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 99.312

alignment_block:
 US-09-240-675-1 x R71723

Align seg 1/1 to: R71723 from: 1 to: 436

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77 CCCATGGGTGTCGCCGCGCGCGGTGGAATAATCTAAATCTCTC 126
17 YProTrpAlaLeuSerAlaAlaAlaGlyLysAlaLeuLysSerProG 34
127 AAAAGTAGAGTGCATCATAGATGACAACTTATCTGTGGTGGAG 176
34 LInyValGluValAlaSerAlaLeuAlaGlyLysAlaLeuLysSer 50
177 AGAGCGATGAGTGTGCGGAGTGTGCTTTCATTCGATTAACAAA 226
51 ArgSerAspGluSerValGlyAlaValThrPheSerPheAspTyrGlu 67
227 AACGGGATGATATTTGGATTAATTTGTCGGGTGTGAGAAATTA 276
67 SThrGlyLeuAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleTr 84
277 GTACCAATGCAACTTTCTCAGCAAGTGAATGTTATGAGAATTT 326
84 eTrhLysCysAsnPheSerSerLeuLysLeuValTyrGluGluIle 100
327 AAATTGCTATPAGACAGAAAAAGAAACCTTCTCATGAGTATGAG 376
101 LysLeuAlaGlyIleArgAlaGluLysGlnAsnThrSerSerTrpTyr 117
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117 LAspSerThrThrProPheArgLysAlaGlnIleLysProProGluVal 134
427 ATTAGAAGCTGAAGATAGCAATAGTATGATACATCTCCGAGACA 476
134 LsLeuGluAlaGluLysLysAlaIleValIleHisIleSerProGlyThr 150
477 AAAGTATAGTGTATGCGCTTTGGATGTTAAGCTTATACATATAG 526
151 LysAspSerValMetTrpAlaLeuAspGlyLeuSerPheTrpTyrSer 167
527 ACTATATCGAAAAACCTCTCAGGTGTAGAGAAAGATTAATAATTT 576
167 uLeuIleTrpLysAsnSerSerGlyValGluGluLysIleGluAsnIle 184
577 ATTCGAGATAAATTTATTAACCTCTCAGAGAGACTTATATGTCTA 626

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184 YrSerArgHisLysIleTyrLysLeuSerProGluThrThrTyrCysLeu 200
627 AAAGTAAAGCAGCAGTACTTACTCATGGAATAATGGTGTATAGTCC 676
201 LysValLysAlaAlaLeuLeuThrSerTrpLysIleLysValTyrSer 217
677 AGTACATGTATTAAGACACAGTGAATAATGAATCTCCACACAGAAA 726
217 oValHisCysIleLysThrThrValGluAsnGluLeuProProGlu 234
727 AATAGAAGCAGGCTCCAAATCAGAAATGATGCTTAATGGAGTAT 776
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777 ACATATGCAAAACATGACCTTTCAAGTTCAGTGGCTCCAGCCCTTT 826
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927 GGAATTCCTCTCCGCTACAGCATCTGATGAAATATACATCTTT 976
301 GlyIleTyrLeuLeuArgValGlnAlaSerAspGlyAsnAsnThrSer 317
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1127 GATTATGAATTTATTTTGGGAAAAACATTCAAATGCTGAGAGAAAA 1176
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1177 TTATCGAGAAAAAACATGATGTATACAGTCTCAATTTGAACACAG 1226
384 LelIleGluLysLysThrAspValThrValProAsnLeuLysProLeu 400
1227 GTATATTTGTGAAAGCAGACAGCAGCAGCATGATGAAAGTGAATA 1276
401 ValTyrCysLeuLysAlaArgAlaHisThrMetAspLysLeuAsn 417
1277 AAGAGGTGTTTATGATGACCTGTATGTGAGAAAAACAAACAGGAATA 1326
417 sSerSerValPheSerAspAlaValCysGluLysTrpLysProGlyAsn 434
1327 CCTCTAAA 1334
434 HisSerLys 436

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seq_name: A_Geneseq_36:W21805

seq_documentation_block:
 ID W21805 standard; protein; 434 AA.
 AC W21805:
 DT 23-SEP-1997 (first entry)
 DE Spliced-deleted interferon alpha-receptor form 1.
 KW Interferon alpha-receptor; IFNAR.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT domain 1..427

FT /label- Extracellular domain
FT /note- "comprises amino acids 1-427 of the
FT transmembrane IFNAR"
FT 428..434
FT domain /label- S_domain
PD AU9475977-A.
PN 11-MAY-1995.
PF 20-OCT-1994: 075977.
PA 24-OCT-1993: IL-107378.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (ABRAV) ABRAMOVICH C.
PI Abramovich C, Ratovitski E, Revel M;
DR MPI: 95-200634/27.
PT New mammalian soluble interferon alpha-receptor forms - used for
PT inhibiting, modulating or modifying the activities of interferon(s)
PS Example 2; Fig 7; 46pp; English.
CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 1
CC (W21805) is characterised by a new domain (S) which follows an
CC end-deleted extracellular domain when compared to transmembrane
CC IFNAR (W21804). There is no transmembrane domain. The amino acid
CC sequence is predicted from a cDNA clone (see also T73520) obtd.
CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR
CC splice-deleted forms 1 and 2 (see also W21806) probably regulate
CC the response of human cells to IFNs, either by acting as IFN
CC antagonists or by regulating the activity of the multiple IFN
CC subtypes. They can be expressed in host cells and used to inhibit,
CC modulate or modify the activities of IFNs alpha and beta in cells,
CC tissues and organisms, or for diagnostic purposes.
SQ Sequence 434 AA;

alignment_scores:
Quality: 2260.00 Length: 427
Ratio: 5.305 Gaps: 0
Percent Similarity: 99.766 Percent Identity: 99.766

alignment block:
US-09-240-675-1 x W21805

Align seq 1/1 to: W21805 from: 1 to: 434

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1 MetMetValValLeuLeuGlyAlaThrThrLeuValValAlaValAlaG1 17
77 CCCATGGGTGTTCGCCAGCCGAGGTGGAATAATCTCAATCTCTCTC 126
17 YProTrpValLeuSerAlaAlaAlaGlyGlyLeuValLeuValSerProG 34
127 AAAAGTAGAGGTGACATCTATGATGACAACTTATCTGAGGTGAAC 176
34 IndValAlGluValAlaPheIleLeuPheSerPheIleLeuArgTrpAsn 50
177 AGGAGCATGAGTCTGCGGAGTGTGACTTTTCATTCGATATCAAAA 226
51 ArgSerPheLeuSerValGlyAsnValThrPheSerPheAspTrpGlu 67
227 AACTGGATGAGTAATGATTAATAATGTCTGGGTGCAGAAATATCTA 276
67 sThrGlyMetAspAsnTrpIleLeuSerGlyCysGlnAsnIlePheS 84
277 GTACCAATGCAATTTTCTTCACTCAAGCGAATGTTTATGAAGAATT 326
84 eThrTrpCysAsnPheSerSerLeuValValTrpGluGluIle 100
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377 TGACTATTACACCATTTGCAAAAGTCAGATGTTCTCCAGAAAGTAC 426
117 LAspSerPheThrProPheArgGlyAlaGlnIleGlyProProGluValH 134

427 ATTAGAAGCTGAAGATAAGCAATAGTGTATACATCTCTCTCGAAC 476
134 LsLeuGluValGluValAlaIleValIleHisIleSerProGlyThr 150
477 AAAGATAGTGTATGCGGCTTGGATGAGTTTAACTTACATAGTCT 526
151 LysAspSerValMetTrpAlaLeuAspGlyLeuSerPheThrTrpSer 167
527 ACTTATCTGAAAAAACTCTCAGGTGTAGAAAGATGAAATAATTT 576
167 uLeuIleTrpLysAsnSerSerGlyValGluGluValArgIleGluAsnThr 184
577 ATTCACACATTAATAATTATTAATCTCCACACAGACTACTTATGCT 626
184 YSerAlaGlnHisLysIleTrpLysLeuSerProGluThrTrpTrpCysLeu 200
627 AAAGTTAAACAGACACTTACTAGTCATGAAATGGTGTATGCTC 676
201 LysValLysAlaAlaLeuLeuThrSerTrpLysIleLeuValTrpSerTr 217
677 AGTACATTGTATTAAGACACACAGCTTGAAATGAACTACCTCAC 726
217 oValHisCysIleLysThrThrValGluAsnGluLeuProProGlu 234
727 ATATGAGTCACTGTCACAAATCAGACACTATGTTCTTAATGAGTAT 776
234 snIleGluValSerValGlnAsnGlnAsnTrpValLeuLysTrpAspTr 280
777 ACATATGCAAAACAGCTTCAAGTCAAGTGGCTCCAGCCCTTTTAA 826
251 ThrTrpAlaAsnMetThrPheGlnValGlnTrpLeuHisAlaPheLeu 267
827 AAGGAATCTGGAACCATTTGTATTAATGAAACAAATACGTAGTGT 876
267 sArgAsnProGlyAsnHisLeuTrpLysTrpLysGlnIleProAspCys 284
877 AAAATGCAAACTACCCAGTGTCTCTTCTCAAAAGCTTTCCAAAA 926
284 LAsnValLysThrThrGlnCysValPheProGlnAsnValPheGlnLys 300
927 GGAATTACTCTTCGCGGTACAGATGATGAGAAATACATCTT 976
301 GlyIleTrpLeuLeuTrpValGlnAlaSerAspGlyAsnAsnThrSerP 317
977 TTGGTGTGAAGATTAAGTTTGTATCTGAAATACAACTTCTCTACT 1026
317 eTrpSerGluGluIleLysPheAspThrGluIleGlnAlaPheLeuLeuP 334
1027 CTCGAGCTTTAATCATTAAGTCCCTTAGTATTCATTCATATCTAT 1076
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1077 GGTGCTCAAAAACAGCTGGAACACAGCTGTATCCAGATTAATCCAT 1126
351 GlyAlaProLysGlnSerGlyAsnThrProValIleGlnAspTrpProLe 367
1127 GATTATGAATTAATTTTGGAAAAACATTCMAATGCTGAGAGAAAA 1176
367 uIleTrpGluIleIlePheTrpLeuAsnThrSerAlaGlnAlaArgLysI 384
1177 TTATCGAAGAAAAACGTGATGTACAGTTCCTTATTTGAAACACAGT 1226
384 IleIleGluLysIleThrAspValThrValProAsnLeuLysProLeuThr 400
1227 GTATATGTGTGAAGACAGACAGACACACATGATGAAAGCTGAATA 1276
401 ValTrpCysValLysAlaArgAlaHisThrMetAspGluLysLeuAsn 417
1277 AACGAGTGTTTTATGACGCTGTATGTAG 1307
417 sSerSerValPheSerAspAlaValCysGlu 427
seqName: A_Geneseq_36:W21806

seq documentation block:

ID W21806 standard; Protein: 496 AA.
 AC W21806;
 DT 23-SEP-1997 (first entry)
 DE Spliced-deleted interferon alpha-receptor form 2.
 KW Interferon alpha-receptor; IFNAR.
 OS Homo sapiens.

FT key Location/Qualifiers
 FT domain 1. 419

FT /label= "Extracellular domain
 /note= "comprises amino acid residues 1-413 and
 422-427 of transmembrane IFNAR"
 FT 420. 496

FT domain

FT /label= "intracellular domain
 /note= "comprises amino acids 481-557 of
 transmembrane IFNAR"

PN AU9475977-A

PD 11-MAR-1995

PE 20-OCT-1994; 075977

PR 24-OCT-1993; IL-107378

PA (YEDA) YEDA RES & DEV CO LTD

PI (ABRA/) ABRAMOVICH C

DR WPI; 95-200634/27

PT New mammalian soluble interferon alpha-receptor forms - used for
 PT inhibiting, modulating or modifying the activities of interferon(s)
 PS Example 3; Fig 7; 46pp; English.

CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 2

CC (W21806) is characterised by a double deletion when compared to

CC transmembrane IFNAR (W21804). The extracellular domain is

CC shortened by 6 amino acid residues and is followed by a truncated

CC intracellular domain. There is no transmembrane region. The amino

CC acid sequence is predicted from a cDNA clone (see also T73521) obtd

CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR

CC splice-deleted forms 1 (see also W21805) and 2 may regulate the

CC response of human cells to IFNs, either by acting as IFN

CC antagonists or by regulating IFN activities. They can be expressed

CC in host cells and used to inhibit, modulate or modify the

CC activities of IFNs alpha and beta in cells, tissues and organisms,

CC or for diagnostic purposes.

SO Sequence 496 AA.

alignment scores:

Quality: 2208.00 Length: 427
 Ratio: 5.282 Gaps: 1
 Percent Similarity: 97.892 Percent Identity: 97.892

alignment block:

US-09-240-675-1 x W21806

Align seg 1/1 to: W21806 from: 1 to: 496

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 1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGly 17
 77 CCCAAGGCTGTGCTCCGCGAGCGAGTGAAGAAAATCTAAATCTCTCC 126
 17 yProTyrPalleuSerAlaAlaAlaGlyGlyAlaSerLeuLeuSerProG 34
 127 AAAAAGTAGAGGTGACATCATGATGACAACTTATCTGAGGTGAGAC 176
 34 InLysValGluValAlaSerPheIleAspAspPheIleLeuArgTyrPasn 50
 177 AGGACGATGAGTCTGCGGGAATGCTTTTATCTGATATCAAAA 226
 51 ArgSerAspGlnSerValGlyAlaValThrPheSerPheAspTyrGlnLys 67
 227 AACTGGATGATATGATGATAAATGCTGCGGTGACAAATATATTA 276
 67 sThrLysMetAspAsnTyrPheIleLysSerGlySerGlnAsnIleThrS 84

277 GTACCAATGCAACTTTCTTCACTCAAGCTGATGTTATGAGAAAT 326
 84 erThrLysCysAsnPheSerSerLeuLysLeuValTyrGlnGlnIle 100
 327 AATTCGCTTAAAGACAGAAAAAAGAAACCTTCTTCATGATAGAG 376
 101 LysLeuArgGlyLeuArgAlaGlnLysGlnAsnThrSerSerTyrPyrGln 117
 377 TGACTCATTCACACATTTCCAAAGCTCAGATGCTGCTCCGAAAGTAC 426
 117 LysSerPheThrProPheArgLysAlaGlnIleGlyProProGlnValH 134
 427 ATTGAGAGCTGAAGATAGCAATAGTATGATACATCTCTCTGAGACA 476
 134 LysLeuGlnAlaGlnAlaPlyAlaIleValIleHisIleSerProGlyThr 150
 477 AAGATAGTGTATGAGGCTTGGATGTTAAGCTTACATATAGCTT 526
 151 LysAspSerValMetTyrPalaLeuAspGlyLeuSerPheThrTyrSerIle 167
 527 ACTATCTGGAAGAAACCTCTCAGGTGAGAAAGAGATGAAATATTT 576
 167 uLeuIleTyrLysAsnSerSerGlyValGlnGlnArgIleGlnAsnThrT 184
 577 ATTCCAGACATAAATTTATTAACCTCTCACCAGACACTTCTTGTCTA 626
 184 ySerArgHisLysLysIleTyrLysLeuSerProGlnThrTyrCysLeu 200
 627 AAGTTAAGCAGACACTTACTGATGATGAAATAGGTGTCTATAGTCC 676
 201 LysValLysAlaAlaLeuLeuThrSerTyrPlyIleLysValTyrSerP 217
 677 AGTCATGTTATTAAGACACAGTGAATGAACTACCTCCACAGAA 726
 217 oValHisCysIleLysThrThrValGlnAsnGlnLeuProProGln 234
 727 ATATAGAGAGCTAGTCCAAATCAGAACTATGTTCTTAATGGATAT 776
 234 snIleGlnValSerValGlnAsnGlnAsnTyrValLeuLysTyrPaspTyr 280
 777 ACATATGCAACATGACCTTCAAGTCACTGCTCCACCCCTTTTAA 826
 251 ThrTyrAlaAsnMetThrPheGlnValGlnTyrPheHisIleAlaPheLeu 267
 827 AAGGAATCTGGAACCATTTGATTAATGAAACAAATACCTGACTGTG 876
 267 sArgAsnProGlyAsnHisLeuTyrLysTyrPlyGlnIleProAspCysG 284
 877 AAATGTCAAACTACCCAGTGTGCTTCTTCCAAAACGTTTCCAAA 926
 284 LysAsnValLysThrThrGlnCysValAlaPheProGlnAsnValPheGln 300
 927 GGAATTAACCTTCTCCGCGTACAGCATCTGATGAAATTAACACTTT 976
 301 GlyIleTyrLeuLeuArgValGlnAlaSerAspGlyAsnAsnThrSerP 317
 977 TTGCTGAGAGATTAAGTTGATGACTGAAATACAAAGCTTCTCTCTC 1026
 317 etPserGlnGlnIleLysPheAspThrGlnIleGlnAlaPheLeuLeuP 334
 1027 CTCGAGCTTTAACATTAGATCCCTTAGTATTCATTCATCATATATC 1076
 334 ropProValPheAsnIleArgSerLeuSerAspSerPheHisIleTyrIle 350
 1077 GGTCTCCAAACAGCTGGAACAGCCGTGATCCAGATATATCAACT 1126
 351 GlyAlaProLysGlnSerGlyAsnThrProValIleGlnAspTyrProLe 367
 1127 GATTATGAATATATTTTGGAAAAACACTTCAATGCTGAGAGAAAA 1176
 367 uIleTyrGlnIleIlePheThrProLysAsnThrSerAsnAlaGlnArgLys 384

1177 TTATCGGAAAAAAGTATGATGCTTCTATTTGAACACAGTACT 1226
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 384 lletleulyslysthrasvalthrvalproasnlleulysprolethr 400
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 1227 GTATTATGTGTGAAGCCAGACGACACCATGATGATAAGCTGATTA 1276
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 401 ValTTCysVallylsAlaArgAlaHstHrMetAspLuu..... 413
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 1277 AAGCAGCTTTTATGACGCTGATGTGAG 1307
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 414SerAspAlaValCysGlu 419

seq_name: A.Geneseq_36:W52296

seq_documentation_block:
 ID W52296 standard; Protein: 325 AA.

AC W52296;
 DT 23-JUN-1998 (first entry)
 DE CRFB4 protein.
 KW CRFB4, interleukin-10, IL-10, IL-10 receptor; allograft rejection;
 KW vaccine; photosensitivity; inflammation; autoimmune disease;
 KW septic shock; immune response; organ rejection; gene therapy.
 OS Homo sapiens.
 PN W09802542-A1.
 PD 22-JAN-1998.
 PF 17-JUL-1997: U12455.
 PR 17-JUL-1996: US-683743.
 PA (UINE-) UNIV NEW JERSEY.
 PI Kolenko SV, Pestka SJ.
 DR MPI: 98-110590/10.
 N-PSDB: V19874.
 PT New recombinant DNA - comprises sequences encoding interleukin-10
 and CRFB4 linked to operator, useful, e.g. preventing allograft
 rejection.
 PS Claim 2: Page -: 79pp; English.
 CC This sequence is the human CRFB4 sequence, DNA encoding it is used in the
 CC recombinant DNA (1) of the invention. (1) comprises a sequence (S1)
 CC encoding the interleukin-10 (IL-10) receptor (IL10R) and a sequence (S2)
 CC encoding CRFB4, both operably linked to expression control sequences.
 CC Cells containing (1) may be used to identify agonists/antagonist of
 CC IL-10. Agonists are potentially useful, e.g. for preventing allograft
 CC rejection, as vaccine adjuvants, for treatment of photosensitivity,
 CC inflammation, autoimmune disease and septic shock, while antagonists are
 CC potentially useful for increasing immune responses against tumours,
 CC viruses, bacteria and parasites (especially intracellular pathogens) and
 CC for preventing organ rejection. A vector containing (1) is used to
 CC restore, e.g. by gene therapy, IL-10 sensitivity to a cell that expresses
 CC a dysfunctional IL10R and is able to bind IL-10 but not to transduce a
 CC signal. Antisense CRFB4 sequences (especially ribozymes), can inhibit
 CC IL-10 activity in cells. Antibodies specific for CRFB4 are used to
 CC measure and localise CRFB4, for diagnosis of defective IL-10 activity.
 CC Fragments of (1) are used as primers or probes to assay CRFB4-specific
 CC RNA. Agonists/antagonists may be administered parenterally, orally or
 CC rectally, especially by intravenous injection or directly into a tumour or
 CC allograft.
 SQ Sequence 325 AA.

alignment_scores:
 Quality: 228.50 Length: 224
 Ratio: 1.693 Gaps: 8
 Percent Similarity: 60.268 Percent Identity: 29.911

alignment_block:
 US-09-240-675-1 x W52296

Align seg 1/1 to: W52296, from: 1 to: 325

81 TGGGTGTGTCGCGACCGCGAGTGAATAATCTAAATCT..... 122
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 3 Trpserleuglysertrpleuglyglycylserleuvalseralaleugl 19
 |||||
 123CCTCAAAAAGTAGAGCTGCATCATATGATGACAACT 159

19 ymetValProProGloGluAsnValArGmetLysSerValAspPheLysA 36
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 160 TTATCGTGAAGTGAACAGAGACGATGACTGCTCGGATGTGACTTTT 209
 |||||
 36 snlleuglntrprgluserproAlaPheAlaLysglLysnleutrPhe 52
 |||||
 210 TCATGTGATTAACAAAACCTGGGATGATTAATGGATTAATGTCTGG 259
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 53 ThrAlaGlnTyr.....LeuSerTyrArgIlePheGlnAspLys 65
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 260 GTGTCAGATATATTAAGTATGACCAATGCAATGTTTCTGACGCAAGCTA 309
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 65 scYsMetAsnThrThrLeuThrGluCysAspPheSer.....LeuS 80
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 310 ATGTTATGAAAGAAATTAATTCGCTATTAAGACAGAA...AAGAAAC 356
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 80 erLysTyrGluAspRstHrLeuArgValArgAlaGluPheAlaAspGlu 96
 |||||
 357 ACTTTTCATGTGATGAGTGTGACATGATTTACACCATTTGCGAAAGCTA 406
 |||||
 97 HisSerAspTyrValAsnIle...ThrPheCysProValAspAspPheX1 112
 |||||
 407 GATTGGCTCCGAGAGTACATTTAGAGCT...GAAGATTAAGGCAATG 453
 |||||
 112 eileGlyProGlyMetGluValGluValLeuAlaAspSerLeuHis 129
 |||||
 454 TGATACACATCTCTCCGACAAAGAAATAGTGT...ATGTGGCTTGG 500
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 129 eLarPheLeuAlaProLysIleGluAsnGluTyrGluThrTrpHrMet 145
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 501 GATGCTTA.....AGCTTTACATATGCTTACTTATCTGAAACATC 544
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 146 LysAsnValTyrAsnSerTrpThrTyrAsnValGluTyrTrpLysAsnI 162
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 545 TTGAGGTGTGAAGAAAGGATTAATAATTTATTCAGACATTAATTT 594
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 162 yThrAspGluLysPheGlnIleThrProGlnTyrAspPheGluValLeu 179
 |||||
 595 ATTAAGTCTCACAGAGACTTATGCTTAATAAGCTTAAGCAGCAGCTA 644
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 179 rGsnLeuGluProTrpThrThrTyrCysValGlnValArgGlyPheLeu 195
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 645 CTTACGTGATGAAATGCTGTCTATGTCACGATCATTTGATAAGAC 694
 |||||
 196 ProAspTyrGsnLysAlaGlyIleTrpSerGluProValCysGluGln 212
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 695 CACAGTTGAAGAAAGCACTACT 716
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 212 TrpHisAspGluThrValPro 219

seq_name: A.Geneseq_36:R75782

seq_documentation_block:
 ID R75782 standard; Protein: 332 AA.

AC R75782;
 DT 13-NOV-1995 (first entry)
 DE IFN-gamma receptor beta subunit.
 KW Interferon-gamma receptor beta subunit; muIFN;
 KW Interferon-gamma antagonist.
 OS Mus sp.
 FH Key
 FT peptide

FT Location/Qualifiers
 FT 1..18
 FT /label= Sig_peptide
 FT 19..242
 FT /label= Extracellular_domain
 FT 243..266
 FT /label= Transmembrane_anchoring_domain
 FT 267..332
 FT /label= Cytoplasmic_domain
 PN domain
 PD W09516036-A.
 PF 15-JUN-1995
 PF 07-DEC-1994: U14277.

PR 09-DEC-1993; US-164596.
 PA (AGDE/) AGDET M.
 PA (BOEH/) BOEHNI R.
 PI (HEMM/) HEMMI S.
 PI Aguet M, Boehni R, Hemmi S;
 DR MPI; 95-224321/29.
 DR N-PSDB; 090808.
 PT Novel interferon gamma receptor beta chain polypeptide - for
 treatment of inflammatory bowel disease and liver damage
 PS claim 3; Fig. 2a; 86pp; English.
 CC The IFN-gamma receptor beta-subunit encoded by a cDNA clone derived
 CC from mouse B-cells is given in R75782. Recombinant beta-subunit,
 CC pref. with the transmembrane anchoring domain deleted or
 CC inactivated and with the cytoplasmic domain deleted, may be
 CC used to treat pathological conditions associated with endogenous
 CC IFN-gamma production.
 SO Sequence 332 AA;

alignment_scores:
 Quality: 203.00 Length: 229
 Ratio: 1.471 Gaps: 13
 Percent Similarity: 60.262 Percent Identity: 30.131

alignment_block:
 US-09-240-675-1 x R75782

Align seg 1/1 to: R75782 from: 1 to: 332

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87 TTGTCGCCGAGCCGAGGTGGA.....AAAATCTAATAATCTCC 124
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16 LeuGIYAlaAlaIaSerSerProaspSerPheSerGlnLeuAlaIaPr 32
125 TCAAAAGTAGAGGTGCACATAGATAGACACTTATCTCGTAGGTGA 174
|:::|||||:|||||:|||||:|||||:|||||:|||||:|||||
32 oleuAsnProArgLeuHisLeuTyraAsnAspGlnIleLeuThrIpe 49
175 ACAGAGCGATGAGTCT.....GTCCGGAATGTGACT 206
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
49 IuproSerProSerSerAsnAspProArgProValIaIaIaGln 65
207 TTTTCATTCGATTATCAAAAACGCGATGAT..AATGGATAAAT 253
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66 TySerPhe.....IleAspGlySerTrpHisArgLeu 76
254 G.....TCTGGTGTCAAGATATTACTAGTACCAATCAACTTTCT 297
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
76 uleuGlnProAsnCysThrAspIleThrGlnThrIleCysAspLeuThr 93
298 CA.....CTCAAGCTGAATGTTATGAA..GAATTAATTCGCT 335
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93 IyGIyGIyArgLeuIleuLeuPheProHisProPheThrValPheLeu 109
336 ATAAGAGAGAGAAAAGAAAC..ACTTCTCATGCTGATGAGTTGATC 382
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
110 ValAlaAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 126
383 ATTATACACATTTGCAAGCTCAGATGTCTCCAGAA..GTACATT 429
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126 oPheGlnHisIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 143
430 TAGAAGCTGAAGATAGGCAATAGTATGACATCTCTCTGAAACAAA 479
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143 aIThrProGlyIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 159
480 GATAGTGTATAGTGGCTTGAAGCTTATACATATACATTAATCT 529
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
160 .....ValPheHisGlyAlaIaIaIaIaIaIaIaIaIaIaIa 171
530 TATCTGAAAAACTCTTCAAGGTAGAGAAAGAGATTAATAATTTAT 579
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
171 sTyIThrIuIySerGlnIuIaIaIaIaIaIaIaIaIaIaIaIaIa 188

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580 CCAGACATAAATTTAT.....AAACTCCACAGAGACTACTATTGT 623
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 188 IySerAsnSerIleValIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 204
 624 CTAAAGTTAAACACACACTA..CTTACGTCATGGAATTT..... 662
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 205 LeuGlnThrGlnIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 221
 663 GGGTCTATAGTCAGTACATGTTAATAAGCCACA 698
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 221 sGlyLeuLeuSerAsnValSerCysHisGlnThr 233

seq_name: A.Geneseq_36:W79159

seq_documentation_block:
 ID W79159 standard; Protein: 553 AA.

AC W79159;
 DT 20-NOV-1998 (first entry)
 DE Zcytor7 cytokine receptor polypeptide.
 KW Zcytor7; cytokine receptor; ligand-binding polypeptide; kidney; pancreas;
 KW type 2 cytokine receptor family; CRF2; prostate tissue; nervous tissue;
 KW agonist; cell proliferation; cell differentiation; renal disease; human;
 KW neural disease; pancreatic disease.
 OS Homo sapiens.
 FH Key
 FT Domain Location/Qualifiers
 FT 30..250 /note="extracellular (ligand-binding) domain;
 FT 275..553 /note="intracellular domain"

FT Domain W09837193-A1.
 FT 27-AUG-1998.
 PF 18-FEB-1998: U03029.
 PR 02-OCT-1997: US-943087.
 PR 20-FEB-1997: US-803305.
 PA (ZIMO) ZIMOGENTICS INC.
 PI Adams RL, Farrar TM, Jellmeberg AC, Kuo CJ, Lok S,
 PI Whitmore TE;
 DR MPI; 98-480798/41.
 DR N-PSDB; V57515.
 PT Novel human Zcytor7 DNA encodes a type 2 cytokine receptor - useful
 PT for treating renal, neural, pancreatic and prostatic diseases
 PS Claim 1; Pages 55-59; 72pp; English.
 CC This represents the Zcytor7 cytokine receptor. Zcytor7 is a ligand-
 CC binding receptor polypeptide and is a novel member of the type 2 cytokine
 CC receptor family (CRF2). An expression vector containing the Zcytor
 CC polynucleotide, operably linked to transcription promoter, a sequence
 CC encoding a transmembrane and intracellular domain, or both, and a
 CC transcriptional terminator can be used to transform host cells for the
 CC recombinant production of the polypeptide. The sequences can be used to
 CC study the Zcytor7 gene and to isolate ligands binding to it. Zcytor7 is
 CC preferentially expressed in the kidney, pancreas, prostate or nervous
 CC tissue. Agonists of Zcytor7 can be used to stimulate proliferation and
 CC differentiation of cell in these organs. The antagonists and agonists can
 CC also be used in the treatment of renal, neural, pancreatic and prostate
 CC diseases.
 SO Sequence 553 AA;

alignment_scores:
 Quality: 198.00 Length: 433
 Ratio: 0.908 Gaps: 17
 Percent Similarity: 50.346 Percent Identity: 21.016

alignment_block:
 US-09-240-675-1 x W79159

Align seg 1/1 to: W79159 from: 1 to: 553

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57 CTAGTCTCTCGCCGCGCCCATGG.....GTGTGTCGACGCCCC 100
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18 LeuLeuLeuLeuLeuAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 34

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101 AGGTGAAAAAATCTAAATCTCTCAAAAGTAGAGTCACATCATAG 150
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34 rglgly.....LeuProlyProAlaAsnIleThPheLeuSerIleA 49
    ||||| ||||| ||||| ||||| ||||| |||||
151 ATGACACATTATTCCTGAGTGAAGAGAGCGATGCTGCGG... 197
    ||||| ||||| ||||| ||||| ||||| |||||
49 snMetLysAsnValLeuGlnIleThProProGlnGlyLeuGlnVal 65
    ||||| ||||| ||||| ||||| ||||| |||||
198 AATGACCTTTTCATTCGATATACAAAACCTGGATGATTAATGAT 247
    ||||| ||||| ||||| ||||| ||||| |||||
66 LysValIleThrThrValGlnIleThrPheIleThrGlyGlnLysIle 82
    ||||| ||||| ||||| ||||| ||||| |||||
248 AAAATGCTGGGTGAGATATTAATTAAGTACCAATGCAATCTTCT 297
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82 uAsnLysSerGlnCysArgAsnLysAsnArgThrTyrCysAspLeuSer 99
    ||||| ||||| ||||| ||||| ||||| |||||
298 CACTCAAGCTGAATGTTATGAAGAAATTAATGCTATAGAGCA... 344
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99 IacIleThrSerAspTyrGlnIleGlnIleThrValLysValIle 115
    ||||| ||||| ||||| ||||| ||||| |||||
345 GAAAAAAGAAACACTTCTCATGATGATGAGTGAATTAACACATT 394
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116 TrpGlyThrLysCysSerLysTrpAlaGlnSerGlyArgPheTyrPro 132
    ||||| ||||| ||||| ||||| ||||| |||||
395 TCCCAAGCTCAGATGCTGCTCCAGAGTACATTTAGAGCTGAAGATA 444
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132 eLeuGlnThrGlnIleGlyProProGlnValAlaLeuThrThrAsp 149
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445 AGGCAATAGTATACATCTCTCCGAAACAA... 479
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149 ySerIleSerValIleLeuThrAlaProGlnLysTrpLysArgAsnPro 165
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480 .....CATAGTGTATGCGGCTTGATGATGTTAAGCTTTAC 517
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166 GlnAspLeuProValSerMetGlnGlnIleTyrSerAsnLeuLysTyr 182
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518 AATAGCTACTATCTCGAAACCTTCAGCTAGTAGAAGAGATTG 567
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182 nValSerValLeuAsnThrLysSerAsnArgThrTTPSerGlnCysVal 199
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568 AAAATATTATTCACACATTAATTAATTA...CTCTCCACAGAG 611
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199 hAspN.....HisThrLeuValLeuThrPheGlnIleProAsn 211
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612 ACTACTTATTTCTAAAGTTAAAGCAGACCTACTAGCTAGGAAAT 661
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212 ThrLeuTyrCysValHisValGlnSerPheValProGlyProArgAr 228
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662 TGGTCTATAGTCAGTACATGTTAAAGACACAGCTGAAAGAA 710
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228 gAlaGlnProSerGlnLysGlnLysAlaArgThrLeuLysAspGlnSer 245
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711 .....CTACCTCCACAGAA 725
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245 eGlnPheLysAlaLysIleIlePheTrpTyrValLeuPro... 258
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726 AATATGAGTCAAGTCCAAATAGAACTATGTTCTTAATGGATTA 775
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259 .....IleSerIleThrVal.....Ph 264
    ||||| ||||| ||||| ||||| ||||| |||||
776 TACATGCAACATGACCTTCAACT...CAGTGGCCACGCTTT 822
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264 eLeuPheSerValMetGlyTyrSerIleTyrArgTyrIleHisValGly 281
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823 TAAAGAGATCTGGAACCAATTGTAATGAAACAAATACCTGAC 872
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281 yGlnLysHisProAlaAsnLeuIle..... 289
    ||||| ||||| ||||| ||||| ||||| |||||
873 TGTGAAAAGTCAAACTACCAAGTGTCTTCTCAAAAGCTTTCA 922
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290 .....LeuIleTyrGlyAsnGlnPheAs 297
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923 AAAGGAAATTAAGTCTCTCCGGGTAACACATCTGATGAATTAACAT 972
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297 pLysArgPhePheVal.....ProAlaGlnLysIleValIleA 310
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973 CTTTGGTCTGAAAGATTAAGTTGATACGAATA.....CAA 1013
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310 snPheIleThrLeuAsnIleSerAspSerLysIleSerHisGlnAsp 326
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1014 GCCTTCTTACTCTCCAGCTTTAAACATTAGATCCCTTAGATTCATT 1063
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327 MetSerLeuLeuGlyLysSerSerAspValSerSerLeuAsnAsp... 341
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1064 CCATATCTATATCGGTGCTCCAAACAGCTGGAACAGCCTGATCC 1113
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342 .....ProGlnProSerGlnLysLeuArgProProG 352
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1114 AGGATTATCCAGTATTTATGAAT... 1139
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352 GlnGlnGlnGlnGlnValLysHisLeuGlyTyrAlaSerHisLeuMetGln 368
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1140 ATTTTGGGAAAACACTTCAATGCTGAGAGAAAAATTAAGAGAAAA 1189
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369 IlePheCysAspSerGlnGlnLysAsnThrGlnGlyThrSerPheThrGln 385
    ||||| ||||| ||||| ||||| ||||| |||||
1190 AACTGATCTT...ACAGTCTCTAATTGGAACACGACTGATAT 1232
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385 nGlnSerLeuSerArgThrIleProProAspLysThrValIleGlnTyr 401
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seq_name: A_Geneseq_36:R71035

seq_documentation_block:

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ID R71035 standard; Protein; 337 AA.
AC R71035;
DE 11-OCT-1995 (first entry)
DE Human IFN-gamma accessory factor-1.
KW Interferon-gamma; AF-1; tumour.
OS Homo sapiens.
PN W09505847-A.
PD 02-MAR-1995.
PF 22-AUG-1994; 009438.
PR 20-AUG-1993; US-110119.
PA (UTNE-) UNIV NEW JERSEY.
PI Cook JR, Donnelly RJ, Emanuel S, Kotenko S, Mariano TM;
PI Pestka S, Schwartz B, Soh J;
DR WPI: 95-106679/14.
DR N-PSDB: 084697.
PT Suppressing tumours in mammals with accessory factor 1 (AF-1) -
PT for interferon gamma, specifically induction of class I HLA
PT antigens, including use of AF-1 DNA in gene therapy
PS Disclousure; Fig 21A; 114pp; English.
CC The sequence is that of human interferon-gamma accessory factor-1.
CC Incorporation of AF-1 into immune and tumour cells re-establishes
CC normal function with elimination of malignant cells.
SO Sequence 337 AA;

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alignment_scores:

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Quality: 155.50 Length: 300
Ratio: 1.030 Gaps: 14
Percent Similarity: 50.333 Percent Identity: 22.333

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US-09-240-675-1 x R71035
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9 LeuLeuLeuLeuLeuGlyValPheAlaAlaAlaAlaAlaAlaProProAs 25
    ||||| ||||| ||||| ||||| ||||| |||||
108 .....AAAATCTAAATCTCTCAAAAGTGAAGCTGACATCATAG 150
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25 ProLeuSerGlnLeuProAlaProGlnHisProLysIleArgLeuTyrA 42
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59 ArgProValAlaTrpGlnValGlnPheLysTrpThrAspSerLys... 73
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233 GATGATTAATGGATTAATTTGCT.....GGGTGC 264
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74 .....TriphethrAlaAspIleMetSerIleGlyValAsnCysT 87
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265 AGAATATTACTAGTACCAATGCACTTTCTCA..... 299
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87 hrcInIleThrAlaThrGluCysAspPheThrAlaAlaSerProSerAla 103
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300 .....CTCAAGCTGATGTTATGAGAATTAATTCGTATAG 340
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104 GlyPheProMetLaspPheAsnVal.....ThrLeuArgLeuAr 116
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341 AGCAGAAAAAGAAAAACT...TCTTCATGATAGAGTTGACTATTTA 387
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116 galaglulenglValAlaLeuHisSerAlaTrpValThrMetProTrpPheG 133
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388 CACCAATTGCCAAGCTCAGATTGGCTCCAGAGTACATTAGAA... 434
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seq_documentation_block:
Sequence 10, Application US/08328256
Patent No. 5643749
GENERAL INFORMATION:
APPLICANT: REVEL, Michel
APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RIVOTITSKY, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
NUMBER OF SEQUENCES: 12
PREPARATION AND USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: REVEL-13
REFERENCE/DOCKET NUMBER: 25,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

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US-08-328-256-10

alignment scores: Quality: 2313.00 Length: 436
 Ratio: 5.305 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment block:
 US-09-240-675-1 x US-08-328-256-10

Align seg 1/1 to: US-08-328-256-10 from: 1 to: 557

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127 AAAAAGTGAAGGTGACATCATAGATGACAACTTATCTGAGTGGAAC 176
34 InlyValGluValAspIleIleAspAspAspHeilleuArgTrpAsn 50
177 AGGAGCGATGAGTCTGCGGGAATGCTTTTTCATTCGATTATCAAA 226
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTrpGlu 67
227 AACTGGAGTGAATTAATGATTAATTTGCTGGTCAAGATATATACCA 276
67 sthGlyMetAspAsnTrpIleLeuSerGlyGlyGlnAsnIleTrs 84
277 GTACCAAAATGCACTTTTCTCTCACTCAAGCTGAATGTTATGAGAA 326
84 erThrLysCysAsnPheSerSerLeuLysAsnValTrpGluIle 100
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117 LasPheSerHehrProPheArgLysAlaGlnIleGlyProProGluVal 134
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134 AsLeuGluAlaGlyLysAlaIleValIleIleSerProGlyThr 150
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301 GlyIleTrpLeuLeuArgValGlnAlaSerAspLysAsnTrpSer 317
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seq name: /cgn2.6/prodata/1/aa/5A.COMB.pep:US-08-471-454-2

seq documentation block:

Sequence 2, Application US/08471454

Patent No. 5731169

GENERAL INFORMATION:

APPLICANT: MOGENSEN, Knud E.

APPLICANT: UZE, Gilles

APPLICANT: LOTFALLA, Georges

TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR

TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE

TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHAYE P. C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

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 351 GYALAPROLYSGINSEKLYSNTFHPROVALILEGLIAPTYRPROLE 367
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 1177 TTATCGAGAAAAAACTGATGTACAGTCTCAATTTGAACACAGTACT 1226
 384 IALLGLULYSYSHRASPVALTHVALPROMSNULEUSYSPROLEUTH 400
 1227 GTATATGTGTGAAGCCAGACACACACCATGGATGAAGCTGAATTA 1276
 401 VALTYRCYVALLYSALHARGALHSTHMETLAPGLULYLEUSNULY 417
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 1327 CCTCTAA 1334
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seq_name: /cgn2_6/prodata/1/lae/5B_COMB.pep:US-08-471-453-2

seq_documentation_block:
 : Sequence 2, Application US/08471453
 : Patent No. 5886153

GENERAL INFORMATION:

APPLICANT: MOGENSEN, Knud E.

APPLICANT: UZE, Gilles

APPLICANT: LUTFALLA, Georges

APPLICANT: GRESSER, Ion

TITLE OF INVENTION: cDNA FRAGMENT CODING FOR THE GENE FOR

TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERBYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471.453

FILING DATE: 06-JUN-1995

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/900,642

FILING DATE: 15-JUN-1992

APPLICATION NUMBER: FR 89/13770

FILING DATE: 20-OCT-1989

ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205

REFERENCE/DOCKET NUMBER: 960-7

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

TELEX: 200797 NIXN UR

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 557 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-471-453-2

alignment_scores:
 Quality: 2313.00 Length: 436
 Ratio: 5.305 Gaps: 0
 Percent similarity: 100.000 Percent identity: 100.000

alignment_block:
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Align seg 1/1 to: US-08-471-453-2 from: 1 to: 557

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 1 METETVALVALLEULENGLYALATHRTHLEUVALLEUVALALVALGI 17
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 17 YPOTRIPVALLLEUSERALALALAGLYGLYASNULEUSYSPROG 34
 127 AAAAAATGAGGTGACATCATAGTACAACTTATTCCTGAGGTGAC 176
 34 INLYSVALGLIIVALASPILEILEASPSASPANPEILELEADRGTPASN 50
 177 AGGACGATGAGTGTGCGGGAATGTGACTTTTCATTCGATTCACAAA 226
 51 ARGSEKASPSLUSERVALGLYSNALTHRPHESERPHESAPTRYGLNLY 67
 227 AACTGGATGATTAATGGATAAATGTCTGCGGTGTCAGATATTAATA 276
 67 STHCGLYMETASPANTRIPLEYLSLEUSERGLCYSELNSNLERHS 84
 277 GTACCAATGCACTTTCTTCACCTCAAGCTGAATGTTATGAAGAAAT 326
 84 ERTHLVSCYASNPHESEKSERLEUSLEUASVALTYGLUGLUILE 100
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 377 TGACCATTTACACCATTTGCGAAAGCTCAGATTGCTCCACAAAGTAC 426
 117 IASPERPHERTHRPHOPHARGLYSALAGLILEGLYPROFROGLIUA 134
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 seq_documentation_block:
 : Sequence 11, Application US/08328256
 : Patent No. 5643749
 : GENERAL INFORMATION:
 : APPLICANT: REVEL, Michel
 : APPLICANT: ABRAMOVICH, Carolina
 : APPLICANT: RATOVITSKI, Edward
 : TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
 : NUMBER OF SEQUENCES: 12
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: BROWDY AND NEIMARK
 : STREET: 419 Seventh Street, N.W., Suite 300
 : CITY: Washington
 : STATE: D.C.
 : COUNTRY: USA
 : ZIP: 20004
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin, Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/328,256
 : FILING DATE: 24-OCT-1994
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: IL 107378
 : FILING DATE: 24-OCT-1993
 : ATTORNEY/AGENT INFORMATION:
 : NAME: BROWDY, Roger L.
 : REGISTRATION NUMBER: REVEL-13
 : REFERENCE/DOCKET NUMBER: 25,618
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 202-628-5197
 : TELEFAX: 202-737-3528
 : TELEX: 248633
 : INFORMATION FOR SEQ ID NO: 11:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 434 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
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 : Alignment scores:
 : Quality: 2265.00 Length: 427
 : Ratio: 5.304 Gaps: 0
 : Percent Similarity: 100.000 Percent Identity: 100.000
 : Alignment block:
 : US-09-240-675-1 x US-08-328-256-11
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seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-328-256-12

seq documentation block:
Sequence 12 Application US/08328256
Patent No. 5643749
GENERAL INFORMATION:
APPLICANT: REVEL, Michel
APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RAYOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
TITLE OF INVENTION: PREPARATION AND USE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Use #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: REVEL-13
REFERENCE/DOCKET NUMBER: 25,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-373-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO.: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-328-256-12

Alignment scores:
Quality: 2213.00 Length: 427
Ratio: 5.282 Gaps: 1
Percent Similarity: 98.126 Percent Identity: 98.126

Alignment block:
US-09-240-675-1 x US-08-328-256-12

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 1 MetMetValValLeuLeuGlyAlaThrThrLeuValAlaValAla 17
 77 CCCATGGGCTGTGTCGCGACCGCGAGTGGAAAAATCTAAATCTCC 126
 17 ProTrpValLeuSerAlaAlaGlyGlyLeuLeuLeuLeuSerPro 34
 127 AAAAGTATAGGTCGACATCATAGTACACTTATCTGAGGTGAGAC 176
 34 InLysValGluValAspIleIleAspAspAspPheIleLeuArgPasn 50
 177 AGAGAGATGAGTCTCTCGGATGTGACTTTTTCATTCGATTATCAAA 226
 51 ArgSerAspGluSerValGlyLysValThrPheSerPheAspGlyGln 67
 227 AACTGGGATGATTAATGATTAATTTGCTGGGTCTCAATATTACTA 276
 67 SerThrGlyMetAspAsnTrpIleLeuLeuSerGlyGlyGlnAsnIleThr 84
 277 GTACCAATGCAACTTTCTCTCAGCTGAGTGAATGTTATGAGAAAT 326
 84 ThrThrLysCysAsnPheSerSerLeuLysLeuValIleGlyGlnIle 100
 327 AATTCGCTATAGACGAGAAAAAGAAACACTTCTTCATGTATGAGGT 376
 101 LysLeuArgIleArgAlaGlyGlyGlnValThrSerSerTrpGlyGlu 117
 377 TGACTATTATACCATTTGCGCAAGCTCAGATTGGTCTCCAGAAATAC 426
 117 LaspSerPheThrProPheArgLysAlaGlnIleGlyProGlnValThr 134
 427 ATTACAGCTGAAGATAGGCAATAGTGTATACATCTCTCTGGAACA 476
 134 ILeuGluValGluValAspLysAlaIleValIleHisIleSerProGlyThr 150
 477 AAGATAGTGTATGTGGCTTGGATGGTTTAACTTATACATAGCTT 526
 151 LysAspSerValMetTrpAlaLeuAspGlyLeuSerPheThrLysSer 167
 527 ACTATCTGGAATAACTCTTCAGGTGTAGAGAAAGATGAAAAATTT 576
 167 ThrLeuIleTrpLysAsnSerSerIleValGlyGluValGlyLeuAsnIle 184
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 184 LysSerArgHisLysIleTrpLysLeuSerProGlnThrThrTrpCysIle 200
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 201 LysValLysAlaAlaLeuLeuThrSerTrpLysIleGlyValLysSer 217
 677 AGTACATGTATTAAGCAGCTGAAAAATGAACACCCACCGAGAAA 726
 217 ValHisCysIleLysThrThrValGluValGlnLeuProProGln 234
 727 ATTAGAGTCACTGTCCAAAACAGAACTATGTTAATGGATTAT 776
 234 snIleGluValSerValGlnAsnGlnAspTrpValLeuLysTrpAspTrp 280
 777 ACATATGCAAACTGACCTTCAAGTCACTGCTCCAGCGCTTTTAA 826
 251 ThrThrAlaAsnMetThrPheGlnValGlnTrpLeuHisIlePheLeu 267
 827 AAGCAATCCGGAACCATTTGATTAATGAAGAAACAAATCCGACTGG 876
 267 SerGlnProGlyAsnHisLeuTrpLysTrpLysGlnIleProAspCys 284
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 284 LysValValLysThrThrGlnCysValPheProGlnValPheGlnLys 300

927 GGAATTACCTTCTCCGCGTACAGCATCTGATGAATAACACATCTTT 976
 301 GlyIleTrpLeuLeuArgValGlnAlaSerAspGlyAsnAsnThrSer 317
 977 TTGCTCTGAAGATTAAGTTGATTAATGAAATCAAGCTTCTTACTTC 1026
 317 TrpSerGlnIleLeuLysPheAspThrGlnIleGlnIlePheLeuLeu 334
 1027 CTCCAGCTTTTAACTTATGATCCCTAGTATTCATTCATATCATATC 1076
 334 TrpValPheAsnIleArgSerLeuSerAspSerPheHisIleTrpLe 350
 1077 GGTGCTCCAAAACAGCTGTGAACACCGCTGTGATCCAGATTATCC 1126
 351 GlyAlaProLysGlnSerGlyAsnThrProValIleGlnAspTrpPro 367
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 367 ValLeuTrpIleIlePheTrpGluAsnThrSerAsnAlaGluArgLys 384
 1177 TTATCGAGAAAAAAGCTGATGATGATCCATAATTGAACCACTGACT 1226
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 1227 GTATATTGTGGAAGCCAGACACACACATGATGAAAGCTGAAATTA 1276
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seq_name: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep: PCT-US94-14277-3
 seq_documentation_block:
 : Sequence 3, Application PC/TUS9414277
 : GENERAL INFORMATION:
 : APPLICANT: Aguet, Michel
 : APPLICANT: Bonni, Ruth
 : APPLICANT: Hemmi, Silvio
 : TITLE OF INVENTION: Receptor Subunit Polypeptides
 : NUMBER OF SEQUENCES: 8
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Genentech, Inc.
 : STREET: 460 Point San Bruno Blvd
 : CITY: South San Francisco
 : STATE: California
 : COUNTRY: USA
 : ZIP: 94080
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: 5.25 inch, 360 KB floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: patin (Genentech)
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: PCT/US94/14277
 : FILING DATE: 07-DEC-1994
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/164596
 : FILING DATE: 09-DEC-1993
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Love, Richard B.
 : REGISTRATION NUMBER: 34,659
 : REFERENCE/DOCKET NUMBER: 866PCT
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 415/225-5530
 : TELEFAX: 415/952-9881
 : TELEX: 910/371-7168
 : INFORMATION FOR SEQ ID NO: 3:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 202 amino acids
 : TYPE: amino acid

TOPOLOGY: linear
PCT-US94-14277-3

Alignment scores:
Quality: 490.50 Length: 202
Ratio: 3.337 Gaps: 1
Percent Similarity: 72.772 Percent Identity: 48.515

Alignment block:
US-09-240-675-1 x PCT-US94-14277-3

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158 CTTATCCGAGGTGGACAGGAGCATGCTCGGGGAAATGACTT 207
17 ntyrthleuysrpsrserhisclyuasermetglyservalthrp 34
208 TTTGATTCGATATCAAAAAGTGCATGATTAATGATTAATGCTT 257
34 heseraleuylarghlylsasprgluarglyserpleuys**pro 50
258 GGGTGCAGAAATTTACTAGTACCAAAATCAACTTTCTCACTCAAGT 307
51 glucysglnhishthrtthrtthrtlyscysglnphserleuysph 67
308 GAATGTTTGAAGAAATTAATGCTATAGAGACAGAAAAGAAAC 356
67 rsn**tyrileysrhglnpheargvalargalaglugluglgnst 84
357 ACTTCTCAGATGATGAGTGTGACTCATTTACACCAATTCGCAAGT 404
84 erthserseptrangluvalasprphelerotheryrthala 100
405 CAGATGTCCTCCAGAGTACATTTAGAACTGGAAGATAGGCAATGAT 454
101 hsmetserprogluvalargleugluargluasprlyalalele 117
455 GATACACATCTCCTCGAAGAAAGATAGTGTATGCGGTTGGAG 504
117 uvalhishserprogluylglnasprlysnmetrpalaleugln 134
505 GTTATGCTTACATATACCTTACTATCTGAAAAAAGCTTCAGGTGA 554
134 ysrproserpheserlyrthleargilletrglnlyserseerisap 150
555 GAGAAAGATGAAATTTATTCAGACATTAATTAATTAACCTTC 604
151 lyslysrthleasnserthrtlyrvalglnlyleprogluileu 167
605 ACCAGAGTACTATGCTTAAGTAAAGTAAACACACTACTAGTCT 654
167 urprogluhtthrtlyrcysleugln**lysalleenhsproserleu 184
655 GGAATATGCTGTATAGTCCAGTACATTTATTAAGACACAGTGA 704
184 ysllyshiserasrlyserthr**glnhcylieserthrtthrtala 200
705 AATGA 710
201 asnlys 202
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seq_name: /cgr2_6/protodata/1/aa/PCTUS_COMB.dep.PCT-US94-14277-4

seq_documentation_block:

sequence 4, Application PC/TUS9414277

GENERAL INFORMATION:

APPLICANT: Aguet, Michel

APPLICANT: Bohnl, Ruth

APPLICANT: Hemml, Silvio
TITLE OF INVENTION: Receptor Subunit Polypeptides
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14277
FILING DATE: 07-DEC-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/164596
FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 866PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US94-14277-4

Alignment scores:
Quality: 466.50 Length: 208
Ratio: 3.049 Gaps: 3
Percent Similarity: 73.558 Percent Identity: 44.712

Alignment block:

US-09-240-675-1 x PCT-US94-14277-4

Align seg 1/1 to: PCT-US94-14277-4 from: 1 to: 200

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1 metprovalprogluasnleuglnvalaspraleuglnlylserlyrva 17
761 TCTTAAGGGATAT ..CATATGCAAGATGACCTTCAAGTTCAGT 807
17 lleuysrpsrpyrthleaseraleasprvalleupheargalegnt 34
808 GGGTCCAGGCGCTTTTAAAGAAATCTGGAACATTTGTATAAATGG 857
34 rleuprogluyltysrlyserseergerglyserhiserasrlystr 50
858 AACAATACTGACTGGAAGATGCAAAATCAACCCAGTGTCTTCC 907
51 lysprolleprothrcysalasnvalglntthrtthrtlyscysvalphese 67
908 TCAAGCGTTTCCAAAAGATTAACCTTCCGCGGTAAACACATCTG 957
67 rglasprhr**tyrthrglythrphneleleenisvalglalaseg 84
958 ATGAAATTAACACATTTTGTGTGAGAGATTAAGATTTGATATGAA 1007
84 lnglyasnhihshserphetrpserglugluysrphelieasprseln 100
1008 ATACAGCTTTCCTACTCTCCAGTCTTAACATTAAGATCCCTAGTGA 1057
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alignment_scores:      Quality: 228.50      Length: 224
                       Ratio: 1.693      Gaps: 8
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Alignment_block:
US-09-240-675-1 x US-08-683-743-4

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3 TtpserleuglysertripleuglyglycysleuvalseralaleuGl 19

123 .....CCTCAAAAGTAGAGGTGCACATCATAGATACAACT 155
||| |||||:||||| ||||| ||||| ||||| ||||| |||||
19 ymelvalProProProGluuValAlaGmetAsnSerValAsnphelysa 36

160 TTATCCTGAGGTGAGAACAGAGCAGCATGAGTGTGCGGAAATGACTTT 209
|||||:|||||:||||| ||||| ||||| ||||| ||||| |||||
36 snlleuclntrpcoluserProalaphelialySglYasnleuthrPhe 52

210 TCATTGCATTCAAAAAAACTGGATGATGATTAATGATAAATTGTCTGC 259
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53 ThrAlaGlnTyr.....LeuserTyrArgIlePheGlnAspIly 65

260 GGTGAGAAATNTACTACTACCAATATGCACCTTTCTCACTCAAGCTGA 309
|||||:||||| ||| |||||:||||| ||||| ||||| |||||
65 scYserAsnThrTrleuthrGlnCysAspPheSer.....Leus 80

310 ATGTTATGACGAATTAATTAAATGGCTTAAGACAGAA.....AAGAAAC 356
::: ||| ||||| ||||| ||||| ||||| ||||| |||||
80 erlyTyrGlyAspIsthrleuArgValAlaGlnAluPheAlaAspIu 96

351 ACTTCTCATGGATGAGGTGACTCATTTACACCATTTGCCAAAGCTCA 406
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97 HisSerAspTrpValAsnIle...ThrPheCysProValAspAspThrIl 112

407 GATTGCTCTCCAGACAGACTATTAGAAAGCT..GAAGTAAGCAATAG 453
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112 elledlyProGluMetGlnValGlnValLeuAlaAspSerleuHisM 129

454 TGATACACATCTCTCCGGAACAAAGATAGTGT...ATGTGGCGTTTG 500
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129 eArgPheleuAlaProCysIleGluAsnGlnTyrGlnTrpIleMet 145

501 GATGGTTA.....AGTTACTATAGCTTACTTATCTGAAAAATC 544
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146 LysAsnValIlyAsnSerTrpThrTyrAsnValGlnTyrTrpYsAsnGl 162

545 TTCAGGTGTACAGAAAGAGTGAATTAATTATTCAGACATAAAAATT 594
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162 YThrAspIuLysPheGlnIleThrProGlnTyrAspPheGlnValLeuAla 179

595 ATAAACTCTCACAGACACTACTATTATGTCTAAAGTAAAGCAGCACA 644
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179 TgAsnleuGlnProTrpThrThrTyrCysValGlnValAlaGlyPheLeu 195

645 CTTACGTCATGAAAAATGGTGTCTATAGTCCAGTCATATTGTATAAGC 694
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196 ProAspArgAsnLysAlaGlnGlyIuTrpSerGluProValCysGlnIuTh 212

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seq_name: /cgn2_6/prodata/1/1aa/PC/TUS.COMB.pep.pct-US94-14277-2
seq_documentation_block:
Sequence 2, Application PC/TUS9414277
GENERAL INFORMATION:

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ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Luuu, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELELEX:

SIREN: 1201 Eastlake Avenue East
 CITY: Seattle
 STATE: WA
 COUNTRY: USA


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seq_documentation_block:
: Sequence 16, Application US/08943087
: Patent No. 5945511
:
: GENERAL INFORMATION:
: APPLICANT: Lok, Si
: APPLICANT: Kuo, Choon J.
: APPLICANT: Jelmerig, Anna C.
: APPLICANT: Adams, Robyn L.
: APPLICANT: Whitmore, Theodore E.
: APPLICANT: Farrah, Theresa M.
: TITLE OF INVENTION: CYTOKINE RECEPTOR
: NUMBER OF SEQUENCES: 60
:
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: ZymoGenetics, Inc.
: STREET: 1201 Eastlake Avenue East
: CITY: Seattle
: STATE: WA USA
: COUNTRY: WA USA
: ZIP: 98102
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/943,087
: FILING DATE:
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/803,305
: FILING DATE: 20-FEB-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Lund, Paul G
: REGISTRATION NUMBER: 32,743
: REFERENCE/DOCKET NUMBER: 96-24C1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 206-442-6627
: TELEFAX: 206-442-6678
:
: TELEX:
: INFORMATION FOR SEQ ID NO: 16:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 553 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FRAGMENT TYPE: internal
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: US-08-943-087-16
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: alignment_scores:
: Quality: 198.00 Length: 433
: Ratio: 0.908 Gaps: 17
: Percent Similarity: 50.346 Percent Identity: 21.016
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: alignment_block:
: US-09-240-675-1 x US-08-943-087-16
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: Align seg 1/1 to: US-08-943-087-16 from: 1 to: 553
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: 101 AGGTGGAAAAATCTAAATCTCTCAAAAAGTAGAGTGCACATCATAG 150
: 34 TGIYELY.....LeuProLysProAlaAsnIleThrPheLeuSerIleA 49
: 151 ATGCAACTTATCTGAGTGAACAGACGATGAGTGTGCGG... 197
: 49 smLeuLysAsnValLeuGlnIleThrPheProPheGlnGlyLeuGlnGlyVal 65

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198 AATGACTTTTTCATTCATATCAAAAACTGGGATGATTAATGAT 247
: 66 LysValThrTyrThrValGlnIleThrPheIleTyrGlnIleValTyrPhe 82
: 248 AAAATGCTGTGGTGTCAAAATATCTAGTACCAAAATGCAATCTTCT 297
: 82 uasnLysSerGlnCysArgAsnIleAsnArgThrTyrCysAspLeuSerA 99
: 298 CACTCAAGCTGAATGTTTATGAAGAAATTAATTCGCTAAGACA... 344
: 99 IeGlnThrSerAspTyrGlnIleGlnIleTyrTyrAlaLysValLysAlaIle 115
: 345 GAAAAAGAAACACTTCTCATGTATGAGTGTGACTATTACACAT 394
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: 395 TCGCAAGCTCAGATGTCCTCCAGAACTACATTAATGAGTGAAGATA 444
: 132 eLeuGlnThrGlnIleGlyProPheGlnValAlaLeuThrThrAspGlnL 149
: 445 AGCAATAGTGAACACATCTCTCGAACA... 479
: 149 ySerIleSerValLeuValLeuThrAlaProGlnLysTyrLysArgAsnPro 165
: 480 .....GATAGCTTATGTCGCTTGATGATGTTTAAGCTTAC 517
: 166 GluAspLeuProValSerMetGlnIleTyrSerAsnLeuLysTyrAs 182
: 518 ATATAGCTTACTATCTGAGAAACCTCAGGTGAGAGAAAGATG 567
: 182 nValSerValLeuAsnThrLysSerAsnArgThrTyrSerGlnCysValT 199
: 568 AAATATTTTATTCACACATATAATTTATTA...CTCCACACAGAG 611
: 199 hAsn.....HisThrLeuValLeuThrTyrPheGlnProAsn 211
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: 662 TGGTGTATAGTCCAGTACGATGTTAAGACCAAGTGAAGAAATGA 710
: 228 gAlaGlnProSerGlnLysGlnCysAlaArgThrLeuLysAspGlnSerS 245
: 711 .....CTACCTCCACCGAA 725
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: 259 .....IleSerIleThrVal.....Phe 264
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: 823 TAAAAAGAACTCTGGAACCAATTTGTATAATGGAACAATACCTGAC 872
: 281 ySGlnLysHisProAlaAspLeuIle..... 289
: 873 TGTGAAATGTCAAACTACCAAGTGTCTTCTCAAAAGCTTTTCA 922
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: 1014 GCTTCTTACTCTCCAGTCTTTTACATTAAGTCCCTAGTATTCATT 1063

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1064 CCATATCTATATGCGTCTCCAAACAGCTCGAAACACGCTGTGATCC 1113
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352 InGIuGIuGIuValLysHisLeuGIYTyraIaSerHisLeuMetGIu 368
1140 ATTTTGGAAACACTTCAATGCTGAGAGAAAAATTATCGAGAAAA 1189
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1190 AACTGATGT.....ACAATTCTAATTGAACCACTGACTGTATAT 1232
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385 ngIuSerLeuSerArgThrIleProProAspLysThrValIleGIuTyr 401

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OM of: US-09-240-675-1 to: PIR_63: * out_format: pfs
 Date: Jun 1, 2000 5:46 PM

About: Results were produced by the Gencore software, version 4.5,
 Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

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 -O=/cgn2_1/USPTO.spool/US09240675/runat.30052000.165118.2984/app-query.fasta.1
 -DB=PIR_63 -QFT=fastan -SUFFIX=modif.rpt -GAPOP=12.000
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 -TRAN=human40.cdi -LIST=45 -DOCALLIGN=200 -THR.SCORE=Pct
 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
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Search information block:

Query: US-09-240-675-1
 Query length: 1343
 Database: PIR_63: *
 Database sequences: 168808
 Database length: 58629743
 Search time (sec): 70.990000

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PIR2:G01418	233.50	341.31	1.4e-11	273	1	Cytokine receptor family II, me
PIR2:A47003	228.50	332.32	3.8e-11	325	1	Cytokine receptor family class
PIR2:J06311	221.50	331.29	5.0e-10	349	1	Interferon receptor class II cy
PIR2:AA9947	203.00	294.19	5.0e-09	332	1	Interferon gamma receptor beta
PIR2:118500	155.50	223.36	4.3e-05	337	1	Interferon gamma receptor acces
PIR2:T13822	129.00	171.56	0.0081	1375	1	frazzled gene protein - fruit
PIR2:T13823	129.00	170.64	0.0082	1526	1	neogenin - chicken (fragment)
PIR2:150600	127.50	168.90	0.0109	1443	1	insulin receptor precursor - h
PIR2:A36080	127.00	168.53	0.0119	1383	1	interferon gamma receptor precu
PIR2:A31555	124.50	173.95	0.0168	489	1	190K protein - human
PIR2:S42167	123.50	162.90	0.0233	981	1	receptor tyrosine kinase - h
PIR2:S31604	118.00	158.15	0.0634	1005	1	interleukin-10 receptor - mouse
PIR2:A49667	118.00	157.94	0.0636	575	1	tumor suppressor - African cl
PIR2:T15169	117.50	154.11	0.0731	1427	1	probable protein-tyrosine-phos
PIR2:T19121	117.50	153.19	0.0741	1585	1	titin, muscle - chicken (fragme
PIR2:A48721	117.00	158.27	0.0749	1372	1	protein-tyrosine phosphatase -
PIR2:A41517	116.00	153.72	0.0800	1912	1	hypothetical protein FK2A10.4 -
PIR2:A56118	116.00	149.31	0.1011	1912	1	hypothetical protein FK2A10.4 -
PIR2:T16040	115.50	157.94	0.0970	658	1	165K myofibrillar M-band struc
PIR2:A44027	115.00	150.25	0.1181	1450	1	protein-tyrosine kinase (EC 2.7
PIR1:138344	113.00	124.56	0.1715	26926	1	titin, cardiac muscle - human
PIR1:0C4166	113.50	152.41	0.1475	880	1	protein-tyrosine phosphatase
PIR2:BA9502	113.00	146.33	0.1754	1615	1	protein-tyrosine phosphatase
PIR2:S46216	113.00	145.54	0.1774	1767	1	leukocyte antigen-related prot
PIR2:T77934	113.00	133.65	0.1790	1898	1	hypothetical protein ZK617.1a
PIR2:S57242	113.00	133.64	0.2109	6831	1	hypothetical protein ZK617.1b
PIR2:T27935	113.00	133.23	0.2121	7160	1	Down syndrome cell adhesion p
PIR2:708851	111.50	142.69	0.2384	1896	1	hypothetical protein T20F10.4 -
PIR2:T25036	109.00	152.30	0.3165	416	1	B6-1 protein - rat
PIR2:158164	109.50	143.30	0.3908	1028	1	hybrid receptor ScfLA precurs
PIR2:T009123	108.50	137.61	0.4264	2033	1	receptor protein-tyrosine kinas
PIR2:178843	108.00	136.85	0.4311	2215	1	insulin receptor precursor - h
PIR1:1NH0R	107.50	140.26	0.4465	893	1	receptor-like tyrosine kinase -
PIR2:S51603	107.00	143.35	0.4646	893	1	interleukin-10 receptor - human
PIR2:156215	107.00	146.43	0.4835	578	1	interleukin-10 receptor - human

PIR2:A44147 + 107.00 140.85 0.5244 1091 1 calcium channel protein
 PIR2:S47489 + 106.50 141.81 0.5627 898 1 receptor tyrosine kinase
 PIR2:A54100 + 106.00 136.88 0.6580 1447 1 tumor suppressor protein
 PIR1:AA0091 + 105.50 140.52 0.6791 878 1 interleukin-3 receptor b

seq_name: PIR2:A32694

seq_documentation_block:

Interferon alpha/beta receptor precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 22-Jun-1990 #sequence, revision 22-Jun-1990 #text_change 22-Oct-1999
 C:Accession: A32694; S17112
 R:Oze, G.; Lutfalla, G.; Gresser, I.
 Cell 60, 225-234, 1990
 A:Title: Genetic transfer of a functional human interferon alpha receptor into mo
 A:Reference number: A32694; MID:90124632
 A:Accession: A32694
 A:Molecule type: mRNA
 A:Residues: 1-557 <OZE>
 A:Cross-references: GB:J03171; NID:q184645; PIDN:AA52730.1; PID:q306914
 R:Lutfalla, G.
 Submitted to the EMBL Data Library, July 1991
 A:Description: The structure of the human interferon alpha/beta receptor gene.
 A:Reference number: S17112
 A:Accession: S17112
 A:Molecule type: DNA
 A:Residues: 1-16, 'A', 18-329, 'V', 343-557 <LUT>
 A:Cross-references: EMBL:X60459; NID:q32671
 C:Genetics:
 A:Gene: GDB:IFNAR1; IFNAR; IFRC
 A:Cross-references: GDB:120078; OMIM:107450
 A:Map position: 21q22.1-21q22.1
 A:Intons: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3
 C:Keywords: cytokine receptor; glycoprotein; transmembrane protein
 F:1-21/Domain: transmembrane #status predicted <TRN2>
 F:337-455/Domain: transmembrane #status predicted <TRN2>
 F:50/58, 81, 88, 110, 172, 254, 313, 314, 376, 416, 433, 507, 518, 537/Binding site: carbohydrate

alignment_scores:

Quality: 2313.00 Length: 436
 Ratio: 5.305 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-240-675-1 x A32694

Align: seq 1/1 to: A32694 from: 1 to: 557

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 1 Metcervallaleuenglyalatrthleuvalleuvalleu 17
 77 CCATGGGTTCCTCCGACCCGAGGTGAAAAATCTAAATCTCTC 126
 17 YPOTTPVallleuseralalalacglylysasnleuylserpro 34
 127 AAAAGTAGGTCGACATCATGAGACACTTATCTGAGGTGAC 176
 34 Inlysalgluvalleualllelleaspaspasnhelleuagtrp 50
 177 AGAGGAGTAGCTCTCGGAGATGACTTTTCATGATGATGAAA 226
 51 Argseraspjuseralglgysnvaltrhpserpheaspyglu 67
 227 AACTGGATGATTAATGATTAATAATGTCTGGGTGACGAATTA 276
 67 stringlymetaspasntripileysenserglycglasalleth 84
 277 GTACAAAGGCACTTTCTCACCACCAAGCTGAATTTTGAAGAA 326
 84 ethrlyscysasnpheserleuylsleuasnvaltryglu 100

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101 LysleuagllleuAlaGluLysGlnSerSerTrpGluVal 117
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117 LAsperPheThrProPheArgGlyAlaGlnLeuProGluVal 134
427 ATTGAGACGTAGATAGGCAATAGATACATCTCTCTGAGACA 476
134 LsleuGlnAlaGlnLysPylalileValleHisLsSerProGlyThr 150
477 AAGATAGTATGATGGCTTGGATGGTTAAGCTTACATATAGCT 526
151 LysAspSerValMetTrpAlaLeuAspGlyLeuSerPheThrTyrSerle 167
527 ACTTATCTGGAAGAACTCTTACAGCTGATAGAGAAAGATGAAATATT 576
167 uleuileTrpLysAsnSerSerGlyValGluGlnArgileGlnAsnile 184
577 ATCCGACATATAAATTTTAACTCTCAGCAGAGACTTATGCTTA 626
184 ySerTrpHisLysLysLysLeuSerProGlnThrThrTyrCysleu 200
627 AAGATTAAGCAGACACTACTAGCTATGAGAAATGGTGTATAGTCC 676
201 LysValLysAlaAlaLeuLeuThrSerTrpLysileGlyValTyrSer 217
677 AGTACATGTTATTAAGACACACATTTGAAATGAACTCTCCACAGAAA 726
217 oValHisCysileLysThrThrValGlnGlnGlnLeuProProGln 234
727 ATTTAAGCTAGCTGCCAAAACAGACATCTCTTAAAGGATTTT 776
234 snlleuValSerValGlnAsnGlnAsnTyrValLeuLysTrpAspTyr 250
777 ACATATGCAACATGACCTTCAAGTTCAGTGGCTCCAGCTTTTAA 826
251 ThrTyrAlaAsnMetThrPheGlnValGlnTrpLeuHisAlaPheLeu 267
827 AAGCAATCTCGAAGAACATTTGATTAAGGAAACAAATACCTGACTG 876
267 sArgAsnProGlyAsnHisLeuTyrLysTrpLysGlnileProAspCys 284
877 AAAATGCAAACTACCCAGCTGTCTTCCCAAAAGCTTCCAAAA 926
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927 GGAATTTACCTCTCCGCTACAGCATGTATGAAATTAACATCTT 976
301 GlyileTyrleuLeuArgValGlnAlaSerAspGlyAsnAsnThrSerP 317
977 TTGGCTGAGAGATTAAGTTTGAATGATGAAATCAAGCTTCCCTC 1026
317 eTrpSerGlnGlnileLysPheAspThrGlnileGlnAlaPheLeu 334
1027 CTCAGCTTAAATAGATCCCTTATGATTCATCATCTATCTATATC 1076
334 roProValPheAsnileArgSerleuSerAspSerPheHisileTyrile 350
1077 GGTGCTCCAAAACAGCTGGAACACGCTGTATCCAGATTAATCCAT 1126
351 GlyAlaProLysGlnSerGlyAsnThrProValileGlnAspTyrProle 367
1127 GATTATGAATTTATTTTGGGAAAAACATTAATGCTGAGGAAAA 1176
367 uileTyrGlnilelePheThrPylAsnThrSerAsnAlaGlnArgLys 384
1177 TTATCGAGAAAAAATGATGATTCATCTATTTGAACACATCTACT 1226
384 leileGlnLysLysThrAspValThrValProAsnLeuLysProLeuThr 400
1227 GTATATTTGTGTAAAGCAGACACACATGATGATGAAAAAGTGAATA 1276

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401 ValTyrCysValLysAlaArgAlaHisThrMetAspGlnLysLeuAsn 417
1277 AAGCAGCTTTTATGATGACGCTGATGATGAGAAACAAACCGGAATA 1326
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1327 CCTCTAAA 1334
434 hrserLys 436
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seq_documentation_block:
interferon alpha receptor type 1 precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S27387; S33770
R:Mouchel-Viehl, E.; Luitfalla, G.; Mogensen, K.E.; Uze, G.
FEBS Lett. 313, 255-259, 1992
A:Title: Specific antiviral activities of the human alpha interferons are determined by the amino acid sequence of the human alpha interferon
A:Reference number: S27387; MIMD:93076908
A:Accession: S27387
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-560 <MOU>
A:Cross-references: EMBL:X68443; NID:9431; PIRN:CAA48484.1; PID:9432
R:Lim, J.K.; Langer, J.A.
Biochim. Biophys. Acta 1173, 314-319, 1993
A:Title: Cloning and characterization of a bovine alpha interferon receptor.
A:Reference number: S33770; MIMD:93305725
A:Accession: S33770
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-421, V, 423-560 <LINK>
A:Cross-references: EMBL:L06320; NID:9163187; PIRN:AAA02571.1; PID:9163188
A:Experimental source: lung
A:Keywords: antiviral; cytokine receptor; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-560/Product: interferon alpha receptor type 1 #status predicted <MAT>

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Quality: 1507.00 Length: 439
Ratio: 3.987 Gaps: 6
Percent Similarity: 86.105 Percent Identity: 64.920

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alignment_block:
US-09-240-675-1 x S27387

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Align seg 1/1 to: 527387 from: 1 to: 560

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80 ATGGGCTGTGTCGCGGACGCGCAGTGGAATAAATCAATCTCTCAA 129
|||||
16 gTrpAlaLeuProAlaHisSerGlyGlnAlaAsnLeuLys..ProGln 32
130 AAGTAGAGTCAACATCATATGATGACAACTTATTCAGGTGAGGAG 179
|||||
32 snValGlnleuHisileleAspAspAsnPhePheLeuLysTrpAsnSer 48
180 AGCGATGAGTCTGTGGGAAATGATGCTTTTATTCATGATTAACAAA 229
|||||
49 SerSerGlnSerValLysAsnValThrPheSerAlaAspTyrGlnile 65
230 TGGGATGATTAATGATTAATGCTGTGCTGATGATGATTAATGATTA 279
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65 uGlyThrAspAsnTrpLysLeuSerGlyCysGlnHisileThrSer 82

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327 AATTCGCGATATAGACAGAAAA... GAAACACTCTTCATGGTATCA 373
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99 GluLeuArgIleArgIleGluGluGlnGlnAsnAsnThrSerThrTyrGlu 115
374 GGTGACATATATACACATTCGCAAGCTGAGATGGTCCGCAAG 423
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115 uValGluProPheValProPheLeuGluLeuGlnIleGlyProProAsp 132
424 TACATTAAGCTGAGATAGCAATGATATACACTCT... CCT 470
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132 AHisLeuGlnValGluAspLysAlaIleIleLeuSerIleSerPro 148
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149 GlyThrLysAspSerIleLeuThrPalaMetAspArgSerSerPheArg 165
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165 rSerValValIleTyrLysAsnSerSerLeuGluGlnArgGlnGlu 182
571 AATTTATCCAGACATAAATTTATTAACCTCTCACACAGACTCTAT 620
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721 CAGAAATATAGAGTCAAGTGTCCAAATACAGATATTTTAAAG 770
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232 rGluGlnIleGlnIleAsnAlaAspAsnGlnIleTyrValLeuLys 248
771 GATTATACATATGCAACATGACATCTTCAGTTCAGTGGCTCCAGC 820
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821 TTTTAAAGGAATCTGGAACCATTTGTATTAATGAAACAAATAC 870
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265 rPheLysLysIleProGlnLysAsnIleSerAspLysTyrGlnIle 282
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282 rSerGluGlnAsnValThrSerThrHisCysValPheProArgGlu 298
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315 rSerPheThrPheSerGluGlnLysGluPheAsnThrGluMetLys 332
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332 rPheProProValIleSerValLysSerValThrAspAspSerLeu 1348
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432 rGluLysAsnThrSerLys 437
seq_name: p1r2:A45283
seq_documentation_block:
interferon alpha/beta receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 25-Mar-1993 #sequence revision 18-Nov-1994 #text change 05-Nov-1999
C:Accession: A45283; I48423; I48424; I48425; I48426; I48427; I48428; I48429
R:Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992
A:Title: Behavior of a cloned murine interferon alpha/beta receptor expressed in J
A:Reference number: A45283; M0ID:92262522
A:Accession: A45283
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-590 <UZE>
A:Cross-references: GB:M89641; NID:g194111; PIDN:AAA37890.1; PID:g194112
A>Note: sequence extracted from NCBI backbone (NCBIN:102357)
R:Lutfalla, G.; Uze, G.
Gene 148, 343-346, 1994
A:Title: Structure of the murine interferon alpha/beta receptor-encoding gene: hL
A:Reference number: I48423; M0ID:95047447
A:Accession: I48423
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 118-125 <RS>
A:Cross-references: NID:g497103; PIDN:AAA65003.1; PID:g755810
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A>Status: preliminary; translated from GB/EMBL/DBJ
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A:Cross-references: EMBL:006239; NID:g497106; PIDN:AAA65004.1; PID:g510261
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A>Status: preliminary; translated from GB/EMBL/DBJ
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A:Accession: I48429
A>Status: preliminary; translated from GB/EMBL/DBJ
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A:Residues: 473-590 <RE7>
A:Cross-references: EMBL:006244; NID:g497114; PIDN:AAA65008.1; PID:g510265
C:Genetic:
A:Gene: IFNAR
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A: Introns: 177/3: 331/1
C: Keywords: cytokine receptor; transmembrane protein

Alignment scores: Length: 436
Ratio: 3.230 Gaps: 4
Percent similarity: 75.917 Percent identity: 48.624

Alignment block:
US-09-240-675-1 x AA5283

Align seg 1/1 to: AA5283 from: 1 to: 590

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180 AGCGATGAGTCTGCGGAAATGACTTTTCATTCGATTATCAAAAC 229
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230 TGGGATGATGATGATGATGATGATGATGATGATGATGATGAT 279
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280 CCAATGCACTTTCTTCACTCACTCACTCACTCACTCACTCACT 329
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577 ATTCAGACATTAATTTATTAATCTCACAGAGACTTACTTATGCT 626
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627 AAAGTTAAAGCAGACTTACTGATGAGAAATGGTGCTATAGCC 676
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677 AGTCATGTTTAAAGCAGACTGAGAAAGAAAGTGAATGCTCAGCA 726
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727 ATATAGAGTCACTGTCGAAATCAAGACTATGTTTAAATGGATAT 776
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1124 ACTGATTTATGAATTTATTTTGGAAACACTTCAATGCTGAGAGA 1173
   |||.....|.....|.....|.....|.....|.....|
360 yLeuAsnTyrGlnIleIlePheTrpGlnAsnThrSerAsnThrLys 377
1174 AATTTTGCAGAAAACACTGATGATGATGATGATGATGATGATG 1223
   |||.....|.....|.....|.....|.....|.....|
377 erMetGlnLysAspGlyProGlnPheThrLeuLysAsnLeuGlnPro 393
1224 ACTGATTTATGTTGTTGAAAGCCAGACACACACATGATGAAAGCT 1273
   |||.....|.....|.....|.....|.....|.....|
394 ThrValTyrCysValGlnAlaArgVal..LeuPheArgAlaLeuLeu 409
1274 TAAAGCAGCTGTTTATGAGCTGTATGATGAGAAACAAACAGAGA 1323
   |||.....|.....|.....|.....|.....|.....|
409 nLysThrSerAspPheSerGlnLysLeuGlnLysLysThrArgPro 426
1324 ATACCTCT 1331
426 erPheSer 428

```

seq_name: pir2:G01418

seq_documentation_block:
cytokine receptor family II, member 4 - human
C: Species: Homo sapiens (man)
C: Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
C: Accession: G01418
R: Infalla, G
submitted to the EMBL Data Library, April 1994
A: Reference number: G06935
A: Accession: G01418
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 1-273 <LUD>
A: Cross-references: EMBL:U08988; NID:9571295; PID:9571296
C: Genetics:
A: Gene: GDB:CRFB4; CRF2-4
A: Cross-references: GDB:138168; OMIM:123889
A: Map position: 21q22.1-21q22.2
A: Introns: 17/1: 58/2; 111/1: 166/3; 216/1

alignment_scores: Quality: 233.50 Length: 224

Ratio: 1.704 Gaps: 8
Percent Similarity: 61.161 Percent Identity: 29.911

Alignment block:
US-09-240-675-1 x G01418

Align seg 1/1 to: G01418 from: 1 to: 273

```

81 TGGGTGTTGCCGACGCCGAGTGGAAAAATCTAAATCT..... 122
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
3  Tlpsrleuglsertrpleugllycysleuvalseralaleugl 19
123 ..... CCTCAAAAGTAGAGTGCAGATCATCATAGACACT 159
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
19 ymetvalproprogluasnvalargmetasnservalasnphelysa 36
160 TTATCTGAGGTGGACAGAGCATGATGCTGTGGGATGTGACTTTT 209
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
36 snlleuglntrpqluserproalaphelialysgllyasnleuthphe 52
210 TCATTCGATTATCAAAAAGTGGATGATGATTAATGATGCTGG 259
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
53 Thrleaglndtyr..... leusertryargllephedlnasply 65
260 GTGCAGAAATTTACTAGTACCAATGCAACTTTTCTCACTCAAGCTGA 309
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
65 scysmetasntrhthrleuthrleuglucysasprhser..... leus 80
310 ATGTTATGAGAAATTAATTGCGTATTAAGCAGAA... AAGAAAC 356
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
80 eilysylrglyasphisthrleuthrvalarglialglurhelialasplu 96
357 ACTTCTCAAGTATAGAGGTGACTATTACACCATTTGSCAAAGCTCA 406
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
97 Hisseraptrvalasnle... Thrphesprovalasrparhrl 112
407 GATTGCTCCGAGAGTACATTTAGAACGAGATTAAGGCAATAGTGA 456
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
112 eileglproprogluasnvalgluvalleuadrasrserleuasn 129
457 TACAC... ATCTCTCTGGAACAAAGATAGTGT... ATGTGGCTTGG 500
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
129 etargrheulalarpolysillegluasnclutrgluthrtrhmet 145
501 GATGGTTA... ACCTTACATAGCTTACTTATCTGAAAAATC 544
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
146 lysasnvallytasnsertrhtrlytasnvalglntgtrlyasngl 162
545 TTCAGGTGTGAGAAAGATGAAATTAATTATTCAGACATTAATTT 594
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
162 ythrparglulysrheglndlethrproglntyrasprheglvalleua 179
595 ATAAACTCTCAGACAGACTACTATGTGTAAGATTAAGCAGACTA 644
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
179 rgsnleuglntrpqltrhtrlytgcysvalglndvalarglurheliau 195
645 CTTCAGTCAATGAAATTTGGTGTCTATAGTCCAGTACATGTATTAAGAC 694
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
196 Proasprtagasnlysalaglyglutprsergluprovalcysglnglnt 212
695 CACAGTTGAAATGACACTACT 716
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
212 TTHAsasprgluthrvalpro 219

```

seq_name: p1r2:A47003

seq_documentation_block:

Cytochrome receptor family class II protein CR2-4 precursor - human

C:Species: Homo sapiens (man)

C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 10-Sep-1997

C:Accession: A47003

R:Infalia, G.; Gardiner, K.; Uze, G.
Genomics 16, 366-373, 1993

A:Title: A new member of the cytochrome receptor gene family maps on chromosome 21 a
A:Reference number: A47003; MID:93300510
A:Accession: A47003
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1325 (LUT)
A:Cross-references: GB:Z17227; MID:9393378; PID:9393379
C:Genetics:
A:Map position: 21q
C:Keywords: transmembrane protein

alignment_scores:

Quality: 228.50 Length: 224
Ratio: 1.693 Gaps: 8
Percent Similarity: 60.268 Percent Identity: 29.911

alignment_block:
US-09-240-675-1 x A47003

Align seg 1/1 to: A47003 from: 1 to: 325

```

81 TGGGTGTTGCCGACGCCGAGTGGAAAAATCTAAATCT..... 122
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
3  Tlpsrleuglsertrpleugllycysleuvalseralaleugl 19
123 ..... CCTCAAAAGTAGAGTGCAGATCATCATAGACACT 159
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
19 ymetvalproprogluasnvalargmetasnservalasnphelysa 36
160 TTATCTGAGGTGGACAGAGCATGATGCTGTGGGATGTGACTTTT 209
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
36 snlleuglntrpqluserproalaphelialysgllyasnleuthphe 52
210 TCATTCGATTATCAAAAAGTGGATGATGATTAATGATGCTGG 259
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
53 Thrleaglndtyr..... leusertryargllephedlnasply 65
260 GTGCAGAAATTTACTAGTACCAATGCAACTTTTCTCACTCAAGCTGA 309
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
65 scysmetasntrhthrleuthrleuglucysasprhser..... leus 80
310 ATGTTATGAGAAATTAATTGCGTATTAAGCAGAA... AAGAAAC 356
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
80 eilysylrglyasphisthrleuthrvalarglialglurhelialasplu 96
357 ACTTCTCAAGTATAGAGGTGACTATTACACCATTTGSCAAAGCTCA 406
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
97 Hisseraptrvalasnle... Thrphesprovalasrparhrl 112
407 GATTGCTCCGAGAGTACATTTAGAACGAGATTAAGGCAATAGTGA 453
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
112 eileglproprogluasnvalgluvalleuadrasrserleuasn 129
454 TGTATACATCTCTCTGGAACAAAGATAGTGT... ATGTGGCTTGG 500
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
129 etargrheulalarpolysillegluasnclutrgluthrtrhmet 145
501 GATGGTTA... ACCTTACATAGCTTACTTATCTGAAAAATC 544
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
146 lysasnvallytasnsertrhtrlytasnvalglntgtrlyasngl 162
545 TTCAGGTGTGAGAAAGATGAAATTAATTATTCAGACATTAATTT 594
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
162 ythrparglulysrheglndlethrproglntyrasprheglvalleua 179
595 ATAAACTCTCAGACAGACTACTATGTGTAAGATTAAGCAGACTA 644
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
179 rgsnleuglntrpqltrhtrlytgcysvalglndvalarglurheliau 195
645 CTTCAGTCAATGAAATTTGGTGTCTATAGTCCAGTACATGTATTAAGAC 694
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
196 Proasprtagasnlysalaglyglutprsergluprovalcysglnglnt 212

```

```

695 CACAGTGTGAATGACTACT 716
      |||| : : : : : |||
212 TTTHTSASPGLTHTRVAlPro 219
seq_name: p1r2:JC6311

```

```
seq_documentation_block:
interferon_receptor-class II cytokine receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
```

```
alignment_scores:
  Quality: 221.50
  Ratio: 1.582
  Percent Similarity: 61.404
  Length: 228
  Gaps: 10
  Percent Identity: 28.070
```

alignment_block:
US-09-240-675-1 x JC6311

Align seg 1/1 to: JC6311 From: 1 to: 345

```

121 GTGGGCCCATCGGGTGTCTCCGACGCCGCCGATGGGAAAAAACTAAATC 121
122 TCCCTCAAAAAGTAGAGGTGACATCATAGATGACACTTTATCCTGAGGT 171
123 oProGluLysValAlaPheMetAsnSerValAsnPheLysAsnIleLeuGlnT 40
172 GGAACAGAGAGCCGATGAGTCTGTCCGGAATGACTTTTCATTCAGTTAT 221
173 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 221
40 rpgIuValProAlaPheProLysThrAsnLeuThrPheThrAlaGlnTyr 56
222 CAA.....AAACGGGATGATATATTCGAAATAATGTCTGGTGTGTA 265
57 GluSerTyrArgSerPheGlnAspHis.....CysLys 67
266 GAAATTTACTAGTACCAATGCAACTTTTCTTCACGACGTGAATGTTT 315
67 sarGThrLaserThrGlnCysAspPheSer.....HisLeuSerLysT 82
316 ATGAGAAATTAATTTGGGTATTAAGACGAA...AAAGAAAACATTCT 362
82 yrgLysAspTyrThrValArgValArgAlaGlnIleuAlaAspGlnHisSer 96
363 TCAGGATTTGAGGTTGACACTATTCACATTTCCGAAAGCTCAGATTGG 412
99 GluTTPValAsnVal...ThrPheCysProValGlnAspThrIleIleGln 114
413 TCTCTCACAAGTACATTAGAAGCTGACAGATAGACCAATAGTATACACA 462
114 yProGluMetGlnIleGlnSerLeuAlaGlnSerLeuGlnIleuArgp 131
463 TCTCT.....CTCGAACAAGATAGTGTATG 491
131 heserAlaProGlnIleGlnAsnGlnProGlnThr..... 142
492 TGGGGTTTGGAGGTTA.....AGCTTACATATAGTTACTATATCTG 535
143 TrpThrLeuLysAsnIleLysThrAspSerTyrPalaThrArgValGlnTyrTr 155

```

[illegible]

```

seq_documentation_block:
  interferon gamma receptor beta subunit - mouse
N:Alternate names: IFN-gamma R beta chain; IFN-gamma R species-specific cofactor; ty
C:Species: Mus musculus (house mouse)
C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A49947
C:Hemmi, S.; Bohml, R.; Stark, G.; Di Marco, F.; Agniet, M.
Cell 76, 803-810, 1994.
A:Title: A novel member of the interferon receptor family complements functionality
:Reference number: A49947; MIMD:94170381

```

alignment_scores:		
Quality:	203.00	Length: 229
Ratio:	1.471	Gaps: 13
Percent Similarity:	60.262	Percent Identity: 30.131

alignment_block:
US-09-240-675-1 X A49947

Align seg 1/1 to: A49947 from: 1 to: 332

[illegible]

```

110 VALTALHLYSARGLYSNLEUTHSERTYSTIPVALGLYLEUHLPT 126
383 ATTTACACCATTTTCGCAAGCTCAGATTGCTCCAGAA...GTACATT 429
126 ORPHEGLNHLSTYGLASNLVHLVHLGLYPROPOLYSANLLESERY 143
430 TGAACCTGAAATGAAGGCAATGATACATCTCTCCGACAAA 479
143 ALTHPRGLYSLYSERLEUVALILLHISPHESERPROPHESAP 159
480 GATAGCTATGCGGCTTGATGCTTAAGCTTACATATAGCTTACT 529
160 .....VALPHEHISGLYALATHPHEGLNTHYLEUVALH 171
530 TATCTGAAAACTCTTCAGCTGATAGAAAGATTGAATATATATT 579
171 STYTRPGULYSSERGLNTHGLNGLNGLNGLNGLYPROPH 188
580 CCAGACATATAATTTAT.....AACTCTCAGACAGACTTATTGT 623
188 YSSERANSERILEVALLEUGLYSLNLEUYSAPROLYALYVALTYCY 204
624 CTAAAGTTAAAGCAGACTA...CTTACGTCATGGAATTT..... 662
205 LEUGLNTHGLVALGLNLEUHLLEUYSANLYSLYSILLEUPTROH 221
663 :GGTGTATAGTCCAGTACATTTGATTAAGACCA 698
221 SGLYLEUHLSEASANVALSERCYSHISGLNTHPT 233
seq_name: p1r2:138500

```

seq_documentation_block:

```

Interferon gamma receptor accessory factor-1 precursor - human
C:Species: Homo sapiens (man)
C>Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 05-Nov-1999
C:Accession: I38500; I38501
R:Sch, J.; Donnelly, R.J.; Kotenko, S.; Mariano, T.M.; Cook, J.R.; Wang, N.; Emanuel, S.
Cell 76, 793-802, 1994
A:Title: Identification and sequence of an accessory factor required for activation of
A:Reference number: A49946; MIMD:94170380
A:Accession: I38500
A:Molecule type: mRNA
A:Residues: 1-337 <RES>
A:Cross-references: EMBL:U05875; NID:9463549; PIDN:AA16955.1; PID:9463550
A:Experimental source: clone pK1
A:Accession: I38501
A:Molecule type: mRNA
A:Residues: 1-63, 'Q', 65-337 <RES>
A:Cross-references: EMBL:U05877; NID:9463551; PIDN:AA16956.1; PID:9463552
A:Experimental source: clone pS3
C:Genetics:
A:Map position: 21
C:Keywords: cytokine receptor

```

alignment_scores:

```

Quality: 155.50 Length: 300
Ratio: 1.030 Gaps: 14
Percent Similarity: 50.333 Percent Identity: 22.333

```

alignment_block:

```
US-09-240-675-1 x I38500
```

```
Align seg 1/1 to: I38500 from: 1 to: 337
```

```

60 GTGCTGCGCGCGGCGCCATGGGTGTTCGCGCGCGCGGCGTGA...107
9 LeuLeuLeuLeuGlyValAlpHeAlaAlaAlaAlaAlaAlaProProAs 25
108 .....AAAATCTAAATATCTCCCAAAAGTAAGGTCCAGATCAG 150

```

```

25 PROLEUSERGLNLEUPROALARPROGLNHLSPROLYSILEARGLEUTYA 42
151 ATGACAACTTTTCTCGAGGTGG.....AACAGAGC 182
42 SNLGLGLNGLNVALLEUSERTIPGLUPROVALALEUSERSERTHT 58
183 GATGAGCTGTGCGGAATGTGACTTTTTCATTCGATTCGATTACAAAATCG 232
59 ARGPROVALVALTYALGVVALGLNPHLEUSTYTHLPASERLYE.... 73
233 GATGATANTTGCATTAATTTCTT.....GGGTCTC 264
74 .....TRPPHEHISGLYALASPILEMSERTILEGLYVALAENCYST 87
265 AGAATATTACTGTGACCAATGCAATCTTTCTCA..... 299
87 HGLNHLERHVALTHRGULCYASRPHEHIALALASERPROSERLA 103
300 .....CTCAAGCTGAATGTTATGAGAAATTAATTAATTCGCTAAG 340
104 GLYPHEPROMETASRPHEASNLV.....THLEUHLGULHPT 116
341 AGCAGAAAAAGAAACACT...TCTCATGCTATGAGGCTGACTATT 387
116 GVALGLNLEUGLYALALEUHLISERLATRPVALTHMETPROTPRHEG 133
388 CACCAATTCGCAAGCTCAGATGCTCTCCAGAAAGTACATTAGAA... 434
133 LNHLSTYALGASNLVATHVALGLYPROPROGLN...ASNILLEGLVAL 148
435 .....GCTGAAGATAGGCAATAGTATACACATCTCTCCGAAACAA 478
149 THPRGGLYGLNGLYSERLEUHLLEALRGHSESERTPROPHESAP 165
479 AGATAGCTGTATGCGGCTTGATGCTTAAGCTTACATAGCTTAC 528
165 EALASPRHSERTHLPHE.....PHECUSTYLYLYVALH 178
529 TTATCTGAAAACTCTTCAGCTGATAGAAAGATTGAATATATTTAT 578
178 ISTYTRPGULN....LYSGLYGLYILLEGLNGLNGLYGLYPROPHE 192
579 TCCAGACATATAATTTAT.....AACTCTCAGCAGAGACTATTATG 622
193 ARGSERANSERLIESELEUASPNLEUYSEROSERHVALTYCY 209
623 TCTAAAGTTAAGCAGACTACTTACGCTA.....TGCAAA 660
209 SLEUGLNVALGLNGLNLEUHLLEUHPANLYSERANLLEHPTGV 226
661 TTGGTGTCTANRGCCAGTACTGTATTAAGCCACAGTTGAATGA 710
226 ALGLYHLSLEUSERSANLLESERCYSTYGLNTHKELALASPALASER 242
711 CTACCTCCACCAAGAAATATAGAGTCAGTCTC..... 743
243 THRGLEUGLNGLNVALLEUHLLESERVALGLYTHRPHESERLEUDE 259
744 .....CAAAATCCAGACT 756
259 USERVALLEUHLGLYALACYSRPHLEUVALLEUPLYTYALRGLYL 276
757 ATGTTCTTAATGGATTTATACATNTCCAAACAGACTTCAAGTCA 806
276 EUHLSTYTRTPPHEHISHTHPRPROSERILEPROLEUHLNGLN 292
seq_name: p1r2:113822

```

seq_documentation_block:

```

frazzled gene protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T13822

```

R:Kolodziej, P.A.; Timpe, L.; Mitchell, K.J.; Goodman, C.S.; Fried, S.; Jan, L.Y.; Jan, Cell 87, 197-204, 1996
A:Title: Frazzled encodes a Drosophila member of the DCC immunoglobulin subfamily and is
A:Reference number: 217780
A:Accession: J13822
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1375 <XOL>
A:Cross-references: EMBL:U71001; NID:91621114; PIR:91621115; PIR:AA047314.1
C:Genetics:
A:Gene: frazzled
A:Map position: 2
C:Function:
A:Description: may function in vivo as a receptor or component of a receptor mediating N

Alignment scores:

Quality: 129.00 Length: 622
Ratio: 0.542 Gaps: 22
Percent Similarity: 38.264 Percent Identity: 16.399

Alignment block:

US-09-240-675-1 x J13822

Align seg 1/1 to: J13822 from: 1 to: 1375

```
102 GGTGGAATAATCTAAATCT.....CC 124
147 GYGLYLYSPROLEUSPSEGLYLEUGLALARGLEUPROSERGLNP 463
125 TCAAAAGTAGAGTCGACATCATAGTACAACTTATC...CTGAGGT 171
463 CATGASPLEVALALAGLILEVALYSSERARGPHEVALTHLEUSERT 480
172 GG..... 173
480 rpaValGluProLeuGlnAsnAlaGlyAspValValTyrTyrThrValTyr 496
174 .....AACAGAGCGATGATGCTGTCGGAAATGCTTTTCAT 214
497 TYLYSMETASNSERGLUARGLUGLILYMETVALTHLYSSETH 513
215 CGATTTCAAAACCTGATGATGATGATGATGATGATGATGATGATG 264
513 SASPARGLUGLILEUVALINLEGLINLEUVALINLEUVALINLEU 530
265 AGAATATTAAGTACCAATGCAACTTTCTCA..... 299
530 InPheArgValGluAlaAsnThrAsnPhelGlySerGlyAlaSerSerAla 546
300 ..CTGAGGTGATGTTTATGAAGAATTAATGCGT..... 335
547 PROLEUGLILEUVALINLEUVALINLEUVALINLEUVALINLEUVAL 563
336 .....ATAAGAGCAGAAAAGAAAACACTTTCATGAT 369
563 GASNPHGLUGLYTYRGLALARGSERHISLYSGLILETYRVALLYSTRP 580
370 ATGAG..... 374
580 LUGLUPROTHRVALTHRASNGLYGLILEUVALYSTRARGVALTYR 596
374 ..... 374
597 SERGLUASNPSERGYLAASPLEUTYRHLASPSERTHRALALUGL 613
375 .....GTGACATCATTA 387
613 VALVALLEUTHRGILEUVALGRONHSTHRASPTYRVALILESERVAL 630
388 CACCATTTGCGAAAGCTCAGATGCT..... 413
630 ALPROPEASNPARGASNGLYMETGLYASPSERSERVALGLILEARGVAL 646
```

```
414 .....CCTCCAGAGTACATTAGA 433
647 LYSTHRPHESESERTHRPROSERGLUPROFROASNPVALINLEUGL 663
434 A...GCTGAAATAGGCAATAGATACATCTCTCCGGAACAAAG 480
663 VALTHRSERSESERILETHRVALINLEUVALINLEUVALINLEUVAL 680
481 ATAGTGTTATGTCGCTTGGATGTTTAACTTACATTAACCTTACTT 530
680 LUASPARGASNGLYGLILEUVALYSTRGLYSTRGLYSTRGLYSTRGL 695
531 ATCTGAAAACCTCTCAGGTAGACAGAAAGATTAATATTATTATTC 580
696 ..PHELYSAPRALAPROGLINVALYSSERTHRPROLEASNTLE..Ar 710
581 CAGACATTAATTTATTAATCTCCACGACAGACTATTTGCTTAAG 630
710 GTYRPHGLILEUVALINLEUVALINLEUVALINLEUVALINLEUVAL 727
631 TTAAGCAGACACTACT.....ACGTCATGGAAT 662
727 LEALALEMETHRVALASNGLYSERGLYPROPHETHRGLUTRPSNARG 743
663 GGTGTCATAGTCCAGTACATTTGTTAAAGACACAGTGAATGAACT 712
744 Ala.....AsnThrLeuGlnAsnAspLe 751
713 ACCT..... 716
751 USRPLUTHRGVALPROGLYSPROILETRPILSEERILENISPARG 768
717 .....CCACCGAATAATAGAACTC 737
768 LYALASNPALLEALALEUHNSTRGLYPROFROGHNHSPROGLILE 784
738 AGTGTCCAAAATCAGACTATGTTCTTAATG..... 770
785 LYSILE.....ArgAsnTyrValLeuGLYTRPGLYARGGLYILEPROAS 799
770 ..... 770
799 POLUSNTHRILEGLILEUVALYSTRGLUARGYRHLISILEUVAL 816
771 .....GATTA 776
816 SNLEUGLUSERASNPETASPTYRVALSERLEUARGALARGASNPAL 832
776 ..... 776
833 LYSGLYASRGLYPROPROILETYRASPANILELUSTHRARGASRGLUGL 849
776 ..... 776
849 UPROVALSPRALPROTHRPROLEUGLVALPROVALGLYLEUVALAI 866
777 ..ACATATGCAAAACATGACCTTCAAGTCAAGTCCACGCTTTTAA 824
866 LEITHMETSESERSESERILEVALYSTRPILLESPTHRMETLEU 882
825 AAAAGGAA..... 833
883 ASNLYASNPASNGLNHISVALTHRASNPARGHNISTYRTHRVALSER 899
834 .....CCTGGAACCATTTGTATTAATGGAACAAATACCTGCTGAA 879
899 YLIEHTRGLYSEASNPARGYRGLY.....HISA 910
880 ARGTCAAAACCTACCCAGTGTCTTCTCCAAAGCTTTGCAAAAAGGA 929
910 SNTHRTHRASPLEUASNPENYSMETILE..AsnAspLeuArgProAsnThr 925
```


Species: Gallus gallus (chicken)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #ext-change 13-Sep-1996
R:Accession: F50600
R:Velmetter, J.; Kayem, J.F.; Roman, J.M.; Dreyer, W.J.
J. Cell Biol. 127, 2009-2020, 1994
A:Title: Neogenin, an avian cell surface protein expressed during terminal neuronal
A:Reference number: A55193; MVID:95105243
A:Accession: F50600
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1443 <VIEW>
A:Cross-references: EMBL:U07644; NID:9641965; PID:9641966

alignment_scores:
Quality: 127.50 Length: 415
Ratio: 0.644 Gaps: 19
Percent Similarity: 47.711 Percent Identity: 22.169

alignment_block:
US-09-240-675-1 x F50600

Align seg 1/1 to: F50600 from: 1 to: 1443.

```
87 TTGTCCGACCGCAGCGTGGAAAAATCTAAATCTCTCAAAAAGTAGA 136
||||| |||||
416 LeuAlaProIaIeThrIleProIeuProIhAlaProIaGAspValVa 432
137 GTGTGACATCATGATGATGACACTTATC...CTGAGGTGGACAG... 179
||||| |||||
432 AlaIaIeValIeSerThrArgPheIleArgLeuThrIlePArgIleProV 449
180 ..AGCATGAGTCTGTCCGGAAATGCACTTTTCATGCAATATCAAAA 227
||||| |||||
449 aIeSerPProGInglYAspAsnIeuthrIYSerIlePheIYThrIYs 465
228 ACTGCGATGATTAATGATTAATGATTAATGCTGGGTGTCAGAAATTA 277
||||| |||||
466 GluGly.....IleAsnArgIuArgValGluAsn...Thre 477
278 TACCAATGCACTTTCTTCACTCAAGCTGAATGTTATGAAGAAATTA 327
||||| |||||
477 ArgProGluGluThrGluValMetIleGlnAsnIeMetProGluThrV 494
328 AATGCTCATTAAGACGAGAAAAAAGAACCTCTCATGATGATGAGTT 377
||||| |||||
494 aIYTrValPheArgValValAlaIeGlnAsnIYsIeGluIeGlyGlu... 509
378 GACATCTTACACCATTTCCGAAAGCTCAAGTGGTCTCCAGAACTACA 427
||||| |||||
510 ..SerSerIaIeProIeuIYsValIaIeThr.....GlnProIuValG 523
428 TTTAGAAGCTGAAGATAGGCAATAGTATGATACACATCTCCCGAGACA 477
||||| |||||
523 nIeupProGluProIaIeProAsnIleArgAlaIeArgIYArgIeSerPro 540
478 AAGTAAGCTTAAGTGGCTTTC.....GATGGTTTAACCTT 515
||||| |||||
540 eValIThrValIleThrIlePgluThrProIeuSerIYsngIuIeGln 556
516 ACATATAGCTACTTATCTGGAAGAAACCTCTCAAGGTGTAAGAAAGAT 565
||||| |||||
557 AsnIYTrIYsIeuthrIYTrMetGluIYsGluGlnAspSerIuGlnAsp 573
566 TGAATAATTTATTATCCAGACATAAATTTATTAACCTCAACCGAGACTA 615
||||| |||||
573 IAspValAlaIeIYleuSerIYThrIleThrIeGlyLeuIYsIeYThr 590
616 CTATATGCTAAAGTTAAAGACAGCACTACTTACGTATGGAAGAAATG 665
||||| |||||
590 IuYTrSerPheArgValValAla.....TYrIeAsnIYsIeGlyProGlu 604
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666 GCTATATGCTCAAGTACATGTTATTAAGACACAGCTTGAATTAAGAA 715
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605 valserthnglnaspvalvalvalnlythleuseraspvalproseral 621
716 TCACACAGAAATATATAGAGTCACTGTCACAAAT...CAGACTATGTC 762
621 aalaproglinsleuthleuclalalargshserisletleucl 638
763 TTAATGGGATATATCATATGCAACACGACCTTCAAGTTCAGTGGC 812
638 euH1STF6LProProProala..... 645
813 CACGCTTTTAAAGAAATCCGAAACATTTG..... 848
646 .....glythrhisserglynliethr 654
849 TATATAGCAAAATATACCTGATGCAAAATGCAAACTACCACT 897
654 YTYLlyllearglytyrarglyvalserarglyseraspvalthrglus 671
898 GTGCTCTCCCAAAACGTTTCCA.....AAGCAAT..... 932
671 ervalglyglythrglnleupheglnleuileglylyleuglnargly 687
933 TACCTTCGCCGCTACAGCATCTGATGAATACCA..... 971
688 ThrglutyranphearglylealalameThryalaenglythrglypr 704
972 TCTTTGGCTGAGAGATTAAGTTGATGCAATACCAAGTT 1017
704 calthrasprrpvalseralagluThrphegluserasplespglus 721
1018 TCTACTCTCCCACTC.....TTAACATTAGATCCCTTAGTAT 1058
721 eraAgvalproglvalproserSerleuH1SvalArgProleuValthr 737
1059 TCATTCATATCTATATCGGTGCTCCAAACAGCTGGAACAGCGCTGT 1108
738 Serile...valvalsertrpThrProglinsnglnasile...Va 752
1109 GATCCAGATATCCACATGATTTATGAATATTTTGGAAAAACCTT 1158
752 lvalargglytyralalleglytyrglyle.....glyserp 765
1159 CAAATGCTGAGAGA...AAATATCGAAAAAACTGATGTACAGTT 1205
765 roH1salaglnThrleuvalaspTyrglylserglndarglytyrThrile 781
1206 CTPAATTTGAACACGACGTATATGTGTGAACGACAGCA 1250
782 GlusnleuaspProserSerHisTyValleThrleuysala 796
seq_name: p1r2.A36080
seq_documentation_block:
Insulin receptor precursor rat
C.Species: Rattus norvegicus (Norway rat)
C.Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 18-Jun-1999
R.Goldstein, B.J., Dudley, A.L.
MOL. Endocrinol. 4, 235-244, 1990
A.Title: The rat insulin receptor: primary structure and conservation of tissue-specific
A.Reference number: A36080; M0ID:90331337
A.Accession: A36080
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-1383 <GOL>
A.Cross-references: GB:M28016; NID:9204953; PIDN:AA41441.1; PID:9204954
C.Keywords: ATP; autophosphorylation; hormone receptor; phosphoprotein; transmembrane pr
F:1022-1298/Domain: protein kinase homology <KIN>
F:1030-1038/Region: protein kinase ATP-binding motif

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472 Serglthrglysglyargglnlualrg.AsnaspillealeuysThr 488
175 ACAGAGCGATGAGTCTGCGGAATGACTTTTCACTGATTAACA 224
488 snglyaspGlnalserCysglusnglnleuLysPheSerPhele 504
225 AAACTGGATGATTAAT..... 242
505 ArgthrserPheaspLyslleleuLeuargTTPolProTyrrPropr 521
243 .....TGATAAATTCGTGGGT 261
521 oAsPheargspLeuenglyPheMetleuPheTylysglnalProt 538
538 YrglnasnhvalThrglnPheaspelyglnaspalacs..... 550
300 CTCAGCTGAATGTTATGAAGAAATTAATTCGCTATAGACAGAGAAA 349
550 ..... 550
350 AGAAACACTCTTCATAGGTATGAGTTGACTCATTTACACCATTTGCA 399
551 .....GlySeransertrpThrValasp..... 559
400 AAGCTCAGATGTGCTCCAGAGACTGATTTAGAGCTGAAGATAGGCA 449
560 .....leaspProProglin.....ArgserAasnaspProlys 570
450 ATAGGTATACACATCTCTCGAACAAGATAGTGTATGGCGCTT 499
571 SerglnthrProserHisProgly.....trPleuMe 581
500 GGATGTTTAAAGCTTACATATAGCTTACTTATCTGAAAAACTCTCAG 549
581 largly..... 583
550 GTGTAGAGAAAGATGGAATATTTATTCAGACATAAATTTATAAA 599
583 ..... 583
600 CTCACACAGAGACTTATTTGTAAAGTTAAAGCAGCACTACTTAC 649
584 leuLysProtrpThrglnThryalallePhevallyThrleuvalthrph 600
650 GTATAGGAAA.....ATTGGTCTATAGCTCCAGTACATTTATATA 690
600 eserApsglualrgThrTyrclylalysseraspilleTyValg 617
691 AGACCAAGTTGAAAGACATACCTCCACAGAGAAATATGAAAGTCA 740
617 lnthraspalathrasnProserValProleuaspProleueserValser 633
741 GTCAAAATCAGAACTATGTTCTTAATG.....GATATATCAAA 781
634 AsnserSerSerlnlleleuLysstrpLysProProserAproAs 650
782 TCGAAACATGACCTTCAAGTTCAAGTGGCTCCACGCTTTTAAAGGA 831
650 ngllyasnliethr..... 654

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832 ATCTGGAACCATTTGATAAAGC...AAACAAATACCTGACTGTGA 878
 655HISTYLEUVALTYTRPGIUAAGLALAGLUSPSEGIU 668
 879 AATGCAAAACACACAGTGTCTTTCTCTCAAAAGCTTTCCAAAAG 928
 669 LEUPHEGLULEUSPPTYCYSEU.....LYSGL 678
 929 AATTACCTT.....CTCCGCGTACAAGAT 954
 678 YLEUYSLEUPROSERARGTHTRPSEPRORPHEGLUSEASAPSPS 695
 955 CTGATGAAATACACATCTTTTGTCTGAAGACATA..... 992
 695 ERLGLYHISASNGLSERGLUTYRASPSPSERALASERGLUCYSPS 711
 993AAGTTGATCTGAATAACAAAGCTTCTCTCTCTCCACT 1033
 712 SERCYSPPOLYSTRHASPSEGLINILEULYSGULDEGLUSE 728
 1034 CTTTACATTAATGATCCCTTATGATTCATATATATATATATATAT 1083
 728 RHEARG...LYSTRHESGLUSPPTYCYSEUHSASVALALPHEVALP 744
 1084 CAAAACAG...TCTGGAAC..... 1100
 744 RCRGLYSTRHESERGLYASNGLYALAGLUSPTRYRARGPROSERARG 760
 1101ACGCTGT 1108
 761 LYSARGATSERLEUGLUGLVALGLYASVALTHALATHRTRPCH 777
 1109 GATCCAGATTAATCCACTGATTTATGAAATATTTTGGAAAACACT 1158
 777 LEUPROASPHERPPOASNILESERSETRILE.....ALAPROTHS 792
 1159 CAATCTGAGAGAAAATTTATGAGAA.....AAACTGATGT 1199
 792 ERHSISLUGLUNHSARGPROPHGLULYSVALVALASNDYSGULSERLEU 808
 1200 ACAGTTCCTAATTTGAACACAGCTGATATTTGTGTGAACCCAGAG 1249
 809 VALIISERGLYEUARGHISPHETHGLYTRARGILEGLULEUGL 825
 1250 ACACACATGATGAGAAAAGCTGATAAAGACAGTGTATTTAGACGCTG 1299
 825 ACYSASNGLUSPSPROGLUGLUSPSEGLYVAL...ALALATYV 841
 1300 TATGTGAAAACAAAACCA 1319
 841 ALSERIALARGTHRMETPRO 847
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 Interferon_gamma_receptor_precursor...human
 CSpecies: Homo sapiens (man)
 CDate: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 23-Jul-1999
 CAccession: A31555
 RAgnet: M; Dembic; 2; Merlin; G
 Call: 55, 273-280, 1988
 ATitle: Molecular cloning and expression of the human interferon gamma receptor.
 AReference: A31555; MIM:89003065
 AAccession: A31555
 A.Molecule type: mRNA
 A.Residues: 1-489 ->AGD-
 A.Cross-references: GB:J03143; NID:J184650; PIDN:AA52721.1; PID:9306915
 C.Genetics: GDB:IFNGRI, IFNGR
 A.Gene: GDB:IFNGRI, IFNGR
 A.Cross-references: GDB:120688; OMIM:107470
 A.Map position: 6q23-6q24
 C.Superfamily: Interferon_gamma_receptor

C.Keywords: cytokine receptor; transmembrane protein

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 ratio: 0.666
 Percent Similarity: 53.276 Percent Identity: 22.222

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 83 GGTGTTCGCCAGCC...GCAGTGGAAAACCTAAATCTCTCAAA 129
 17 AGLUMETGLYTRHAPLEUGLYPROSERSEVALPROTHRPROTHA 34
 130 AAGTACAGCTGACATCTATATGACAACTTATCCAGAGTGGAAACAG 179
 34 SNVALTHRIIEGLUSERTYRASNMETASNPROILEVALTYTRPGLUTY 50
 180 AGCATGAGTGTGTCGGATGTG...ACTTTTCATTCGATTAACAAA 226
 51GHLIEMEPROGINVALPROVALPHEHVALGLIUVALLYSAS 65
 227 AACTGGATGATATATGATAAATGCTGTGGGTGACGATAATTAATA 276
 65 DTYGLVALYLYSASNSERGLUTRIPLEASPLACYSILEASNILESERH 82
 277 GTACAAATGCACTTTCTCTACCTGACAGCTGATATGTAAGAAT 326
 82 LSHIITYCYASNILESERASPHISVALGLYASPPROSERASNSERLEU 98
 327 AATGCGGTATAGACA.....GAAAAGAAAACACTTCTTCATG 367
 99 TRPVALLGLVALYALARGVALGLIYGLINYSGLU.....SERALTY 113
 368 GTATGAGGTGACTTATTAACCATTTCCGAAACCTGATATGCTCTC 417
 113 RLALYSSERGLUGLUPHEALVALYCARSPGLYLSILEGLYPROP 130
 418 CAGAACTATTTAGACSTGAAATAGGCAATGATGATACACTCTCT 467
 130 ROLYSLEUSPILLEARGYSGULYSGINLIEMETILESPLE... 145
 468 CCTGGACAAAAGATAGTGTATGTGGCTTTGATGTTAAGCTTAC 517
 146PHEH 147
 518 AATACCTTACTTATCTGAAAACCTCTGAGGTGATAGAGAAAGATG 567
 147 SPROSERVALPHEVAL.....ASNOLYSPGLUGLUGLVALA 160
 568 AATATTTATTCAGACATAAATTTAATCTGACACAGACTACT 617
 160 SP.....TYRASPPOGLUTHRH 166
 618 TATTCCTAAAGTTAAACAGCACTACTTACGTGATGAAAATGTGTCT 667
 167 CYSGLYLLIARGVALYTRASNVALTYRVALARGHETANGLY.....S 181
 668 CTATACCTCAAGTAC...ATTGTATAAGACACACAGTGAATGAAGTAC 714
 181 ERLIULEGINTYRYSILEUTHRGULYGLUSPSPCYSPSGULU 197
 715 CTCACACAGAAAATATAGAAAGTCAAGTCCAAATCAGAACTATGCTC 762
 198 IIEGLICYGLINLEUALALEPROVALSERSELEUSASNSERGLINTYCY 214

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763 .....TTAATGGATTATACATATGCAACATGACCTTTCAGTTCA 805
214 sValSerAlaIleuGluValLeuHisVal.....TTPG 225
806 GTGGCTCCACGCCCTTTTAAAAAGAAATCTCGAACCAATT..... 846
225 lValThrThrGluLysSerLysGluValLysIleThrIlePheAsnSer 241
847 TGTATTAATGGAACAAATACCTGACGTGTAAGAAATGCAAACTACCCAG 896
242 SerIleLysIleSerLeuTrp.....IleProVa 251
897 TGTGTCTTCTCCCAAAAGCTTTTCCAAAAGAAATTTACCTTCGCCGT 946
251 lValAlaIleLeuLeuPheValLeuSerIleValPheIleCysP 268
947 ACAAGCATCTGATGAAATACACATCTTTTGTCTGAAGAGATAAAGT 996
268 he.....TyrIleLysLysIleAsnProLeuLysGluLysSer 280
997 TTGATATGAAATACAGCTTCTTCTACTCTCCAGCTTACATTAGA 1046
281 lIleIleLeuProLysSerIleSerValValArgSerAlaThrLeuG 297
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297 u 297

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seq_documentation_block:

190K protein - human
 C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
 C:Accession: S42167
 R:Viteketer, U.; Obermann, W.; Weber, K.; Fuerst, D.O.
 J:Cell. Sci. 106, 319-330, 1993
 A:Title: The globular head domain of titin extends into the center of the sarcomeric M
 A:Reference number: S42166; MUID:94095665
 A:Accession: S42167
 A:Status: preliminary
 A:Molecule type: mRNA
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US-09-240-675-1 x S42167

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201 ..GTGACTTTTCATTCATTCATCAAAAACCTGGATGATATGGA 246
404 oIleuGluGlyThrPheIleAspLysCysGluValGlyThrAspSerTrp 420
247 TAAATTTCTGCTGGTGTGAGATATTAATTAATCAAAATGCAACTTTCT 296
421 .....SerGlnCysAsnAspThr 426
297 TCACCAAGCTGATCTTTATGAGAAATTAATG..... 332
427 ProValLysPheAlaArgPheProValThrGlyLeuIleGluGlyArgSe 443

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477 LeuLysSerPro.....LeuSerThrLeuAspTrpThrValIleVal 490
458 ACACATCTCTCGAGCAAAAGATAGTGTATGCGCGCTTGAGATGTT 507
490 lThrGluGluGluProSerGlyIleValProGlyProThrAspL 507
508 TAAGCTTTTACA.....TATAGCTTACTTATCTGAAA... 539
507 eSerValThrGluAlaThrArgSerTyrValValLeuSerTrpLysPro 523
540 .....ACTCTTCAGCTGTAGACAAAGAGATTGAAAATATTTA 577
524 ProGlyGluArgGlyHisGluGlyIleMetTyrPheValGluLysCysG 540
578 TTCC..... 581
540 uAlaGlyThrGluAsnTrpGlnArgValAsnThrGluLeuProValLys 557
582 .....AGACATTAATTTATTAACCTTCACACAGACATCTATTTGCTCA 626
557 eProArgPheAlaLeuPheAspLeuAlaGluGlyLysSerTyrCysPhe 573
627 AAAGTTAAAGCAGCAGCTACTACGTACGAGAAATGTGTCTATAATGCC 676
574 ArgValArgCys.....SerAsnSerAlaGlyValGlyGluTrp 586
677 ACTCATTTGTATTAAGACACAGTT..... 701
586 oSerGluAlaThrGluValThrValValGlyAspLysLeuAspIleProL 603
702 .....GAAATGCACTACCTCCACGCAAAATATGAGATGCTGCCAA 746
603 yAlaProGlyLysIleIleProSerArgAsnThrAspThrSerVal... 618
747 AATCAGAACTATGTTCTTAATGGAT..... 773
619 .....ValValSerTrpGluGluLysSerLysAspAlaLysGluLe 631
774 .....TATCATATGCAACATGATACCTTTCACTGATGAGGCTCC 813
631 uValGlyTyrTyrIleGluAlaAsnValAlaGlySerGlyLysTrpGluP 648
814 AGCCTTTTAAAAAGAAATCT...GGAACCATTTGTATTAATGGA 860
648 rCys.....AsnAsnAspProValLysThrHisArgPhe... 659
861 CAATACCTGAGCTGAAATGTAATAAATACCAAGGTGCTTCTCTCA 910
660 .....ThrCysHisGlyLeuValThrGlyLysSer... 669
911 AAAGCTTTTCCAAAAGAAATTTACCTTCTCCGCTACAGCATCTGATG 960
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1011 CAAGCTTCTTACTCTCTCA.....GTCTTAAACATTAG 1045
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791 AlaValSerGlyCysPheLysCysGluGlu 800

seq_name: p1r2:S51604

seq_documentation_block:
receptor-like tyrosine kinase Etk-1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 29-May-1998
C:Accession: S51604
R:Matcomletter, P.C.; Barzoueta, N.X.; Yancopoulos, G.D.
OncoGene 8, 3277-3288, 1993
A:title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase fam
A:Reference number: S49015; M0ID:9406777
A:Accession: S51604
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-981 <MAT>
A:Cross-references: EMBL:S68029
A:Note: the authors translated the codon GAC for residue 170 as Glu
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C:Keywords: ATP; transmembrane protein
F:651-917/Domain: protein kinase homology <KIN>
F:659-667/Region: protein kinase ATP-binding motif

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Percent Similarity: 42.795 Percent Identity: 20.067

alignment_block:
US-09-240-675-1 x S51604

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150 GATGACAACTT .....ATCCGAGAGTGA 174
181 aspserphenhyrargluLeuaspLeuGlyAspArgValMetLysLeuA 198
175 ACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 215
198 snthgluValArgAspValGlyProLeuSerLysGlyGlyPheTyrLeu 214
216 GATTATCAAAACCTGAGATGATATGATTAATATGTCGGGTGCA 265
215 AlaPheGlnAspValGly.....AlaCysIle 223
266 GAATATTAAGTAGTACC.....AAAGCAACTTTTCTTAC 300

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240 rghIleuAlaValPheProasp.....ThrIleThrGly 251
351 GAAACACTTCTTCATGATGATGAGTTGACATTTACACCTTTGGCA 400
252 AlaAspSerSerGlnLeuLeuValSerGlySerCysValAsnHisSe 268
401 AGCTCAGATGTGCTCCAGAGTACATTTAGACCTGAAAGTAAAGGCA 450
268 rValThrAspProProLysMetHisCysSerAlaGluGlyIleTrpL 285
451 TAGTGATACATCTCTCTCGAGAGAGAGAGAGAGAGAGAGAGAGAG 500
285 euVal.....ProIleGlyLysCysMetCys..... 293
501 GATGTTTAAAGCTTATACATATAGCTTACTATCTGAGAAACCTTCAG 550
294 .....LysAlaGlu 296
551 TGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 597
296 yTyrGluGluLysAsnGlyThrCysGlnValCysArgProGlyPhePhe 313
598 AACTCACCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 647
313 yAlaSerProHisSerGlnThrCysSerLysCysProPro..... 326
648 AGCTATGAGAAATTTGTGTATAGTCCAGATCAT ..... 683
327 .....HisSerTyrThrHisGluGluAlaSerThr 336
684 .....TGTATTAAGACACAGTGTGAATATGACTACCTCCA..... 719
336 rSerCysValCysGluLysAspLysPheArgArgGluSerAspProPro 353
720 .....CCAGAAATATAGAGTCACT 740
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370 ValAsnGlnThrSerValPheLeuGlnIleProProAlaAspThrGlu 386
771 .....GATTATACATATGCAAAACATGACCTTTCAGTCACTGGC 810
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811 TCACAGCCTTTTAAAGAGATCTCGAAGACCATTTGTTAAATGAAA 860
402 erHisAlaGlyValCysGluGluCysGlyGlyLysHisValArg ..... 415
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416 .....TyrLeuProGlu 419
911 AAAGTTTTCAAAAGAGATTTACCTTCCCGGTACAGACATGATG 960
419 nglnIleGlyLeuLysAsnThrSerValMetMetAlaAspProLeuAla 436
961 GAATATACATCTTTTGTGCTGAGAGAGATTAAGTTGATGATGAATA 1010
436 lsrHisAsnTyrThrPhe.....GluIle 443
1011 CAAGCTTCTACTCTCCAGCTTAAATAGATTAATCCCTAGTATTC 1060
444 GluAla.....ValAsnGlyValSerAspLeuSerProGlu 465
1061 ATTGCATATCTATATCGGT.....GCTCCAAACAGCTGTGAAACA 1101

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489 LeuSerTTPGlnGlnProAspArgProAsnGlyIleIleLeuGlnTyrGln 505
1136 AATTATTTTGGAAAAACACTTCAATGCTGAGAGAAAAATTATCGAG. 1184
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505 uIleLysTyrPheGlnLysAspGlnGlnThrSerTyrThrIleIleLysS 522
1185 ..AAAAAACTGATGTACAGTTCTTAATTGAAACCACTGACTATAT 1232
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1233 TGTGTGAAGCAGACACACAC 1256
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539 ValPheGlnIleArgAlaArgThr 546

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 Date: Jun 1, 2000 6:24 PM

About: Results were produced by the GenCore software, version 4.5,
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 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
 -OGAPOP=4.000 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=bloms62
 -TRANS=human40.ctl -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NOM=ext -MINLEN=0
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 -THREDS=1

Search information block:

Query: US-09-240-675-1
 Query length: 1343
 Database: SwissProt_38.*
 Database sequences: 83857
 Database length: 30454973
 Search time (sec): 84.100000

score_list:

Sequence	Strd Orig	Zscore	Escore	len	Documentation
SwissProt_38:INRL_HUMAN + 2313.00	3405.81	7.4e-183	557	P17181	homo sapiens (human)
SwissProt_38:INRL_BOVIN + 1507.00	2214.75	1.6e-116	557	Q04780	bos taurus (bovine)
SwissProt_38:INRL_SHEEP + 1503.00	2208.84	3.4e-116	560	Q28589	ovis aries (sheep)
SwissProt_38:INRL_MOUSE + 1069.00	1567.06	1.8e-80	590	P33896	mus musculus (mouse)
SwissProt_38:CFR4_HUMAN + 228.50	330.47	2.5e-11	335	Q08334	homo sapiens (human)
SwissProt_38:INRS_HUMAN + 155.50	222.27	2.6e-05	337	P38484	homo sapiens (human)
SwissProt_38:INRS_RAT + 127.00	167.38	0.0072	1383	P15127	rattus norvegicus (rat)
SwissProt_38:INRS_HUMAN + 124.50	173.10	0.0097	449	P15260	homo sapiens (human)
SwissProt_38:KWL1_HUMAN + 123.50	161.77	0.0140	1451	P52179	homo sapiens (human)
SwissProt_38:EPAS_RAT + 118.00	156.97	0.0374	1005	P54757	rattus norvegicus (rat)
SwissProt_38:INOR_MOUSE + 117.50	161.28	0.0376	575	Q61757	mus musculus (mouse)
SwissProt_38:INRS_MOUSE + 117.00	152.67	0.0476	1372	P15308	mus musculus (mouse)
SwissProt_38:PPDF_HUMAN + 116.00	148.19	0.0606	1912	P23368	homo sapiens (human)
SwissProt_38:INSE_CHICK + 115.00	149.22	0.0701	1450	Q02173	gallus gallus (chick)
SwissProt_38:IT03_RAT + 113.50	151.32	0.0860	880	P55146	rattus norvegicus (rat)
SwissProt_38:DEC_MOUSE + 111.50	144.06	0.1360	1447	P54756	homo sapiens (human)
SwissProt_38:EPAS_HUMAN + 108.00	141.91	0.2503	1037	P54756	homo sapiens (human)
SwissProt_38:IN11_HUMAN + 107.00	148.46	0.2632	427	P78552	homo sapiens (human)
SwissProt_38:IN10_HUMAN + 107.00	145.72	0.2753	578	Q13651	homo sapiens (human)
SwissProt_38:CIC2_RAT + 107.00	139.97	0.3050	1091	P34290	rattus norvegicus (rat)
SwissProt_38:INRS_HUMAN + 107.00	135.83	0.3168	1382	P34290	rattus norvegicus (rat)
SwissProt_38:DEC_HUMAN + 106.00	135.94	0.3858	1447	P43146	homo sapiens (human)
SwissProt_38:IL13_MOUSE + 105.50	139.72	0.3913	878	P26594	mus musculus (mouse)
SwissProt_38:CIC2_HUMAN + 105.50	137.75	0.4053	1091	P54289	homo sapiens (human)
SwissProt_38:IN12_HUMAN + 104.50	140.80	0.4520	662	P42701	homo sapiens (human)
SwissProt_38:CYRB_MOUSE + 104.00	137.32	0.5217	886	P26595	mus musculus (mouse)
SwissProt_38:NRG_DROME + 104.00	134.39	0.5497	1239	P20241	drosophila melanogaster
SwissProt_38:PPPE_HUMAN + 104.00	130.53	0.5888	1897	P10586	homo sapiens (human)
SwissProt_38:TCF2_TORAC + 104.00	138.86	0.6065	2280	P09976	nicotiana tabacum
SwissProt_38:IL16_HUMAN + 103.50	136.36	0.5758	918	P40189	homo sapiens (human)
SwissProt_38:INGR_MOUSE + 102.50	140.81	0.6263	477	P15651	mus musculus (mouse)
SwissProt_38:TCF2_SPTOL + 102.50	127.26	0.7972	2131	P08873	spinacia oleracea
SwissProt_38:TCF2_ARATH + 101.00	123.11	0.9750	2294	P56786	arabidopsis thaliana
SwissProt_38:CD45_HUMAN + 99.50	133.21	1.17	1304	P08575	homo sapiens (human)
SwissProt_38:CYRB_HA9IN + 99.50	133.66	1.22	897	P43611	haemophilus influenzae
SwissProt_38:5230_PLAFO + 99.50	119.33	1.50	3135	Q08372	plasmidium falcatum
SwissProt_38:TH00_YEAST + 98.50	125.52	1.58	1345	P38800	saccharomyces cerevisiae
SwissProt_38:RPO_TMY + 98.50	123.86	1.63	1615	P03586	tobacco mosaic virus
SwissProt_38:CYAA_YEAST + 98.50	121.81	1.69	2026	P08678	saccharomyces cerevisiae
SwissProt_38:KTR7_YEAST + 98.00	133.43	1.49	517	P40504	saccharomyces cerevisiae

seq_name	SwissProt_38:INRL_HUMAN	SwissProt_38:K128_YEAST +	97.50	137.44	1.50	306	P06242	saccharomyces
SwissProt_38:LEPR_MOUSE +	97.50	125.36	1.86	1162	P48356	mus musculus		
SwissProt_38:CAIC_CHICK +	97.50	126.66	1.89	1256	P11722	gallus gallus		
SwissProt_38:CAIC_CHICK +	97.50	116.41	2.19	3124	P13944	gallus gallus		

seq_name: SwissProt_38:INRL_HUMAN

seq_documentation_block:

ID	INRL_HUMAN	STANDARD	PRT	557	AA
AC	P17181				
DT	01-AUG-1990	(Rel. 15, Created)			
DT	01-AUG-1990	(Rel. 15, Last sequence update)			
DT	15-FEB-2000	(Rel. 39, Last annotation update)			
DE	INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).				
GN	IFNARI OR IFNAR.				
OS	homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
CC	Eutheria; Primates; Catarrhini; Hominoidea; Homo.				
LN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 90124632.				
RA	Uze G., Lutfalla G., Gresser I.,				
RT	"Genetic transfer of a functional human interferon alpha receptor				
RL	into mouse cells: cloning and expression of its cDNA."				
RL	Cell 60:225-234(1990).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 92129376.				
RA	Lutfalla G., Gardiner K., Proudman D., Vleth E., Uze G.,				
RT	"The structure of the human interferon alpha/beta receptor gene."				
RL	J. Biol. Chem. 267:2802-2809(1992).				
RN	[3]				
RP	PHOSPHORYLATION BY TYR2.				
RX	Colamonde J., Yan H., Domanski P., Handa R., Smalley D.,				
RA	Mullersman J., Witte M., Krishnan K., Krolewski J.,				
RT	"Direct binding to and tyrosine phosphorylation of the alpha subunit				
RL	of the type I interferon receptor by p135tyk2 tyrosine kinase."				
RL	Mol. Cell. Biol. 14:8133-8142(1994).				
CC	"FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE				
CC	I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS				
CC	INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-ALPHA AND BETA-				
CC	SUBUNITS THEMSELVES.				
CC	"SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.				
CC	"TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALL TISSUES AND				
CC	EVEN ON THE SURFACE OF MOST IFN-RESISTANT CELLS.				
CC	"PTM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYK2 TYROSINE KINASE.				
CC	"SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.				
CC	"SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation				
CC	at the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
CC	EMBL; J03171; AAA52730.1;				
DR	EMBL; X60459; CAA42992.1;				
DR	PIR; A32694; A32694.				
DR	PIR; S17112; S17112.				
DR	KIM; I07450;				
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KW	Phosphorylation.				
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FT	TRANSMEM	437	457	POTENTIAL.	
FT	DOMAIN	458	557	CYTOPLASMIC (POTENTIAL).	
FT	DISULFID	79	87	BY SIMILARITY.	
FT	DISULFID	199	220	BY SIMILARITY.	

FT	MOD_RES	466	466	PHOSPHORYLATION (BY TYK2) (PROBABLE)
FT	MOD_RES	481	481	PHOSPHORYLATION (BY TYK2) (PROBABLE)
FT	CARBOHYD	50	50	POTENTIAL
FT	CARBOHYD	58	58	POTENTIAL
FT	CARBOHYD	81	81	POTENTIAL
FT	CARBOHYD	88	88	POTENTIAL
FT	CARBOHYD	110	110	POTENTIAL
FT	CARBOHYD	172	172	POTENTIAL
FT	CARBOHYD	254	254	POTENTIAL
FT	CARBOHYD	313	313	POTENTIAL
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FT	CARBOHYD	416	416	POTENTIAL
FT	CARBOHYD	433	433	POTENTIAL
FT	VARIANT	168	168	POTENTIAL
FT	CONFLICT	17	17	G -> A (IN REF 2)
FT	SEQUENCE	557 AA:	63525 MM:	0F674AC8A1ADEB73 CRC64:

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 Ratio: 5.305 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-240-675-1 x INRI_HUMAN

Align seg 1/1 to: INRI_HUMAN from: 1 to: 557

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17 YProTTrValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
127 AAAAGTAGAGTCGACATCATAGATGACAACTTATCTGAGGTGAGAC 176
34 LulysValGluValAlaSerPheIleLeuAspAsnPheIleLeuArgTrpAsn 50
177 AGAGCCATGTCGTCGCGGAGTGTCTTTCATTCATTCATTCATTCATTCAT 226
51 ArgSerAspGlnSerValGlyAsnValThrPheSerPheAspTrpGlyGly 67
227 AACGGGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 276
67 StHcGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleHis 84
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84 eTrHlyLysCysAsnPheSerSerLeuLysLeuAsnValIlyGluGluIle 100
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101 LysLeuValGlyIleArgGluAlaGluLysGluAsnThrSerSerTrpTrpGlyVal 117
377 TGAGTCATTTACACCATTTCCCAAGTCAGATGTCCTCCCAAGATGATGATG 426
117 LAspSerPheThrPhePheArgGlyAlaGlnIleGlyProProGluValH 134
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977 TTGCTGTGAGAGATTAAGTGTATGATGATGATGATGATGATGATGATGAT 1026
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1027 CTCACGCTTAAATTAATGATCCCTTAAGTATGATGATGATGATGATGATG 1076
334 rOProValPheAsnIleArgSerLeuSerAspSerPheHisIleLysIle 350
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351 GlyAlaProLysGlnSerGlyAsnThrProValIleGlnAspTrpProLe 367
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1177 TATCGAAGAAAAGTATGATGATGATGATGATGATGATGATGATGATGAT 1226
384 lIleGluLysLysThrAspValThrValProAsnLeuLysProLeuThr 400
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401 ValTrpCysValLysAlaArgAlaHisThrMetAspGluLysLeuAsn 417
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 ID INRI_BOVIN STANDARD: PRT: 560 AA.
 AC Q04790:
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)

Align seg 1/1 to: INRI_BOVIN from: 1 to: 560

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1 MetLeuAlaLeuLeuGlyAlaThrThrLeuLeuLeuValAla... GlyIle 16
80 AAGGGGTGTGGTCCGAGCCGCGAGGTGGAAAAAATCTAAATATCCCTCAA 129
16 GTrpAlaLeuProAlaAlaSerGlyGlyAlaAsnLeuLys... ProGlu 32
130 AAGTAGCGTGCACATCATAGATACAACTTATCTGAGGTGGAAACG 179
32 snValGlnIleHisIleIleLeuAspAsnProPheLeuLysTrpAsnSer 48
180 AGCGATGAGTGTCCGGGAATGATCACTTTTCATCGCATATACAAAAC 229
49 SerSerGlnSerValLysAsnValThrPheSerAlaAspArgGlnIleLe 65
230 TGGCATGATATATGGAAATATGTGTGGGTGCACAAATATACAGTA 279
65 uGlyThrAspAsnTrpLysLysLeuSerGlyCysGlnHisIleThrSer 82
280 CCAATGCAACTTTCTCTACTCAAGTG... AATGTTTATGAAGAAAT 326
82 hTrpCysAsnPheSerSerValGlnLeuGlnAsnValPheGlnLysIle 98
374 GGTGACTCATTTACACCATTTGGCAAGTCCAGATTGGTCCCGAAG 423
115 uValGlnProPheValProPheLeuGlnAlaGlnIleGlyProProAsp 132
424 TACATTTAGAAGCTGAAGATTAAGCATTAAGTATACACTCT... CCG 470
132 aHisLeuGlnAlaGlnLysAspLysAlaIleIleLeuSerIleSerPro 148
471 GGAACAAAGACTAGCTGTATATGTGGCGTTTGCAGAGGTTTAAGCTTACATA 520
149 GlyThrLysAspSerIleMetTrpAlaMetAspArgSerPheArg 165
552 TAGCTTACTATATCGGAAAAAAGCTTCAGGTGTGAAAGAAAGATGAA 570
199 CysLeuLysValLysAlaGlnIleuAlaGlnLeuSerGlyGlyCys 215
571 TAGCCAGTCACTGTATATAGAACCAACATGAAATGAAATGAACTCTCCAC 720
215 rSerProValThrCysLeuAsnThrThrGlnArgLysValProSer 232
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665 ePheLysLysIleProGlnAsnHisSerAspLysTrpLysGlnIlePro 282
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82 snCysGlnAsnValThrSerThrHisCysValPheProArgGlnValSer 298
21 CAAAAAGAAATTTACTCTTCGCGGTACAAAGCATGTGATGAAATACAC 970


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CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED. EXCEPT
CC CONCEPTUS AT DAY 15 OF PREGNANCY.
CC -1- SIMILARITY: CONTAINS 2 FIBROECTIN TYPE IIT-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC
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CC or send an email to license@sdb.sdb.ch).
CC -----
CC DR EMBL; X95939; CAA65183.1;
CC DR EMBL; U65978; AAB84231.1;
CC DR PFM; PFM0041; fn3; 1.
CC KW Receptor; Transmembrane; Glycoprotein; Signal.
CC FT SIGNAL 1 24 BY SIMILARITY
CC FT CHAIN 25 560 INTERFERON-ALPHA/BETA RECEPTOR ALPHA
CC FT CHAIN.
CC FT DOMAIN 25 437 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 438 458 POTENTIAL.
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CC FT CARBOHYD 47 47 POTENTIAL.
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Align seg 1/1 to: INRL SHEEP from: 1 to: 560

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16 gtrpvalleuproAlaAlaSerGlyAlaAlaSerLeuYSer...GluA 32
130 AAGTAGAGCGAGCATCATGATGACAACTTATCTCGAGGTGAGACAGG 179
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49 SerSerGlnSerValAlaGlnValThrPhSerAlaAspArgGlnIleLe 65
230 TGGGATGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 229
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65 uGlyThrAspAsnIlePArgLysLeuPArgLysGlnIleIlePArgSers 82
280 -CGAATGCAACTTTCTTCACTGACAGTGG...AATGTTATGAAGAAAT 326

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99 GluleuArglleatGalaGluGluGlyAsnAsnThrSerThrTpyrGlu 115
374 GGTGACTCATTTACACCATTTCCGCAAGCTCAGATGGCTCCGCAAG 423
115 uValGluProPheValProPheLeuLysAlaGluLleGlyProProAspV 132
424 TACATTTAGAGCTGAGATTAAGCATGATGATACATCTCT...CCT 470
132 AlHisLeuGluAlaGluAspLysAlaLlelleLeuSerlleSerProPro 148
471 GGAACAAAGATAGCTTATGCTGGCTTGGATGGTTAAGCTTACATA 520
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521 TAGCTTACTATCTGGAAGAACTCTTACGCTGAGAAAGAAAGATTGAA 570
165 rSerValVallleTpyrLysAsnSerSerSerLeuGluGluThrGluT 182
571 ATATTATTCAGACATTAATAATTATTAACCTCAGACAGACACTAT 620
182 hrVallyrProGluAspLyslleTpyrLysLeuSerProGluLleThrTy 198
621 TGCTTAAGATTAAGACAGCACTACTACTGATGATGAAATTTGGTGTCTA 670
199 CysLeuLysVallysalGluLeuArgLeuGlnSerArgValGlyCsty 215
671 TAGCCGATCATCTGTATAAGACACAGCTGAAATGAAATACCTCCAC 720
215 rSerProVallyrCyslleAsnThrThrGluArgHisLysValrProSerP 232
721 CAGAAATATATGAGTACAGTGTCCCAAAATGCACTATGTTCTTAATG 770
232 roGluAsnValGluLleAsnValAspAsnGlnAlaTyrValLleuLysTyr 248
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1021 TACTTCTCAGCTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 1067
332 lePheProProVallleSerMetLysSerlleThrAspAspSerLeuHis 348
1068 ATCTATATCGGTGCTCCAAACAGTCTGAAACAGGCTGATGATGAG 1117
349 ValSerValSerAlaSerGluGluSerGluAsnMetSerValAsnGlnle 365
1118 TTTATCCATATTTATGAATTTATTTTGGGAAACACTTCAATCTG 1167
365 uTyrProLeuVallyrGluValllePheThrGluAsnThrSerAsnAlaG 382
1168 AGAGAAATATATGAGAAAAAAGTATGATGATGATGATGATGATGAT 1217

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382 lndrGlyValLeuGluLysArgThrAspPheThrPheProAsnLeuLys 398
1218 CCACGACTGATATATGTTGGAAGCCAGACACACACATGATGATGAAA 1267
399 ProLeuThrVallyrCysVallysalArgAlaLeuLleGluAsnAspAr 415
1268 GCTGATTAAGACAGTGTTTTATGACGCTGATGAGAAAAAACAAC 1317
415 gTTPAsnLysGlySerSerTyrSerAspThrValCysGluLysThrLysP 432
1318 CAGAAATTAACCTTAA 1334
432 roGluAsnThrSerLys 437

seq_name: SwIsProt_38:INRL_MOUSE
seq_documentation_block:
ID INRL_MOUSE STANDARD: PRT: 590 AA.
AC P33896;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
GN IFNAR1 OR IFNAR OR IFAR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1].
RP SEQUENCE FROM N.A.
RX MEDLINE: 92262522.
RA Uze G., Lutfalla G., Bandu M.T., Proudhon D., Mogensen K.E.;
RT "Behavior of a cloned murine interferon alpha/beta receptor expressed
in homosppecific or heterosppecific background."
RL Proc. Natl. Acad. Sci. U.S.A. 89:4774-4778(1992).
CC - FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
INCLUDING JAKS, TYRK, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
SUBUNITS THEMSELVES.
CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC - SIMILARITY: CONAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC - SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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or send an email to license@sib-sib.ch).
CC
DR EMBL: M89641; AAA37890.1;
DR PIR: A45283; A45283.
DR MGD: MGI:107658; IFNAR.
KW Receptor, Transmembrane, Glycoprotein, Signal.
FT SIGNAL 1 26
FT CHAIN 27 590 INTERFERON-ALPHA/BETA RECEPTOR ALPHA
FT FT
FT FT CHAIN
FT FT TRANSMEM
FT FT DOMAIN 27 429
FT FT DOMAIN 430 449
FT FT DISULFD 78 86 CYTOPLASMIC (POTENTIAL).
FT FT CARBOHYD 199 220 BY SIMILARITY
FT FT CARBOHYD 43 43
FT FT CARBOHYD 109 109
FT FT CARBOHYD 181 181
FT FT CARBOHYD 214 214
FT FT CARBOHYD 314 314
FT FT CARBOHYD 370 370
FT FT CARBOHYD 409 409
FT FT CARBOHYD 413 413
FT SEQUENCE 590 AA: 65776 MW: 76C6DF370185D3A CRC64;
SQ

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alignment_scores: length: 436
 Quality: 1069.00 Gaps: 4
 Ratio: 3.230
 Percent Similarity: 75.917 Percent Identity: 48.624

alignment_block:
 US-09-240-675-1 x INR1_MOUSE

Align seg 1/1 to: INR1_MOUSE from: 1 to: 590

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30 ATGCTCTCTCTCTGGGGGCGACGACCTAGTGTCTGCTGGCGGCGCC
1 MetleuAlaValIglAlaIalAlaLeuValIleuValIalIglAlaPr 17
80 ATGGGTGTGCGCCGACGCGGAGGTGGAAAAATCTAAATCTCTCAA
17 OTTPValLeuProSerAlaIalIglAlaIglAlaLeuValProGluA 34
130 AATGAGAGTGTGACATCATAGATGACACTTATCTTCTGAGGTGGAACAG
34 snIleAspValTyrIleIleAspAsnTyrThrLeuValTyrSerSer 50
180 AGCGATGATGTGCGGGAATGTGACTTTTCATTGATTCAAAAAAC
51 HisGlyIleSerMetGlySerValThrPheSerAlaIglTyrAlaGlyThly 67
230 TGGGATGATTAATGATAAATATGCTGGGTGCGAATATATCTACTA
67 sAspAlaIalAlystrPleuValProGluCysGlnHisThrThrTrt 84
280 CCAATGCAACTTTCTTCACTCAAGCTGAATGTTATGAGAATTAATAA
84 hrLysCysGlnPheSerLeuLeuAspThrAsnValTyrIleLysThrGln 100
330 TTGGGTATAGACGAGAAAAAGAAC...ACTTCTCATGGTATGAGT
101 PheArgValAlaGlnIglAlaIglAlaLeuValSerThrSerThrAsnGlnIva 117
377 TGACATCATTCACCATTTGCGAAGCTGCAATGTGCTCTCCAGAGATC
117 AspProPheIleProPheTyrThrAlaHisMetSerProProGluValA 134
427 ATTGAGAGCTGAGATAGAGCAATAGATGATACATCTCTCTGGAACA
134 rGleuGlnAlaGlnLysPlyAlaIleLeuValHisIleSerProProGly 150
477 AAAGTATGTTATGTGGCTTGGATGGTTAACTTATACATATAGCTT
151 GlnAspGlyAsnMetTrpAlaLeuGlnLysProSerPheSerTyrThrI 167
527 ACTTATGCGAAAACTCTGAGTGTAGAGAAAGATGAGATTAATATTT
527 eArgIleTrpGlnLysSerSerSerAspPlyLysThrIleAsnSerThrT 184
167 eArgIleTrpGlnLysSerSerSerAspPlyLysThrIleAsnSerThrT 184
577 ATTCGACATTAATAATTATTAACCTCTGACAGAGACTATTATGTCTA
200 YTYValIglLysIleProGluLeuLeuProGluThrThrTyrCysLeu 200
627 AAAGTTAAAGCGACACTACTTACGTCATGAGAAATGGGTGTATAGTC
201 GluValLysAlaIleHisProSerLeuLysLysHisSerAspTyrSerTh 217
677 AGTACATGTATTAAGACCAAGTGAATAATAGTACTTCACAGAGAA
217 YValIleGlnCysIleSerThrThrValAlaAsnLysMetProValProGlyA 234
727 AATAGAACTGAGTCCAAAATCAGAACTATGTTCTTAATAGGATAT
234 snLeuGlnValAlaPheIleGlnLysSerTyrValLeuLysTrpAspTyr 250
777 ...ACATATGCAAACTGACCTTTCAGTTCAGTCTCCAGCCCTTTT
251 IleAlaSerAlaAspValLeuPheArgAlaGlnTrpLeuProGlyTyrIse 267

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824 AAAAGAAATCCGAAACCATTTGTATTAATGAAACAAATCTGACT
267 rLysSerSerSerGlySerHisSerAspLysTrpLysProIleProThrC
874 GTGAAATGTCAAACTACCCAGCTGTCTTCTTCCAAAAGTTTTCAA
284 YsAlaAsnValGlnThrThrHisCysValPheSerGlnAspThrValTyr
924 AAGGAATTTACTTCTCCGCGTACAGACATCGATGAGAAATACACATC
301 ThrGlyThrPhePheLeuHisValGlnAlaSerGlnGlyAsnHisThrSe
974 TTTTGTCTGAGAGATAAAGTTGATGTAATCAATCAAGTTTCTTAC
317 rPheTrpSerGlnGlnLysPheIleAspSerGlnLysHisIleLeuPro
1024 TTCTCCAGCTTTTAACATTAGATCCCTTAGTATTCATTCATTCAT
334 rOProProValIleThrValThrAlaMetSerAspThrLeuValTyr
1074 ATGGGTCTCCAAAACAGCTCGAAGACGCCCTGTGATTCAGATATTC
351 ValAsnCysGlnAspSerThrCysAsp.....Gt 360
1124 ACTGATTATGAATATTTTGGGAAACACTTCAATGCTGAGAGAA
360 YLeuAsnTyrGlnIleIlePheTrpGlnAsnThrSerAsnThrLysIleS
1174 AAATATTCGAGAAAAAACTGATGTTACAGTTCTTAATTTGAACACCTG
377 erMetGlnLysAspGlyProGluPheThrLeuLysAsnGlnProLeu
1224 ACTGATATATGTGTGAAGCCAGACACACACATGATGATGAAGTGA
394 ThrValTyrCysValGlnAlaAlaArgVal...LeuPheArgAlaLeuLeuAs
1274 TAAAGCAGATGTTTGTAGTACGCTGTATGTGAGAAACAAACAGGAA
409 nLysThrSerAsnPheSerGlnLysLeuCysGlnLysThrArgProGlys
1324 ATACCTCT 1331
426 erPheSer 428

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seq_name: SwissProt_38:CRF4_HUMAN

seq_documentation_block:

ID	CRF4_HUMAN	STANDARD:	PRT:	325 AA.
AC	008334			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	01-OCT-1996 (Rel. 34, Last annotation update)			
DE	CYTOKINE RECEPTOR CLASS-II CRF2-4 PRECURSOR.			
GN	CRF4.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Catarrhini; Homiidae; Homo.			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=FETAL BRAIN;			
RX	MEDLINE: 93300510.			
RA	Lutfulia G., Gardiner K., Uze G.;			
RT	*A new member of the cytokine receptor gene family maps on chromosome			
RL	21 at less than 35 kb from IFNAR.			
RN	Genomics 16:366-373(1993).			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 96054036.			
RA	Lutfulia G., McInnis M.G., Antonarakis S.E., Uze G.;			
RT	*Structure of the human CRF4 gene: comparison with its IFNAR			
RL	neighbor.			
RD	J. Mol. Evol. 41:338-344(1995).			

01-APR-1990 (Rel. 14, Created).
01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
INSULIN RECEPTOR PRECURSOR (EC 2.7.1.112) (IR).
GN INSR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN
RP SEQUENCE FROM N.A.
RA MEDLINE; 90231337.
RA Goldstein B.J., Dudley A.L.;
RT The rat insulin receptor: primary structure and conservation of
RT tissue-specific alternative messenger RNA splicing." ;
RL Mol. Endocrinol. 4:235-244(1990).
[2]
RN PARTIAL SEQUENCE FROM N.A.
RP STRAIN-SPRAGUE-DAWLEY;
RA Liu Y., Tam J.W.O.;
RT Submitted (May-1997), to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS RECEPTOR BINDS INSULIN AND HAS A TYROSINE-PROTEIN
CC KINASE ACTIVITY.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -1- ENZYME REGULATION: AUTOPHOSPHORYLATION ACTIVATES THE KINASE
CC ACTIVITY.
CC -1- SUBUNIT: TETRAMER OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE
CC BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LIGAND-
CC BINDING DOMAIN, WHILE THE BETA CHAIN CARRY THE KINASE DOMAIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC
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CC
CC EMBL; M29014; AAAA1441.1; -

DR	EMBL	AF005776	AAB61414.1	
DR	EMBL	AF005777	AAB61415.1	
DR	EMBL	U80633	AAB38746.1	
DR	EMBL	U80632	AAB38968.1	
DR	EMBL	U80631	AAB38968.1	JOINED.
DR	EMBL	U80630	AAB38967.1	
DR	EMBL	U80629	AAB38967.1	JOINED.
DR	PIR	A36080	A36080.	
DR	HSPB	P06213	LINK.	
DR	PRINTS	PR00014	ENTPEP11.	
DR	PRINTS	PRO0109	TYRINASE	
DR	PROSITE	PS00107	PROTEIN_KINASE_ATP.1	
DR	PROSITE	PS00109	PROTEIN_KINASE_TYR.1	
DR	PROSITE	PS00239	RECEPTOR_TYR_KIN_II.1	
DR	PROSITE	PS50011	PROTEIN_KINASE_DOM.1	
DR	PFAM	PF00041	tn3.1	
DR	PFAM	PF00069	kinase.1	
DR	PFAM	PF00757	Furin-like.1	
DR	PFAM	PF01030	Recep_L-domain.1	
DR	Transferrase		tyrosine-protein kinase; Receptor; Transmembrane; Glycoprotein; ATP-binding; Phosphorylation; Signal; Repeat.	
KW	SIGNAL	1	26	
FT	CHAIN	27	760	INSULIN RECEPTOR, ALPHA-SUBUNIT.
FT	PROPEP	761	763	REMOVED IN MATURE FORM.
FT	CHAIN	764	1383	INSULIN RECEPTOR, BETA-SUBUNIT.
FT	DOMAIN	764	957	INTRACELLULAR (POTENTIAL).
FT	TRANSEM	958	978	POTENTIAL.
FT	DOMAIN	979	1383	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	619	848	FIBRONECTIN TYPE-III.
FT	DOMAIN	849	949	FIBRONECTIN TYPE-III.
FT	DOMAIN	1024	1299	PROTEIN KINASE.
FT	NP_BIND	1030	1038	ATP (BY SIMILARITY).
FT	BINDING	1058	1058	ATP.
FT	ACT_SITE	1160	1160	BY SIMILARITY.
FT	MOD_RES	1190	1190	PHOSPHORYLATION (AUTO-).
FT	ACT_SITE	1000	1000	IMPORTANT FOR BIOLOGICAL ACTIVITY
FT	DISULFID	461	494	BY SIMILARITY.
FT	DISULFID	550	550	INTERCHAIN (BY SIMILARITY).
FT	CARBOHYD	42	42	POTENTIAL.
FT	CARBOHYD	51	51	POTENTIAL.
FT	CARBOHYD	104	104	POTENTIAL.
FT	CARBOHYD	137	137	POTENTIAL.
FT	CARBOHYD	241	241	POTENTIAL.
FT	CARBOHYD	281	281	POTENTIAL.
FT	CARBOHYD	321	321	POTENTIAL.
FT	CARBOHYD	363	363	POTENTIAL.
FT	CARBOHYD	423	423	POTENTIAL.
FT	CARBOHYD	444	444	POTENTIAL.
FT	CARBOHYD	540	540	POTENTIAL.
FT	CARBOHYD	634	634	POTENTIAL.
FT	CARBOHYD	652	652	POTENTIAL.
FT	CARBOHYD	699	699	POTENTIAL.
FT	CARBOHYD	770	770	POTENTIAL.
FT	CARBOHYD	783	783	POTENTIAL.
FT	CARBOHYD	921	921	POTENTIAL.
FT	CARBOHYD	934	934	POTENTIAL.
FT	CONFLICT	1119	1119	L. > M (IN REF. 2).
FT	SEQUENCE	1383	AA: 16756	MM: 48919565902A944A CRC64;

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  Ratio: 0.645         Gaps: 21
  Percent Similarity: 41.561  Percent Identity: 19.620

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alignment_block:
US-09-240-675-1 x INSR_RAT
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Align seg 1/1 to: INSR_RAT from: 1 to: 1383

125 TCATAAGTAGAGTGCACATCATAGATGACCACTTATCTGAGGTGA 174
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 472 SerGlyThrLysGlyArgIngluArg.AsnAspIleAlaLeuLysThra 488

175 ACAGAGCGCATGAGTCGTGCGGAAAGTGCATTTTCATCGATTAATCA 2244
176 ||| |||
177 AGAGAGCGCATGAGTCGTGCGGAAAGTGCATTTTCATCGATTAATCA 2244
178 ||| |||
488 snc1yaspnlmlaserCysg1uasng1uleuLeuysPheSerPhe1le 5040
225 AAAACTGGGATGGAAAT 2424
505 ArgThrSerPheAspLys1lleLeuLeuArgTlrgLProTyrTrpProF 5211
243 TGGATAAATGCTGGGT 2611
531 oasPheArgAspLeuLeuG1yPheMetLeuPheTyrLysG1uAlaProF 5388
262 GTCGAGAAATTTACT AGTACCAAAAGCAACTTTCTTCA 2399
538 yrg1lansvalthrlcubPheasPrgLysInaspAlaCys 5500
300 CTCAGCTGAATGTTTATGAAAGAAATTAATTGCTATAGACGAGAAA 3449
550 5500
350 AGAAAACACTTTCATGCGTATGAGGTGACATTAATTAACCCATTTGCA 3999
551 GlySerAsnSerTlrgThValValasp 5599
400 AAGCTCAGATTGCTCTCCAGAAAGTACATTTAGAACTGAAGTAAAGCA 4499
350 IleAspTrpProGln ArgSerAsnSProls 5700
450 ATAGATATACATCTCTCTCGAGACAAAGATAGTATGCGGCTTT 4999
571 SerGlnThrProSerHisProls TrpLeu 5811
500 GGAGGTTTAACTTACATATAGCTTACTTATCTGGAAAACCTCTTCAg 5499
581 Lafgely 5883
550 GTGTGAAGAAGATGAATTAATTTATTCAGACATAAATTTATTA 5599
583 5883
600 CTCACACAGAGACTTACTTATGTCTAAAGTTAAGCAGCACTACTTAC 6449
584 LeuLysProlTlrgInG1uThValallePheValLysThrLeuValThrPh 6000
650 GTCATCGAAA ATGGGTCTATAGTCAGTACATTGTATTA 6900
600 eSerAspLumArgThrTyrG1yAlaLysSerAspLleIetyValg 617
691 AGACACAGCTGAAGAAATGAACTACTCTCCAGCAGAAATATATAGTCAgT 7400
617 InthAspAlaThAsnProSerValProlLeuAspProlIeSerValSer 6333
441 GTCGAAATCGAACTATGTCTTAAATG GATTATACATA 7811
634 AsnSerSerSerGlnIleIleLeuLysTrpLysProProSerAspProls 6500
782 TGCAAACATGACCTTCAAGTCAAGTCAAGTGCCTCAGCCCTTTTAAAAAGA 8311
650 nglYasn1leThr 6544
832 ATCTGGAACACATTTGATATAATG AAACAATACCTGACGTGA 878
655 HisTyrLeuValTyrTlrgLuarGlnAlaGlnLaspSerGlu 668
879 AATGTCAAACTACCCAGGTGTCTTCCCTCAAAACGTTTCCAAAAG 928
669 LeuPheGluLeuAspTyrCysLeu LysG1 678
929 AATTACTT CTCGGGTACAGAT 954
678 yLeuLysLeuProSerArgThrTrpSerProPheGluSerAspAs 695


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955 CGATGGAATATACACATCTTTGGTGTGAAGATA..... 992
||| .....
695 eGlnIyShIsAnSngInSerGIuTyAsPAsSerAlaSerGIuScys 711
993 .....AGTTTGATCTAGTCAATATCAAGCTTCTCTCCCTCCACT 1033
||| .....
712 SerCyProIyThrAsPserGlnIleuLySgIuLeuGIuSerse 728
1034 CTTTACATTAGTCCCTTAGTGATCATCTCCATCTATCGGCTGC 1083
||| .....
728 rPheA9g...LySthrPheGlnuSPyrLeuHIsAnSngValPheValP 744
1084 CAAGAAG...TCTGGAAC..... 1100
||| .....
744 rOmArgLySthrSerSerGIuSngLyAlaGlnuSPhrArgProSerArg 760
1101 .....ACGCTGT 1108
||| .....
761 LySArgArgSerLeuGIuValGIyAsnValThAlaThrProth 777
1109 GATCCAGATATCCACTGATTTATGAAATTTTGGGAAACACTT 1158
||| .....
777 rLeuPAsPAsPheProAsnIleSerSerThrIle.....AlaProThIs 792
1159 CAATGCTGAGAGAAATATATGAGAA.....AAACTGATGT 1199
||| .....
792 eThIsGlnGIuHIsArgProPheGlnuLySValAlaSnLySgIuSerIe 808
1200 ACAGTTCCTATTTGAACCACTGACTGTATGTGTGTAACCAAGC 1249
||| .....
809 ValIleSerGIuLeuArgHIsPheThrGIyTyArgIleGIuLeuGlnAl 825
1250 ACACACCAGGATGAAGAAAGCTGATTAACAGCTTTTATGAGCGCTG 1299
||| .....
825 ACySAnSngInuSPSerProGIuGIuArgSerGIyVal...AlaAlaTy 841
1300 TATGTGAGAAACAAACCA 1319
||| .....
841 AlSerAlaArgInMetPro 847
seq_name: SV4SProt_38: INGR_HUMAN
seq_documentation_block:
ID INGR_HUMAN STRAND: PRT: 489 AA.
AC P15260:
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119).
GN IFNGR1
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89003065.
RA Aguet M., Demeis Z., Meriin G.
RT "Molecular cloning and expression of the human interferon-gamma
RT receptor."
RT Cell 55:273-280(1988).
RN [2]
RP DISULFIDE BONDS, PARTIAL SEQUENCE, AND MUTAGENESIS.
RX MEDLINE: 93183911.
RA Stueber D., Friedlein A., Fountoulakis M., Lahn H.-W., Garotta G.;
RT Alignment of disulfide bonds of the extracellular domain of the
RT interferon-gamma receptor and investigation of their role in
RT biological activity.
RT Biochemistry 32:2423-2430(1993).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 26-248.
RX MEDLINE: 95342235.
RA Walter M.R., Windsor W.T., Nagabhushan T.L., Lundell D.J., Lunn C.A.,
RA Zaodny P.J., Narula S.K.

```

```

RT "Crystal structure of a complex between interferon-gamma and its
RT soluble high-affinity receptor."
RT Nature 376:230-235(1995).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 28-122 COMPLEX WITH ANTIBODY.
RX MEDLINE: 98035727.
RA Sogabe S., Stuart F., Henke C., Bridges A., Williams G., Birch A.,
RA Winkler F.K., Robinson J.A.;
RT "Neutralizing epitopes on the extracellular interferon gamma receptor
RT (IFNGAMMAR) alpha-chain characterized by homolog scanning mutagenesis
RT and X-ray crystal structure of the A6 fab-IFNGAMMAR-108 complex."
RT J. Mol. Biol. 273:882-897(1997).
CC -1- FUNCTION: RECEPTOR FOR INTERFERON GAMMA. TWO RECEPTORS BIND ONE
CC INTERFERON-GAMMA DIMER.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- PTM: PHOSPHORYLATED AT SER/THR RESIDUES.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J03143; AAA52731.1;
DR PIR: A31555; A31555.
DR PDB: 1JRH; 25-MAR-98.
DR MM: 107470;
DR MM: 209950;
KW Receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation;
KW Immunoglobulin domain; 3D-structure.
FT SIGNAL 1 17
FT CHAIN 18 489 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.
FT DOMAIN 18 245 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 246 266 POTENTIAL.
FT DOMAIN 267 489 CYTOPLASMIC (POTENTIAL).
FT DISULFID 77 85
FT DISULFID 122 167
FT DISULFID 195 200
FT DISULFID 214 235
FT CARBOHYD 34 34 POTENTIAL.
FT CARBOHYD 79 79 POTENTIAL.
FT CARBOHYD 86 86 POTENTIAL.
FT CARBOHYD 179 179 POTENTIAL.
FT CARBOHYD 240 240 POTENTIAL.
FT CARBOHYD 240 240 POTENTIAL.
FT SEQUENCE 489 AA; 54404 MW; DCF9E574DBF7400 CRC64;
SO
alignment_scores:
Quality: 124.50 Length: 351
Ratio: 0.666 Gaps: 16
Percent Similarity: 53.276 Percent Identity: 22.222
alignment_block:
US-09-240-675-1 x INGR_HUMAN
Align seg 1/1 to: INGR_HUMAN from: 1 to: 489
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1 MetAlaLeuLeuPheLeuLeuProLeuValMetGlnGlyValSerArgAl 17
83 GGTGTGTCGCGAGCC...GCAAGTGGAGAAATATCAATATCCCAAA 129
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17 agIuMetGIyThrAlaAsPLeuGIyProSerValProGIuProThA 34
130 AAGTAAAGTGCATCATATGATGACACTTATCTGAGTGGAACAG 179
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34 snvalthrileglsertyrinsmetasnprollevaltyrtpglutyr 50
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65 ntlygilyvallysasnserserlutrplleasplacysilleasnsiles 82
277 GTACCAATGCACTTTTCTTCTCAAGCGATGATGTTTAAAGAAAT 326
82 tshstlyrlycysasnilleaseraspisvalglyaspproserasnsers 98
327 AAATGCGATTAAGACA...GAAAGAAAACCTCTTCATG 367
99 Trrpvalargvallysalarvalgllyglulysglu.....Serlalatyr 113
368 GTATGAGGTTGACTCATTTTACACATTTGCAAAAGCTCAGATTGGCTC 417
113 talalyserserlunluphealvalcysargaspjlystilleglprop 130
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146 .....Pheh1 147
518 ATATAGCTTACTTATCTGGAACAACTCTCAGGTGAGAGAAAGATG 567
147 sproservalpheyval.....Asnrglyaspjluglunlual 160
568 AAAATATTTATTCAGACATTAATTTATACTGCACCGAGACACT 617
160 sp.....Tyraspproglunthrthr 166
618 TATTTGTTAAAGTTAAAGCAGCACTACTTACGTGAGAAATTTGGTGT 667
167 Cystylleargvaltyrasval.TyrvalArgmetasnly.....S 181
668 CTATAGCCGACTAC..ATGTATTAAGACCAAGCTGAAATGAAGACTAC 714
181 erglulileglnlyrlylethrthrclunlulysgluasppcysaspjlu 197
715 CTCACACAGAAATATAGAGTCAAGTGCCTCAATTCAGAACTAGTTC.. 762
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268 he.....Tyrilleyslileasnsproleuylsuglulys 280
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1047 T 1047
297 u 297
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AC P52179;
DT 01-OCT-1996 (rel. 34, Created)
DT 01-OCT-1996 (rel. 34, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE MYOHEXIN 1 (190 KD TITIN-ASSOCIATED PROTEIN) (190 KD CONNECTIN-
DE ASSOCIATED PROTEIN).
GN MYO1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SKELETAL MUSCLE;
RX MEDLINE: 94095665.
RA Vinckelmeier U., Obermann W., Weber K., Fuerst D.O.;
RT "The globular head domain of titin extends into the center of the
RT sarcomeric M band. cDNA cloning, epitope mapping and immunoelectron
RT microscopy of two titin-associated proteins."
RL J. Cell Sci. 106:319-330(1993).
CC - FUNCTION: MAJOR COMPONENT OF THE VERTEBRATE MYOFIBRILLAR M BAND.
CC - BINDS MYOSIN, TITIN, AND LIGHT MEROMYOSIN. THIS BINDING IS DOSE
CC DEPENDENT.
CC - SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC - SIMILARITY: CONTAINS 7 FIBRONECTIN TYPE III-LIKE DOMAINS.
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb.slb.ch).
CC -----
DR EMBL: X69090; CAA48833.1;
DR MIM: 603508;
DR PFM: PFM0047; fn3, 5.
DR PFM: PFM0047; 19; 3.
DR PRINTS: PR00014; FNTYPEIII.
KW Immunoglobulin domain; Muscle protein; Thick filament; Repeat.
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alignment_scores: Quality: 123.50 Length: 460
Ratio: 0.588 Gaps: 21

RA Lasemann B, Steck A.J. :
 RT Expression and developmental regulation of EphA-1, a neuronal
 RL Etk-like receptor tyrosine kinase in brain.
 CC Neuroscience 63:163-178(1994).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
 CC EPHRIN-A1, -A2, -A3, -A4 AND -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
 CC PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARE PRODUCED BY
 CC ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSED IN THE NERVOUS
 CC SYSTEM. PREDOMINANTLY EXPRESSED IN NEURONS.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
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 CC EMBL: X78689; CAA55357.1; -
 CC HSSP: P00523; 2PTR.
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 DR PRINTS: PRO0109; TYRKINASE.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
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 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
 DR PFAM: PF00041; fn3; 2.
 DR PFAM: PF00069; pkinase; 1.
 DR PFAM: PF01404; EphA1; 1.
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 KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing;
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 551 TGTAGAAGAAAGATTAAGATTAAT... TATTCAGACATTAATTAATTA 597
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 RX MEDLINE: 94068585.
 RA HO A.S.-T., Liu Y., Khan T.A., Hsu D.-H., Bazan J.F., Moore K.W.,
 RT Proc. Natl. Acad. Sci. U.S.A. 90:11267-11271(1993).
 CC -1- FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.

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 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 DR EMBL: L12120; AAA16156.1;
 DR MGD: MGI:96538; IL10RA.
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 16
 FT CHAIN 17 575
 FT DOMAIN 17 241 INTERLEUKIN-10 RECEPTOR.
 FT TRANSMEM 242 262 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 263 575 POTENTIAL.
 FT DISULFID 204 225 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 50 50 POTENTIAL.
 FT CARBOHYD 66 66 POTENTIAL.
 FT CARBOHYD 113 113 POTENTIAL.
 FT CARBOHYD 182 182 POTENTIAL.
 FT CARBOHYD 238 238 POTENTIAL.
 SO SEQUENCE 575 AA; 64248 MW; 820B9CD576F686B7 CRC64;
 Alignment_scores: Quality: 117.50 Length: 389
 Ratio: 0.691 Gaps: 16
 Percent Similarity: 43.702 Percent Identity: 20.308
 Alignment_block:
 US-09-240-675-1 x IIOR_MOUSE
 Align seg 1/1 to: IIOR_MOUSE from: 1 to: 575
 63 CTCGTGCGCGGCGCCATGCGGTGTCGCCAGCCGAGGTGAAAAA 112
 9 LeuValThrIleSerSerLeuSerLeuGluThrIleAlaTyrGlyThrG1 25
 113 TCTAAATCTCTCAAAAAGTAGAGGTGACATCATAGATGACAACTTA 162
 25 uLeuProSerProSerTyrValThrPheGlnAlaArgPheGlnHisI 42
 163 TCCGTAGCTG.....AACAGAGCGATGAGTCTGCGGAGAT 200
 42 IeLeuHisThrLysProIleProAsnGlnSerGlnSerThrTyrTyrGlu 58
 201 GTGACTTTTCATTCGATTATCAAAAACAGCGATGATTAATGGATMAA 250
 59 ValAlaIleu.....LysGlnTyrGlyLysSerThrThrPasnAs 71
 251 ATGTCGTGGTGCAGATATTACTAGTACCAACCAATTTCTTCAC 300
 71 PheHisIleCysArgLysAlaGlnAlaLeuSerCysAspLeuThrP 88
 301 TCAACCTAATGTTATAGAAA.....ATTAATTCGGATAGA 341
 88 heThrLeuAspLeuThrHisArgSerTyrGlyTyrArgAlaArgValArg 104
 342 GCA.....GAAAAAAGAAACCTTTCATCAGTATGAGTGACTCA...TT 385
 105 AlaValAspAsnSerGlnTyrSerAsnThrThrThrGluThrArgPh 121
 386 TACACATTTGCAAAACCTCAGATTGTCCTCCAGAACTACATTAGAG 435
 121 eRh..... 122
 436 CTGAAGATAGAGCATAGTATACATCTCTCTGGAACAAAGATGT 485
 123 ..ValAspGluValIleLeu.....ThrValAspSer 132
 486 GTT...ANGTGGCTTGAAGGTTTAAAGCTTACATATACTACTAT 532

[illegible]

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585 LeuLysProTPrInGIntYrAlaIlePheValLysThrLeuValThrPh 601
600 GTCAATGAAA.....ATTGCTGTATGTGCAGATCAATTGATA 690
601 eSerAspGluArgThrTYrGlyAlaLysSerSpIleIeTYrValG 618
691 AGACCACAGTTGAAATGAACTACTCCACAGAAATTTAGAGCTT 740
618 IntInAspAlaThrAsnProSerValProLeuAspProIleSerValSer 634
741 GTCCAAATCGAACTATGCTTTAAAG.....GATTATACAA 781
635 AsnSerSerSeGlnIleIleLeuLysTrpLysProProSerAspProAs 651
782 TGCAACATGACCTTCAAGTTCAGTGGGTCCAGCGCTTTTAAAAAGA 831
651 nGlyAsnIleThr..... 655
832 ATCCGGAACCACTTTGTATAATG.....AAACAATACCTGACTGTAA 878
656 .....HisTYrLeuValTYrTrpGluArgGlnIleGluAspSerGlu 669
879 AATGCAAAATCAACCCAGTGTCTCTTCTCAAAACGTTTCCAAAAAG 928
670 LeuPheGluLeuAspTrpCysLeu.....LysG 679
929 AATTACCT.....CTCCGGTACAGCAT 954
679 YLeuLysLeuProSerArgThrTrpSerProPheGluSerAspAspS 656
955 CTGATGAAATTAACACATCTTTTGGTCTGAAGAGATA..... 992
696 eGlnIleHisAsnGlnSerGluTYrAspAspSerAlaSerGluCysCys 712
993 .....AACTTGATACCTGAATATCAACGCTTCTCTACTCTCCACT 1033
713 SerCysProLYrThrAspSerGlnIleLeuLysGlnLeuGlnLysSer 729
1034 CTTTAACATTAGATCCCTAGTATGATTCATTCATCTATATACGGTCTC 1083
729 rPheArg.....LysThrPheGluAspTrpLeuHisAsnValAlaPheValP 745
1084 CAAACAGTCT.....GGAAAC..... 1100
745 roArgProSerArgLysArgArgSerLeuGlnIleValGlyAsnValThr 761
1101 .....ACGCTGTGTATCCAGATTTATCCACTATTTATGAATTTATTT 1144
762 AlaThrThrLeuThrLeuProAspPheProAsnValSerSerThrIleVal 718
1145 TTGGGAAACACTTCGAATGCTGAGAGAAATATATCGAGAA..... 1187
778 1.....ProHisSerGlnGluLuhHisArgProPheGlnLysValAla 793
1188 .....AAACTGATGTTCAGTCTCTAATTTGAAACACTGACTGATATATGT 1235
793 sGlyGlnSerLeuValIleSerGlyLeuArgHisPheThrGlyTYrArg 809
1236 GAGAAAGCCAGAGCACACACCACTGATGAAGAACTGAATTAAGCACTGT 1285
810 IlegIleGlnAlaLysAsnGlnAspSerProAspGluArgCysSerVa 826
1286 TTTTAGTACCGCTGTGTGAGAAACAAACCA 1319
826 1.....AlaAlaTYrValSerAlaArgThrMetPro 836
seq_name: swissProt_38:PPPD_HUMAN
seq_documentation_block:
ID PRPD_HUMAN STANDARD: PRT: 1912 AA.
AC P23468:
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)

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FT	DOMAIN	1020	1137	FIBRONECTIN TYPE-III
FT	DOMAIN	1375	1618	PROTEIN-TYROSINE PHOSPHATASE
FT	DOMAIN	1619	1912	PROTEIN-TYROSINE PHOSPHATASE
FT	ACT_SITE	1553	1553	BY SIMILARITY
FT	ACT_SITE	1844	1844	BY SIMILARITY
FT	SITE	1175	1178	CLEAVAGE (POTENTIAL)
FT	CARBOHYD	254	254	POTENTIAL
FT	CARBOHYD	299	299	POTENTIAL
FT	CARBOHYD	724	724	POTENTIAL
FT	CARBOHYD	832	832	POTENTIAL
FT	VARSPLIC	181	189	MISSING (IN KIDNEY ISOFORM)
FT	VARSPLIC	226	229	MISSING (IN KIDNEY ISOFORM)
FT	VARSPLIC	775	783	MISSING (IN KIDNEY ISOFORM)
FT	VARSPLIC	609	1137	MISSING (IN FETAL BRAIN ISOFORM)
FT	MOTAEIN	1178	1178	R-A: 2.5-FOLD REDUCTION IN CLEAVAGE
SO	SEQUENCE	1912 AA	214759 MW	3AB8CB032182B26 CRC64

alignment_scores:	Quality:	116.00	Length:	285
Ratio:	0.768		Gaps:	11
Percent Similarity:	52.982		Percent Identity:	21.754

Alignment block:
US-09-240-675-1 x PRPD_HUMAN

Align seg 1/1 to: PRPD_HUMAN from: 1 to: 1912

537	AAAACTCTCAGCTGTACAGAGAAGATGAAATAT..TATTCAG	563
361	LysAsnSerGlnGluLeuTyrGlnLeuAspGlyAlaLeuThrAr	377
584	ACATAAATTTATAACTCTCCACGACAGACTATGTCTAAATTA	633
377	GTYSeVValAlaGlyLeuSerProTyrSerAspTyrAlaPheArgValV	394
634	AGCAGCAGCTACTAGTCATGGAATATGGTGTCTATAGCCGCTACAT	683
394	AlaAlaValAsn.....AsnIleGlyAlaGlyProProSerGlu	406
684	TGTTAAAGACACACTTGAATAATGACTACT....CCACGAGAA	727
407	ProValLeuThrGlnThrSerGlnAlaProSerSerAlaProAlaG	433
728	TATGAAAGTCAGTGTCCAAATCAACAATACTGTCT..AATGSGATT	774
423	pValGlnAlaArgMetLeuSerSerThrThrIleValValGlnThrP	440
775	ATACATATGCAACATGACCTTCAAGTCAGTGCGCCACGCGCTTTA	824
440	Lupro..GluGluProAsnGlnGlnIleGlnGlyTyrArgValTyrT	455
825	AAAAGAAATCTGGAAACCATTTGTATTAAGGAACAAATACCTGACTG	874
456	ThrMetAspProThrGlnIleValAsnAsnTrpMetLys.....	468
875	TGAATATGCAAAATCAACCAAGTGTCTTCTCCAAAGCTTTCCAA	924
469	HisAsnValAlaAspSerGlnIleThrThrIleGlyAsnIleValProG	485
925	AAGCAATTTACCTTCCCGGACACAGCATGTATGGAATAATACATCTG	974
485	IndySerThrTyrSerValLysValLeuAlaIlePheThrSerIleGly	501
975	TTTTGGTCTGAAGAGATTAAGTTGTATGCAATTAACACTTCTCTACT	1024
502	ProLeuSerSerAspIleGlnValIleThrGlnThrGlyAlaProGlyG	518
1025	TCTCCAGCTTTACATTAATTAATCCCTTAAGTATCATTCATATCTATA	1074
518	nProLeuAsnPheLysAlaGluProGlnSerGlnThrSerIleLeuLeu	535
1075	TCTGCTCTCCAAAGAGTCTGGAACACGCGTGTATCGAGATTATTCGA	1124


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FT DOMAIN 266 364 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 368 464 FIBRONECTIN TYPE-III.
FT DOMAIN 496 592 FIBRONECTIN TYPE-III.
FT DOMAIN 597 693 FIBRONECTIN TYPE-III.
FT DOMAIN 696 794 FIBRONECTIN TYPE-III.
FT DOMAIN 797 898 FIBRONECTIN TYPE-III.
FT DOMAIN 899 990 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 1002 1095 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 1126 1205 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 1225 1312 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 1333 1427 IG-LIKE C2-TYPE DOMAIN.
SQ SEQUENCE 1450 AA: 163400 MW: E313C7D39FE6C6AC7 CRC64;

alignment_scores:
    Quality: 115.00      Length: 425
    Ratio: 0.618        Gaps: 26
Percent Similarity: 43.765 Percent Identity: 21.647

alignment_block:
US-09-240-675-1 x MPSF_CHKCK

Align seg 1/1 to: MPSF_CHKCK from: 1 to: 1450

87 TTGTCGACGCGCGAGGTGGAAAAAATCTAAATCTCTCAAAAAGTACA 136
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
366 LeuIleAlaGlyAlaProGly.....AlaProMetAspVally 378
137 GGTC..GACATCATAGATGACCACTTATCCGAGGTGACACGAGCG 183
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
378 scyHisAspAlaAsnAaGAspIlyrValIleValIhTriPlyserProA 395
184 ATGACTCTGTGGGAAAT....GTGACTTTTCATTCGATTATCAAAA 227
   ::::: ::::: ||| ||| ||| ||| ||| ||| ||| ||| |||
395 srthTrhSerGlnAsnProValIleGlyTrpPheValAspIlyscyGlu 411
228 ACTGGGAGGAAATATGGATAAATTTGTCGCGGTGTCGAATATCTAG 277
   ::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
412 ValGlyLeuGluAsnTrpVal..... 418
278 TACCAAAATGCAACTTTTCTTCACTCAAGCTGAAATGTTTAAAGAAATTA 327
   ::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
419 ..GlnCysAsnAspAlaProValIlyIleCylsLyTrpProValhTrG 434
328 AATFG.....CSTAAAGACGCAAAAAAGAA 353
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
434 IyLeuTrgluIyAlaYrSerTrpIlePheAspValArgAla..... 447
354 AACACTTCTCATGTGTATGATGATGGACATCTTACACCATTTGCGCAAGC 403
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
448 .....ValAsnSerAlaIlyIleSerhArgProse 457
404 TCAGATGTGCTCTCCAGAGTACATTTTAAAGCTGAAGAT...AAGG 447
   ::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
457 rArgValSerGluProValAlaAlaAlaLeuAspProValAspLeuIuArg 474
446 CATATGATATACATCTCTCTCGA.....ACAAAAGT 482
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
474 hGlnhTrpValhIshValAspGluGlyIlyIleValIleSerLysAsp 490
483 AATGTTATGTGGCTTGTGATGT..... 506
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
491 Asp.....LeuGluGlyAspIleGlnIleProGlyProProh 503
507 .....TRAGCTTACATATAGCTTACTTATCGGA 537
   ::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
503 rAsnValhIshAlaSerGluIleSerLysTrpThyValValAsnSerTrpA 520
538 AAAAC..... 542
520 spProProValAlProArgIyAlaTrgluProLeuTrhTrpPheIleGluLys 536
543 .....TCTTCAGGTGTGAGAAAGAGATTGAATAATATTATTTC.. 581

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537 SerMetValGlySerGlySerTrpGlnArgValAsnAlaGlnValAlaVala 553
552 .....AGCATTAATTTATTAACCTCTCCACGAGACTACTTAT 621
553 ILysSerProAlaGlyTAlaValAlaPheAspLeuAlaGlnGlyLysProTyr 570
622 GTCATAAGTTAAAGCAGACACTACTAGTCTAGTGAATAATGCTGTCTAT 671
570 alphaArgVal.....LeuSerAlaAsnLysHisGlyLysSer 582
672 AGTCAGACACTATTGTATAAGACACACAGTGTGAATAATGAACATA..... 713
583 AspProSerGlnIleThrGlnProIleGlnProGlnAspIleValVala 599
714 ..CTCCACACAGAAATATAGAAAGTCAAGTGTCCAAAT.....CAGAACT 756
599 LProSerAlaProGlyArgValAlaIleThrArgAsnThrLysThrSerV 616
757 ATGTCCTAAATGGGAT..... 773
616 alphaValGlnTrpAspLysProLysHisGlnLysAsnLeuTyrGlyTyr 632
774 TATACATATGCAAAACATGACCTTTCAAGTTCAGTGCCTCCACGCTTTT 823
633 TyrIleAspTyrSerValValGlySerAsnGlnTrp..... 644
824 AAAAAGAGATCTGGAACACATTTTATTAATGGAACAAATACCTGACT 873
645 .....GluProAlaAsnHis.....LysProIle..... 652
874 GTGAATAATGTAAACCTACCCAGTGTCTTCCCAAAAGCTTTCCAA 923
653 .....AspTyrAsnArg.....PheValValHisGlyLeuGlu 663
924 AAAGA...ATTACCTTCTCCGCTACAGCATCTGATGA..... 962
664 ThrGlyGlnGlnTyrIlePheArgValLysAlaValAsnAlaValGlyPh 680
963 ..AATACACATCTTTTGTCTGAAAGATTAAGTTATATCTGAAATAC 1011
680 eSerGlnAsnSerGlnGlnSerGlnAlaIleLys.....ValG 693
1012 AAGCTTCTACTCTCCAGCTTT.....ACATAGATCCCTTGT 1055
693 IAlaIleAlaLeuThrCysProSerTyrProHisGlyIleThrLeuLysAsn 709
1056 ..GATTCATTCATATCTATATCGT.....GTCCAAAACAGTCTGG 1096
710 CysAspArgLysLeuSerMetThrLeuGlyTyrPylsAlaProLysTyrSerG 726
1097 AAACAGCCCTGTGATCCAGATTAAT 1121
726 yGlySerProIleLeuGlyTyrTyr 734

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seq_name: SwissProt_38: TYO3_PAT

seq_documentation_block:

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ID 1103_PAT STANDARD; PRT: 880 AA.
AC P55166;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, last sequence update)
DT 15-JUN-1999 (Rel. 38, last annotation update)
DE TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN
DE KINASE SKY).
GN TYRO3 OR SKY.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 96104999

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RA Ohashi K., Honda S., Ichinomiya N., Nakamura T., Mizuno K.;
RT "Molecular cloning and in situ localization in the brain of rat sky
RT receptor tyrosine kinase."
RL J. Biochem. 117:1267-1275(1995).
CC -1- FUNCTION: MAY BE INVOLVED IN CELL ADHESION PROCESSES, PARTICULARLY
CC IN THE CENTRAL NERVOUS SYSTEM.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: ABUNDANT IN THE BRAIN AND LOWER LEVELS IN
CC OTHER TISSUES.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D37880; BAA07119.1;
DR HSSP: P11362; 1FGT.
DR PROSITE: PS00107; PROTEIN_KINASE_AMP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PFAM: PF00041; fn3; 2.
DR PFAM: PF00047; 1g; 2.
DR PFAM: PF00069; pkinae; 1.
DR Receptor: Glycoprotein; Tyrosine-protein kinase; ATP-binding;
DR Transferrase; Phosphorylation; Transmembrane; Signal; Repeat;
KW Immunoglobulin domain.
FT SIGNAL 1 30
FT CHAIN 31 880
FT DOMAIN 31 419
FT TRANSMEM 420 440
FT DOMAIN 441 880
FT DOMAIN 34 115
FT DOMAIN 131 200
FT DOMAIN 214 301
FT DOMAIN 305 401
FT DOMAIN 508 785
FT NP_BIND 514 522
FT BINDING 540 540
FT ACT_SITE 645 645
FT MOD_RES 676 676
FT CARBOHYD 53 53
FT CARBOHYD 75 75
FT CARBOHYD 181 181
FT CARBOHYD 220 220
FT CARBOHYD 230 230
FT CARBOHYD 283 283
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FT CARBOHYD 370 370
FT SEQUENCE 880 AA; 95918 MW; C3751E86AE5FA5B CRC64;

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alignment_scores:

Quality: 113.50 Length: 355
Ratio: 0.701 Gaps: 17
Percent Similarity: 45.634 Percent Identity: 22.254

alignment_block:

US-09-240-675-1.X TYO3_PAT

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15 LeuLeuLeuAlaGlyLeuAlaLeuLeuLeuLeuProly..... 27
83 GGCTGTTCTCCGACGCCAGCTGGAATAAATCTTAATCTCTCAAAAG 132

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28 .....SerAlaAlaAlaGlyLeuLysLeuMetGlyAlaProValLysM 42
133 TA.....GAGTCGACATC 146
42 eThValSerGlnGlyInpValLysLeuAsnGlySerValGlnGly 58
147 ATGATGACAACTTATCTCGAGTGAACAGACGATGCTGTCGG 196
59 MetAspAspProAspLeu...HisThrMetLysAspGlyAlaValGln 74
197 GAT.....GTGACTTTTCATTCGATTATCAAAAAGTGGATGG 237
74 nAsnAlaSerGlnValSerIleSerIleSerGlnGln..... 86
238 ATAAATGATAAATGTGCTGGTGCAGAAATATTACTAGTACCAATGC 287
87 ..AsnTrpIleGlyLeuLeuSerLeuLysSerAlaGlnArgSerAspAla 102
288 AACCTTTCTTCACTCAAGCTGAATGTTATGAGAAATTAATTGGGAT 337
103 GlyLeuTyTrpCysGlnValLysAspGlyGlnGlnThrLysIle..... 117
338 AAGACGAGAAAAGAAAACACTTCTTCATGATGAGTGAAGTCA... 383
118 .....SerGlnSerValTrpLeuThrValGlnGlyValP 129
384 .....TTTACACCATTTCCGAAAGCTCAGATGGTCTCCAGAAATGAT 428
129 rophepethrValGlnProLysAspLeuAlaValProAsnValPro 145
429 TTAGAAGCTGAAGATAGGCAATAGTATACATCTCTCTGGAACAAA 478
146 pheGlnLeuSerCysGlnAla.....ValGlyProProGlnP 158
479 AGATAGCTTATGCTG.....GCTTGAGATGCTTATAGCT 513
158 ovalThrIlePheTrpArgGlyProThrLysValGlyGlyProAlaS 175
514 TTACATATAGCTTACTATCTGAAAAACTCTCAGGTGAGAAAGAG 563
175 erSerProSerValLeu.....AspValThrGlyValThrGlnArg 188
564 ATGAAATATTATTATCCAGACATAAATTATTAACCTCCACAGAGAC 613
189 ThrGlnPheSerCysGlnAlaHisAsnIleLysGlyLeuAlaThrSer 205
614 TACTTATGCTTAAAGTTAAACGACACTACTAGCTATGGAATATG 663
205 gProAlaIleIleArgLeuGlnAla..... 213
664 GTGCTATAGTCCAGTACATTTGATTAAGCACACATGGAATGAAC 713
213 ..... 213
714 CCTCCA.....CCAGAAATATAGAGTC..AGTGTCCAAATATGAA 754
214 ProProAlaAlaProPheAsnIleThrValThrThrIleSerSerSer 230
755 CTATGCTCTTAATG.....GATTATACATATGCAACATG 792
230 nAlaSerValAlaTrpValProGlyAlaAspGlyLeuAlaLeuLeuHis 247
793 CCTTTCAGTTCAGTGCCTCCAGCCCTTTTAAAGAAATCCTGGAAAC 842
247 erGysThrValGlnValAlaHisAla.....ProGly.. 257
843 CATTGTATAATGAAACAAATACTGACTGGAATATGCAAACTAC 892
258 .....GlnTrpGlnAlaLeuAlaValAlaValProValProPro 271
893 CCAAGTGTCTTCTCCAAAAGTTTCCAAAAGAAATTACTCTCTGC 942
..... 111 1111

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271 eThCysLeuLeu...ArgAsnLeuAlaProAlaThrAsnTrpSerLeuA 287
943 GCGTACAGACATCTGATGCAATATACACATCTTTTGGCTGAGAGATA 992
287 rGValArgCysAlaAsnAlaLeuGlyProSerProTyArgLysAspTrpVal 303
993 AAGTTGATCTGAA 1007
304 ProPheGlnThrLys 308

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Mon Jun 5 12:50:59 2000

us-09-240-675-1.modif.rspt

Page 1

OM of: US-09-240-675-1 to: SPTREMBL_12.* out_format: pfs

Date: Jun 1, 2000 6:02 PM

About: Results were produced by the Gencore software, version 4.5.
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL-frame2.p2p.model -DEV-rip
-O/cgml2/US09-240-675-1/unat.30052000.165119.3020/app-query.fasta.1
-DB-SPTREMBL_12 -QFMT-fastan -SUFFIX-modif.rspt -GAP0-12.000
-GAP0-4.000 -MINMATCH-0.100 -LOOPEL-0.000 -LOOPEXT-0.000
-GAP0-6.000 -GAP0-10.000 -GAP0-10.000 -GAP0-10.000
-GAP0-10.000 -GAP0-10.000 -GAP0-10.000 -GAP0-10.000
-DEPOP-6.000 -DELEXT-7.000 -STRAT-1 -MATRIX-dlousum2
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct
-ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext -MINLEN-0
-MAXLEN-1000000 -USER-US09240675 -NCP0-6 -ICPU-3 -NO_XLPHY -WAIT
-THREADS-1

Search information block:

Query: US-09-240-675-1
Query length: 1343
Database: SPTREMBL_12.*
Database sequences: 225878
Search time (sec): 75.460000

Sequence	Strd Orig	ZScore	EScore	Len	Documentation
SP_invertebrate:09YHMO	691.50	1052.51	2.0e-51	569	09YHMO gallus gallus (chicken).
SP_invertebrate:061130	222.50	333.01	3.8e-11	349	061130 mus musculus (mouse).
SP_invertebrate:063953	203.00	303.35	1.8e-09	332	063953 mus musculus (mouse).
SP_invertebrate:09YHMO	189.50	282.29	2.6e-08	341	09YHMO gallus gallus (chicken).
SP_invertebrate:09W609	138.50	195.09	0.0007	918	09W609 gallus gallus (chicken).
SP_invertebrate:014936	132.00	190.56	0.0024	484	014936 homo sapiens (human).
SP_invertebrate:09YHMO	130.00	188.60	0.0028	508	09YHMO gallus gallus (chicken).
SP_invertebrate:09YHMO	130.00	177.80	0.0040	1493	09YHMO mus musculus (mouse).
SP_invertebrate:094537	129.00	176.96	0.0048	1375	094537 drosophila melanogaster.
SP_invertebrate:094538	129.00	176.07	0.0048	1536	094538 drosophila melanogaster.
SP_invertebrate:090610	127.50	174.23	0.0065	1443	090610 gallus gallus (chicken).
SP_invertebrate:098949	123.00	171.60	0.0150	873	098949 gallus gallus (chicken).
SP_invertebrate:092859	122.50	166.41	0.0174	1461	092859 homo sapiens (human).
SP_invertebrate:091562	122.50	166.41	0.0174	1461	091562 homo sapiens (human).
SP_invertebrate:091562	117.50	158.90	0.0468	1427	091562 xenopus laevis (afrikan).
SP_invertebrate:017859	117.50	158.00	0.0473	1585	017859 caenorhabditis elegans.
SP_invertebrate:092673	117.50	155.13	0.0489	2214	092673 homo sapiens (human).
SP_invertebrate:007784	117.00	162.92	0.0488	817	007784 gallus gallus (chicken).
SP_invertebrate:091767	115.50	158.40	0.0564	1284	091767 manduca sexta (tobacco).
SP_invertebrate:009946	115.50	162.46	0.0643	658	009946 caenorhabditis elegans.
SP_invertebrate:097603	115.50	156.12	0.0693	1377	097603 rattus norvegicus (rat).
SP_invertebrate:010466	115.50	156.12	0.1033	26926	010466 homo sapiens (human).
SP_invertebrate:09W675	113.00	155.44	0.1001	1040	09W675 brachydanio rerio (zebra).
SP_invertebrate:024495	113.00	150.12	0.1165	1767	024495 drosophila melanogaster.
SP_invertebrate:064604	113.00	149.51	0.1174	1898	064604 protein-tyrosine phosphatase.
SP_invertebrate:023020	113.00	139.56	0.1319	6048	023020 caenorhabditis elegans.
SP_invertebrate:023550	113.00	138.51	0.1336	6831	023550 caenorhabditis elegans.
SP_invertebrate:023551	113.00	138.11	0.1342	7160	023551 caenorhabditis elegans.
SP_invertebrate:029117	112.00	158.26	0.1268	572	029117 sus scrofa (pig).
SP_invertebrate:063155	111.50	149.53	0.1537	1445	063155 rattus norvegicus (rat).
SP_invertebrate:060468	111.50	149.53	0.1550	1571	060468 homo sapiens (human).
SP_invertebrate:095209	111.50	147.20	0.1579	1896	095209 cyrtolagus canaliculus.
SP_invertebrate:018094	110.00	143.56	0.2158	2213	018094 cyrtolagus canaliculus.
SP_invertebrate:018094	109.00	156.36	0.2223	416	018094 caenorhabditis elegans.
SP_invertebrate:095646	109.00	156.14	0.2238	427	095646 homo sapiens (human).
SP_invertebrate:062682	108.50	147.83	0.2688	1028	062682 rattus norvegicus (rat).
SP_invertebrate:077773	108.50	147.32	0.2704	1091	077773 sus scrofa (pig).
SP_invertebrate:054711	108.50	147.97	0.2880	2033	054711 mus musculus (mouse).
SP_invertebrate:088307	108.50	141.24	0.2905	2215	088307 mus musculus (mouse).
SP_invertebrate:091677	107.00	141.45	0.3794	1651	091677 homo sapiens (human).
SP_invertebrate:064487	106.50	139.50	0.4248	1894	064487 mus musculus (mouse).

SP_invertebrate:061210 + 105.50 138.27 0.5158 1825 061210 caenorhabditis
SP_invertebrate:091286 + 105.00 144.83 0.5224 777 091286 homo sapiens (hum
SP_invertebrate:013332 + 105.00 136.94 0.5732 1948 013332 homo sapiens (hum
SP_invertebrate:009165 + 105.00 120.61 0.6945 13055 009165 caenorhabditis

seq_name: SP_invertebrate:09YHMO

seq_documentation_block:

ID 09YHMO PRELIMINARY; PRT; 569 AA.
AC 09YHMO;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE INTERFERON ALPHA/BETA RECEPTOR 1.
GN IFNARI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA REBOUL J., GARDINER K., MONNERON D., UZE G., LUTFALLA G.
RT "Comparative genomic analysis of the interferon/interleukin-10
receptor gene cluster".
RL Genome Res. 0:0-0(1999).
DR EMBL; AF082664; AAD13669.1;
KW Receptor.
SQ SEQUENCE 569 AA; 64055 MW; F99BC099 CRC32;

alignment_scores:

Quality: 691.50 Length: 455
Ratio: 2.384 Gaps: 14
Percent Similarity: 63.736 Percent Identity: 37.363

alignment_block:

US-09-240-675-1 x 09YHMO ..
Align seg 1/1 to: 09YHMO from: 1 to: 569

12 TCGGGGGCTCCAGATGATGCTGCTCCGCGGCGGCGACACCTACT 61
6 CysAlaSerCylArgLeuAlaValLeuLeu.....CysVal 18
62 GCTGCGCGCGTGGCGCCATGGCTGTCGCCAGCGCGAGTGGAAAA 111
18 IleuValValValSer.....ArgCysAlaLeuGlnThra 31
112 ACTTAATCTCTCTCAAAAGTAGAGTGCATCATATGATGACAACTTT 161
31 SduLeuYserProGlnAspIleGlnValValValAsnThrAspHe 47
162 ATCCGAGGTGAGACAGGAGCATGCTGCGGAGATGACCTTTTC 211
48 ThrLeuMetThrAspThrThrThrThrThrThrThrThrThrThr 63
212 ATTCATTATCA.....AAACTGGATGATTAATGGA 246
63 TAlaGlnThrGlnCysPheAspAspLeuGlnThrSerGlnProGlnI 80
247 TAAATTCGTCGGGTGATGATATTAATTAATGACAAATGCACTTTCT 296
80 YGAlaLeuSerCylCysGlnAsnValSerHisThrGlnCysAspHe 96
297 TACACAGCTGAATGTTATGACAGAAATTAATGCGGATTAAGACGA 346
97 SerAlaIleThrAlaThrThrThrThrThrThrThrThrThrThr 113
347 A...AAGAAAACTCTTCATGATGATGATGATGATGATGATGATGAT 393
113 TAlaGlnThrGlnAlaYserProThrSerSerIleHeGlnIleThrPro 130
394 TTCCGAAAGCTCAATGCTGCTCCAGAGATGATGATGATGATGATGAT 443

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130 yfcilullealeglnileglyproptogluillealeuglnserlleasn 146
444 AAGGCAATAGTGTACACATCTCTCGAACAAGATAGTGT ..... 488
147 GlyAlaIleLysIleAsnIleSerProptogluAlaAsnGlnValArgly 163
489 ATGGGGCTTGGAGTGTAAAGCTTACATACCTTACTTATGTGGA 537
163 smetTP...leuIleSerValPhePheLysTyrAsnValIleTyr 179
538 AAACCTTCAGCTGTGAGAAAGATGAAATTTATTCACACAT 567
179 spnsSerSerAsnVal...GlnLysValArgSerIleLeuProIleAsp 194
588 AAATTTATTAATCTCACAGAGACTTATTTGTTAAAGTAAAG 637
195 ValIleAsnAspLeuAlaProGlnTyrTyrCysLeuLysValGlnAl 211
638 AGCACTACTTACGTATGAAAAATGGTCTATGTCACATCATGTA 687
211 aTrrValProLeuGlnAspLysGlyLeuPheSerProIleHisCysI 228
688 TAAGACACACAGTTGAA...AATGAACTACCTCCACAGAAATATGAA 734
228 IeLysThrThrAlaGlyValAsnAspLeuLysCysProThrAsnValArg 244
735 GTGAGTGTCCAAATCAGAACTATGTTCTTAATGGATATACAT 782
245 ValPheAlaLeuAsnMetLysPheTyrIleLeuTyrAsnHisTyrAs 261
783 GCMAACATGACCTTTCAGCTAGTGGCTCCAGCCCTTTTAAAGA 831
261 ngIuHisValThrTyrThrValGlnTyrLeuThrGlyTyrLeuLysAsn 278
832 ATCTGGAAACCATTTGTATTAATGGAACAATACCTGACGTGAAAT 881
278 eutTyrAspTyrSerSerLysTyrPoiLysValSerGlyCysGlnAsn 294
882 GTCAAACTACCCAGTGT ..... GTCTTCCCTCAAAACGT 916
295 IleThrSerMetLysCysAsnLeuSerSerValIleLysProThrSer 310
917 TTTCACAAAAGAAATTACCTTCCCGCTCAAGCATGTGATGGAATA 966
311 .....AlaSerTyrTyrPheArgValGlnAlaMetAsnGlnTyr 324
967 ACACATTTTGTGCTGAGAGATTAAGTTGTATCTGAATACAAACGT 1016
324 eLysSerCysLeuSerLysAspValGlnValAspProIleValThrAsn 340
1017 TTCTTACTTCCCTCAGCTTATACATTAAGTCTTATGATTCATTC 1066
341 GlnIleGlyProProAspValLysValAspIleSerAspValLeuAsn 357
1067 TATCTATATGCGTGTCCAAACAGCTGGAACACCCCTGTATCCAG 1116
357 sIleLysIleThrProPoiGlyLysProGlnAsnLysIleMetSerAsp 374
1117 ATATTCAGTATTTATGAATTTTGTGGGAAACACTGAAAGCT 1166
374 eutTyrAspPheSerTyrGlnIleLeuTyrTyrLysAsnSerSerAspAsn 390
1167 GACAGAAAAATTAATCGAAAAAAACATGAT ..... GTTACAGTCC 1207
391 GlnGlnIleValLysMetLysGlnThrLysGlnThrIleAlaThrLys 407
1208 TAATTTAAACCACTGATATATGTGTGAAGGCAAGGCAAGCA 1257
407 rAspLeuAlaToserThrLeuTyrCysValLysValGlnAla.....P 422
1258 TGCATGAAAAGCTGAATAAAGCAGTGTTTTAACTGACGCTGATGTAG 1307

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422 heserGluAlaTyrAsnLysSerSerAspPheSerArgGluGlnCysIle 438
1308 AAACAAAACACAGA 1322
439 GlyThrAlaGly 443
seq_name: sp_rudent:061190
seq_documentation_block:
ID 061190 PRELIMINARY; PRT; 349 AA.
AC 061190:
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE CYTOKINE RECEPTOR FAMILY 2, MEMBER 4 (CLASS II CYTOKINE RECEPTOR 4).
GN IL10RB OR CRFB4 OR CRF2-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97199375.
RA GIBBS V.C.; PENNICA D.;
RT *CRF2-4: Isolation of cDNA clones encoding the human and mouse
RT proteins.
RL Gene 186:97-101(1997).
DR EMBL; U53696; AAC53062.1;
DR MGD; MGI:109380; il10rb.
DR PFM; PF00041; fn3.1.
SQ SEQUENCE 349 AA; 39774 MW; 4AC1802A CRC32;
alignment_scores:
Quality: 222.50 Length: 214
Ratio: 1.660 Gaps: 9
Percent Similarity: 62.617 Percent Identity: 26.168
alignment_block:
US-09-240-675-1 x 061190 ..
Align seg 1/1 to: 061190 from: 1 to: 349
711 CTACCTCCACAGAAATATAGACAGTGTCCAAATCAGACTATGT 760
21 IleProProGlnLysValArgMetLysSerValAspPheLysAsnI 37
761 TCTTAATGGAT ..... TATACATATGCAACATGACCTTCAAG 801
37 eleuGlnTyrPoiLysValProAlaPheProLysThrAsnLeuThrPhe 54
802 TTCAGTGGCTCCAGCCCTTTTAAAGAAATCTGGAACCATTTGT 851
54 IeGlnTyr ..... Gln 57
852 AAATGGAACAAATACCTGAC...TGTGAATATGCAAACTACCCAGTG 898
58 SerTyrArgSerPheGlnAspHisCysLysArgGlnAlaSerThrGln 74
899 TGTCTTCTCCAAACGTTTCCAAAGAAATTAACCTTCCGCGTAC 948
74 sAspPhe...SerHisLeuSerLysTyrGlyLysArgTyrValArgVal 90
949 AAGCATGTATGGAATATACATCTTTTGTGTGTGAGAGATTAAGTT 998
90 rGlnIleLysLeuAlaAspGlnLysSerGlnTyr...ValAsnValThrPhe 105
999 GATCTGAAATGCAAGCTTCTTACTGCTCCAGCTTAACTATGATG 1048
106 CysProValGlnAspThrIleIleGlyProProGlnMetGlnIleLys 122
1049 CTTTACTGATTCATTCATATATATATATGAGTGTCCAAACGCTGGA 1098
122 rLeuAlaGlnSerLeuHisLeuArgPheSerAlaPro...GlnIleGln 138

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1099 ACACCCCTGTGATCCAGATTATCACTGATTATGAA..... 1136
1137 ..ATTATTTTGGGAAAACCTTCAATGCTGAGAAAATTTTCGA 1183
155 ArgValIGLTyTTrpLysAsnGLYThrAsnGLuLysPheGlnValIse 171
1184 GAAAAAATGATGATTACAGTTCCTTAATTGAAACCATGACTGATTAT 1233
171 rProtyrAspSerGluValLeuLysAsnLeuGluProtyrThrTyrC 188
1234 GTGTGAACCCAGACACACACATGATGAGAAAAGCTGAATTAACCACT 1283
188 yAlIeGlnValIGlnGLyPheLeuLysAsnPoln.....AsnArgThrGLy 202
1284 GTTTTGTAGTACGCTGTATGTGAGAAAACAAAACAGAAAT 1325
203 GluTrpSerGluProIleCysGluArgThr.....GlyAsn 214
seq_name: sp_rodent:063953

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seq_documentation_block:
ID 063953 PRELIMINARY: PRT: 332 AA.
AC 063953
DT 01-NOV-1996 (TRENBLREL 01, Created)
DT 01-NOV-1996 (TRENBLREL 01, Last sequence update)
DT 01-NOV-1999 (TRENBLREL 12, Last annotation update)
DE INTERFERON GAMMA RECEPTOR 2 (INTERFERON GAMMA RECEPTOR BETA SUBUNIT).
GN IFNGR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
NC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
[2]
SEQUENCE FROM N.A.
RA MEDLINE; 94170381.
RA HEMMI S., BOHNI R., STARK G., DI MARCO P., AGNET M.,
RT "A novel member of the interferon receptor family complements
RT functional of the murine interferon gamma receptor in human
RT cells."
RT Cell 76:803-810(1994).
RN
RP
RC STRAIN-129SV/3.
RX MEDLINE; 97128072.
RA EBERSPERGER C., RHEE S., MUTHUKUMARAN G., LEMBO D., DONNELLY R.,
RA PESTKA S., DEMBIC Z.,
RT "Genomic organization and promoter analysis of the gene IfngR2
RT encoding the second chain of the mouse interferon gamma receptor."
RT Scand J Immunol 44:599-606(1996).
RL
DR EMBL; U65599; AAC52938.1;
DR EMBL; U65594; AAC52938.1; JOINED.
DR EMBL; U65595; AAC52938.1; JOINED.
DR EMBL; U65596; AAC52938.1; JOINED.
DR EMBL; U65597; AAC52938.1; JOINED.
DR EMBL; U65598; AAC52938.1; JOINED.
DR EMBL; S69336; AB30165.1;
DR MGD; MG1107654; IfngR2.
DR PRAM; PF00041; fn3; 1.
SQ SEQUENCE 332 AA; 37471 MW; 0BF24E9E CRC32;

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alignment_scores:
Quality: 203.00 Length: 229
Ratio: 1.471 Gaps: 13
Percent Similarity: 60.262 Percent Identity: 30.131

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Alignment block:
US-09-240-675-1 x 063953

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Align seg 1/1 to: 063953 from: 1 to: 332

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87 TTGCGCAGCCGACGTGCA.....AAAATCTAAATCTCC 124
16 LeuGlyAlaAlaIleSerSerProAspSerPheSerGlnLeuAlaIlePr 32
125 TCAAAAAGTAGAGTCGACATCATGATGACAACTTTATCCAGAGTGA 174
32 OleuAsnProAlaGluHisIleLeuThrAsnAspLeuIleLeuThrTrp 49
175 ACAGAGCCGATGAGTCT.....GTGCGGAATGTGACT 206
49 LuProSerProSerSerAsnAspProAlaGlyValGlyGlnValGlu 65
207 TTTTATTCGATTATCAAAAACGTGGATGGAT...AATGGATAAAT 253
66 TyrSerPhe.....IleAspGlySerThrPheIleArgIle 76
254 G.....TCTGGGTGTCAGATATATATAGTACGCAATGCACTTTGCT 297
76 uLeuGluProAsnCysThrAspIleThrGluThrLysCysAspLeuThr 93
298 CA.....CTCAGCTGAATGTTATGAA...GAATTAATTCGCT 335
336 ATTAAGACGAGAAAAGAAAC...ACTTCTCATGCTGTAGAGTCTACT 382
110 ValArgAlaLysArgGlyAsnLeuThrSerLysTrpValGlyLeuGluPr 126
383 ATTACACCATTTCCAAAGCTCAGATGGCTCCAGAA...GTACACT 429
126 oPheGlnHisThrGluAsnValThrValGlyProProLysAsnIleSerV 143
430 TAGAAGCTGAAACATAGGCAATAGTATGATACATCTCTCTGAGAACAA 479
143 alThrProGlyLysGlySerLeuValIleHisPheSerProProPheAsp 159
480 GATATGTTATGTGGGCTTTGATGTGTTAACTTACATATAGTTCCT 529
160 .....ValPheHisGlyAlaThrPheGlnThrLeuValAlaH1 171
530 TATCTGAAAAACCTTCAGGTGTGAGAAAGATGAAATATATATAT 579
171 sTryTrpGluLysSerGluThrGlnGlnGlnValGluGlyProPheL 188
580 CCAAGCATTAATTTAT...AAACTCACCAGACACTACTATTGT 623
188 ySerAsnSerIleValLeuGlyAsnLeuLysProTyrArgValTyrCys 204
624 CTAAAGCTTAAGCAGCACTA...CTTACGTCAGGAAAT 662
205 LeuGlnThrGluLysGlnLeuIleLeuLysAsnLysLysIleArgProH1 221
663 GGTGTCTATAGTCCAGATCATGATTAAGACCA 698
221 sGlyLeuLeuSerAsnValSerCysHisGluThrThr 233
seq_name: sp_vertebrate:09YGC8
seq_documentation_block:
ID 09YGC8 PRELIMINARY: PRT: 341 AA.
AC 09YGC8
DT 01-MAY-1999 (TRENBLREL 10, Created)
DT 01-MAY-1999 (TRENBLREL 10, Last sequence update)
DT 01-MAY-1999 (TRENBLREL 10, Last annotation update)
DE INTERLEUKIN-10 RECEPTOR 2.
GN IL10R2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
NC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
[1]
SEQUENCE FROM N.A.
RA REBOUD J., GARDINER K., MONNERON D., UZE G., LUTFALLA G.,
RN
RT "Comparative genomic analysis of the interferon/interleukin-10

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468 CCTGGACAAAGATAGTGTATGGCTTGATGCTTAAAC... 512
331 .....SerlysglyProthrIlethrPargThrIleAspValSerProSe 345
513 .....TTACATTAAGTCTACTATCTGAAA.....A 540
345 rProAlaThrIleValArgLeuMetThrPysAlaLeuGluProPheG 362
541 ACTCTTCAGGTGA.....GAGAA 560
362 IuAlaAsnGlyValIleLeuGlnTyrGluValThrIleArgAlaLysPro 378
561 AGGATGAAATATTTATTCAGACATAAATTTAATACCTCA..... 605
379 ProLeuSerHisProProSerThrSerHisValIleThrThrSerLeuTh 395
606 .....CCAGAGACTACTATATGCTTAAAGTTAAGCAGACACTAC 645
395 rLeuLysLeuProAsnGlyThrTyr.....GluValThrValY 408
646 TTACGTATGGAATATGCTGCTATATCCAGTACATGTATTAAGACC 695
408 aAlaHisAsnArgValIleGlyAla...SerProProSerValLeuLeuIle 423
696 ACAGTTGAAATGAACTACCTCCACCAGAAATTAAGAAGTCACTCCA 745
424 ProSerSerAsnSerLysAlaProValLysAsnIleArgThrLeuProLy 440
746 AAATAGACTATATGCTTAAATGGAGATTATACATATGCAACATGACT 795
440 sAspLysLysLeuThrPValIleGlyThrAlaProAsnValIleLeuLST 457
796 TTCAGTTCAGTGCCTCAGCCCTTTTAAAAAGAAATCCGGAACAT 845
457 yValIleGluThrPys.....LeuMetSerAsnSerSerAspYs 470
846 TTGZTAAATGGAACAAATACCTGACTGTAATGTCAAAACATACCA 895
471 IleThrGluThrPglThrGluProLy...AsnIle..... 481
896 GTGTGCTTTCTCTCAAAAGCTTTCCAAAAGA..... 929
482 .....GlnGlyThrTyrLeuLysGlyAspIleLysProPheL 494
930 ATTACTCTCTCCGCTACAGCA.....TCGTGGAATATACCA 971
494 yScyTyrLeuIleThrValTyrProLeuPheAlaAspLysGlnGlySer 510
972 TCTTTTGGCTGAGAGATTAAGTTGATCTGTAATACATCAAGCTTCT 1021
511 Gly.....GlnSerValLysAlaTyrLe 518
1022 ACTTCCT.....CGAGTCTTAACATTAAGATCCCTTA 1053
518 uGlnGlnIleLysArgProSerLysGlyProThrValGlnThrLysLysValG 535
1054 GTGATTCATTCATATC.....TAATGGGTGCTCCAAAAG 1091
535 lLysAlaGlnAlaValLeuThrThrPasnHisLeuThrValAspLysInd 551
1092 TCTGGAACAGCCCTGTATCCAGATATTCACATGATTATGAAATAT 1141
552 AsnGly.....PheIleArgSerTyrThrIleLeuTyrLysThrVa 565
1142 TTTTGGGAAAACACTTAATATGCTGAGAGAAAATTAATGAGAAAAA 1191
565 lAspLysAsnGluThrAlaValSer.....ValAspProSerLysT 579
1192 CTGATGTACAGTTCCTAATTTGAACACATGACGTATATTTGTGAA 1241
579 hGluTyrThrLeuSerSerLeuThrSerAspThrLeuTyrThrValArg 595

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1242 GCCAGACACACACC 1256
596 MetMetAlaIleTyrThr 600

seq_name: sp_human:014936
seq_documentation block:
ID 014936 PRELIMINARY: PRT: 484 AA.
AC Q14936;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89003065.
RA AGUET M., DEMBIC Z., MERLIN G.;
RT "Molecular cloning and expression of the human interferon-gamma
RT receptor."
RL Cell 55:273-280(1988).
RN [2]
RP PARTIAL SEQUENCE FROM N.A.
RX MEDLINE: 97246734.
RA MERLIN G., VAN DER LEEDE B.-J.M., MCKRONE K., KNEZEVIC N.,
RA BANNARATH W., ROMQUIN N., VIEGAS-PEQUIGNOT E., KIEFER H., AGUET M.,
RA DEMBIC Z.;
RT "The gene for the ligand binding chain of the human interferon gamma
RT receptor."
RL Immunogenetics 45:413-421(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA DEMBIC Z.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBD databases.
DR EMBL: U19247; AAC52064.1; JOINED.
DR EMBL: U19241; AAC52064.1; JOINED.
DR EMBL: U19242; AAC52064.1; JOINED.
DR EMBL: U19243; AAC52064.1; JOINED.
DR EMBL: U19244; AAC52064.1; JOINED.
DR EMBL: U19245; AAC52064.1; JOINED.
DR EMBL: U19246; AAC52064.1; JOINED.
SO SEQUENCE 484 AA; 53818 MW; EBC99D1F CRC32;

alignment_scores:
Quality: 132.00 Length: 350
Ratio: 0.714 Gaps: 15
Percent Similarity: 52.857 Percent Identity: 22.000

alignment_block:
US-09-240-675-1 x 014936
Align: seq 1/7 to: 014936 from: 1 to: 484

33 GTCTCTCTCTGGGCGGAGACCCCTAGTCTGCTCCCTGGGCCCATG 82
1 MetAlaLeuLeuPheLeuLysProLeuValMetGlnIleValSerArgAl 17
83 GGTGTGCGCCGACCC...GCAGTGGAAAAAATCTAAATCTCCCTCAA 129
17 aglMetGlyThrIleAspLeuGlyProSerSerValProThrProThra 34
130 AAGTAGAGTCTGACATATGATGACACACTTATCCGAGGTGGAACAG 179
34 snValThrIleGlnSerTyrAsnMetAsnProIleValTyrTpgLutyr 50
180 AGCGATGAGTCTGCGGAGATG...ACTTTTCATTCATATCAAAA 226
51 .....GlnIleMetProGlnValProValPheThrValGlnValLysAs 65
227 AACTGGATGGATTAATGATTAATAAATGCTGGGTGTCAGAAATTACTA 276

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      65 nTyrGlyValLysAsnSerGluThrIleAspAlaCysIleAsnIleSerH 82
      277 GPACCAAAATGCACTTTCTTCACCTCAAGCTGAATGTTATGAAAGAAAT 326
      82 IseIstYrCysAsnIleSerAAspHisValGlyAspProSerAsnSerIeu 98
      327 AAATTCGCGATTAAGACA.....GAAAAAGAAACACTCTTCATG 367
      99 TrpValArgValLysAlaArgValGlyGlnLysGlu.....SerAlaTy 113
      368 GATGAGGTTGACTCATTTACACCATTTGCGCAAGCTGAGATGGCGCC 417
      113 IAlaLysSerGluGlnPheAlaValLysArgAspGlyLysIleGlyPro 130
      418 CAGAACTACATTTAGAACTGAAGAAAGCAATGATGATACACATCTCT 467
      130 rOlYsIeuAspIleArgLysGlnGluLysGlnIleMetIleAspIle... 145
      468 CCTGGACAAAGATAGTGTATGTGGCTTTGATGGCTTTAAGCTTAC 517
      146 .....PheH 147
      518 AATAGCTTACTATCTGAAAAACCTTCAGCTGAGAGAAAGATG 567
      147 sProSerValPheVal.....AsnGlyAspGluGlnGlnValA 160
      568 AAAATTTTATTCACACATTAATTTATTAATCTCACAGAGACTACT 617
      160 sP.....TyrAspProGluThr 166
      618 TATGTCTAAATTAAGACAGACTACTGATGAAATTTGGTGT 667
      167 CysTyrIleArgValTyrAsnValTyrValArgMetAsnGly.....S 181
      668 CTATAGCCGCTGAC...ATTGATAAAGACACAGTTGAAAAATGACTAC 714
      181 eArgIleGlnTyrIleLeuThrGlnLysGlnAspPyrCysAspGlu 197
      715 CTCACACAGAAATATAGAGTCACTGCTCAAAATCAGAACTATGTTCT 764
      198 IleGlnCysIleLeuAlaIleProValIleSerIleAsnSerGlnTyr 214
      765 AAT.....GGGATATATATGCAACATGACCTTCAACTGAG 808
      214 sSerAlaGlnGlyValLeuHisVal.....TyrGlyV 225
      809 GCTCCACGCTTTTAAAGAGATCTGGAACACT.....TGT 849
      225 alhTrhTrgluYsSerLysGlnValCysIleThrIlePheAsnSer 241
      850 ATAATGGAACAAATACCTGACTGTAATGTAATGCAAACTACCACTGT 899
      242 IleLysGlySerLeuThrIleProValAlaIleValIleuSerIle 258
      900 GCTTTCCTCAAAAGCTTTCAAAAGAAATTTACTCTCCGCGACA 949
      258 uValPheIleCysPheTyrIleLysLys..... 267
      950 AGCATGTGAGGAATTAACATCTTTTGTGTGAGAGATAAGTTG 999
      268 .....IleAsnProLeuLysGlnLysSerIle 276
      1000 ATACTGAATACAGCTTCTCTACTCTCTCAGCTCTTAACATTAAT 1047
      277 IleLeuProLysSerLeuIleSerValValArgSerIleAlaThrIleGlu 292
      seq_name: sp_vertedrate:09YH9
      seq_documentation_block:
      ID 09YH9 PRELIMINARY; PRT: 508 AA.
      AC 09YH9;
      DT 01-MAY-1999 (TREMblrel 10, Created)

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DT 01-MAY-1999 (TREMblrel 10, last sequence update)
DT 01-NOV-1999 (TREMblrel 12, last annotation update)
DE INTERFERON ALPHA/BETA RECEPTOR 2.
GN IFNAR2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER.
RA REBOUL J., GARDINER K., MONNERON D., UZE G., LUTPALLA G.;
RT "Comparative genomic analysis of the interferon/interleukin-10
RL genome Res. 0:0-0(1999).
DR EMBL; AF082665; AAD13670.1;
DR HSSP; P13726; ITFH.
KW Receptor.
SQ SEQUENCE 508 AA; 57049 MW; 2DCAE498 CRC32.

alignment_scores:
  Quality: 131.00      Length: 502
  Ratio: 0.567        Gaps: 29
  Percent Similarity: 46.016      Percent Identity: 21.116

alignment_block:
  US-09-240-675-1 x 09YH9
  Align seg 1/1 to: 09YH9 from: 1 to: 508

30. ATGTCGCTCTCTGCGCGCAGC.....ACCTAGTGTGCT 67
   |||||.....
   1 MetGlnThrIleuMetGlyLysProLeuArgPheTyrGlnLeuValPheVal 17
68. CCGCGTGGCCCATGGGTGTGTCGCCAGCCGACAGTGGAAAAATCTAA 117
   |||||.....
   17 IserIle.....LeuCysAlaIleCysTyrSerIleuSerGlu 31
118. AATCTCTTAAAAAGTA.....GAGTCGACATCATGATGACACTTT 161
   |||||.....
   31 YalSerProGluGlnProPheAspAsnLeuGlnMetThrSerAsnAspHe 47
162. ATCTGAGGTGAGAC..AGGACGATGAGTCTGCGG..... 197
   |||||.....
48. GlnHisIleLeuSerTyrPheAlaHisSerAspProThrValProThrTy 64
198. AATGACTTTTTCATTCGATTATCAAAAACTGGGATGATAATT 243
   |||||.....
64. TyrPheArgValLeuLysSer.....SerHisSerAsn 75
244. GGAATAAATGTCGTGGGTGTCAGAAATTAATTAACCAATGCACTTT 293
   |||||.....
75. rPlyAlleLysGlnLysCysSerArgIleValGlnProPheCysAsnLeu 91
294. TCTTCCTCAAGCTGAATGTTATGAGAA.....ATTAATT 331
   |||||.....
92. ThrAspAspPheGlnAlaValSerAspGluTyrSerAlaPheValGlnSe 108
108. rPheValGlyThrGlnValPheAsnSerSerLeuLeuHis..... 121
333. GCGTATAGAGCGAAGAAAGAAACACTTCTCAAGGTAGTAGTTGACT 381
   |||||.....
382. CATTTACACATTTGCGCAAGCTCAGATTTGCTCCCGAAGATACATTTA 431
   |||||.....
122. PheSerProLeuSerGlnThrPheLeuGlyProGluPheAsnLeu 137
432. GAGCTGAAGTAAGCAATGATGATACACATCTCT...CTGGAACA... 476
138. SerSerCysValHisCysAlleAsnIleThrIleLysLeuProProThrH 154
477. ....AAGATAGCTTATGTCGGCTTTGATGGCTTTAAGCTTACAT 519
   |||||.....
154. sLeuArgLysAsnGlyLysLeu.....L 162

```



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1210 ATTGAACACTGACT ..... GTATTGTGTGAACCAAGA 1247
|||||
401 .. LeuserProleuserIryValbaCysrIrrIrySerleuargSerIry 416
1248 GCACAC 1253
417 Serasn 418
seq_name: sp_rpodent:p97798
seq_documentation_block:
ID p97798 PRELIMINARY; PRT; 1493 AA.
AC p97798;
DT 01-MAY-1997 (TREMBLrel_03, Created)
DT 01-MAY-1997 (TREMBLrel_03, Last sequence update)
DT 01-NOV-1999 (TREMBLrel_12, Last annotation update)
DE NEOGENIN (NEOGENIN PROTEIN).
OS NEOL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97407661.
RA KEELING S.L., GAD J.M., COOPER H.M.;
RT "Mouse Neogenin, a DCC-like molecule, has four splice variants and is
RL expressed widely in the adult mouse and during embryogenesis.";
RL Oncogene 15:691-700(1997).
DR EMBL: Y09535; CAA70727.1; -.
DR HSPF: P02751; LITG.
DR MGD: MGI:1097159; Neol.
DR PFAM: PF00041; fn3; 6.
DR PFAM: PF00047; Ig; 4.
DR PRINTS: PR00014; FNTYPEPIT.
SO SEQUENCE 1493 AA; 163159 MW; 98F26676 CRC32;

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alignment scores:
      Quality: 130.00      Length: 415
      Ratio: 0.637      Gaps: 20
Percent Similarity: 49.157      Percent Identity: 21.446

alignment block:
US-09-240-675-1 x P97798 ...

Align seg 1/1 to: P97798 from: 1 to: 1493

      87 TTGTCGCGACGCGGAGGTGGAAAAATCTAAATCTGCTCAAAAGTACA 136
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
461 LEMLARQLALHTHTGGLGYPROLEUPROSELIARPLYQVSPVALYA 477
      137 GGTGCACATCTACATGACACTTTATC..CTGAGGTGAC.....A 177
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
477 LALSERLEUVALERTHTMRPHETLEUYLEHTPTPRGTGPIQA 494
      178 GGAGGATGAGCTGCTGGGAAATGCTTTTCATTTGCAATTTGCAAA 227
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
494 LASERPPTONHISGLYASPSHNEUHTLTYETVALPHEUTHTLYS 510
      228 ACTGGATGATGATTAATTCATTAATTCCTGCGGTGCAGATPTTACTAG 277
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
511 GLUDGLYALAPRAY.....GLUDGLYALGLNLSNDRHSERGII 523
      278 T.....ACCAATGCAACTTTTCTTCACTCAAGCTGA 309
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
523 nPROGLYGLUMLGELINVALHTTEGLINSNEUMLPTROLATHVAL 540
      310 ATGTTTATGCAAGAAATTAATTCGCTATAGACACAAAAGAAACACT 359
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
540 YLLIEPHE.....LYVALMETKALDELINSNLYSHISGLY 551
      360 TCTCTAGGATGATGAGGTGACTCATATTCACCACTTTGCGAAAGCTCAGAT 409
      ||||| ||||| ||||| ||||| ||||| ||||| |||||

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552 SerGly.....GlusSerAlaProLeuArgValGluThr.. 563
410 TGGTCTCCAGAGTACATTAGAAAGCTGACAGATAGCAATAGTCAAC 459
564 ....GlnProGluValGlnLeuProGlyProAlaProAsnIleArgAla 579
460 ACATCTCTCCGGAAACAAAGATAGTATTATGGGCTTG..... 500
579 yAlaThrSerProThrSerIleThrValThrThrGluThrProLeuSer 595
501 ...GANGGTTAAAGCTTACATATAGCTTACTATCTGAAAACCTTC 547
556 GlyAsnGlyGlnIleGlnAsnTyrIleGlyTyrMetGlnGlyGly 612
548 AGGTGTAGAAAGAGAGATGAAATTTATTCACAGACATAAATTATA 597
612 rasPlysglnGlnAspIleAspValSerSerHisSerTyrThrIleAsn 629
598 AACCTCTACAGAGACTACTATTGTCTAAAGTTAAAGCACACTACT 647
629 ILeuLysLysTyrThrGluTyrSerPheArgValAla.....Tyr 643
648 AGCTCATGGAATAATGGTCTATAGTCCAGATGATGATAAAGACAC 697
644 AsnLysHisGlyProGlyValSerThrGlnAspValAlaValArgThr 660
698 AGTTGAAATGAACTACTCCACAGAAAATAGAAAGTCACTGCCAA 747
660 uSerAspValProSerAlaAlaProGlnAsnLeuSerIleGlnValArg 677
748 AT...CAGACTATGTCTTAATG.....GATATACATATGCA 785
677 snSerLysSerIleValIleHisTyrGlnProProSerSerThrThrGln 693
786 AAC.....ATGACTTTCAGATGAGCTCCAGCCTTTTAA 826
694 AsnGlyGlnIleThrGlyTyrIleArgTyrArgLysAlaSerGly 710
827 AAGGAATCTGGAAACCATTTGTATAAATGAAACAAATACCTGACTGG 876
710 sSerAspValThrGluThrLeuValThrGlyThrGlnLeu..... 723
877 AAAATGTCAAACCTACCAGTGTCTTCCCAAACCTTTCCAAA 926
724 .....SerGlnLeuIle.....GlnGlyLeuAspArgGly 733
927 GGAATTAACCTTCCGCGTACAGATCGATGAAATACACA..... 971
734 ThrGluTyrAsnPheArgValAlaAlaLeuThrValAsnGlyThrGly 750
972 ....TCTTTTGGCTGAAAGATTAAGTTGATGAAATACAGCTT 1017
750 oAlaThrAspTyrProLeuSerAlaGluThrPheGlnSerAspLeuAspGlu 767
1018 TCTTACTTCTCCAGTC.....TTAACTATGATCCCTTACTGAT 1058
767 hArgValProGluValProSerSerLeuHisValArgProLeuValThr 783
1059 TCATTCATATATATCGTCTCCAAACAGCTCGAAACGCGCTGT 1108
784 SerIle...ValValSerThrThrProProGlnAsnGlnAsnIle... 798
1109 GATCCAGATATACCTGATTTATGAAATTAATTTTGGGAAACACTT 1158
798 ValAlaGlyGlyTyrAlaIleGlyTyrGlyIle.....GlySer 811
1159 CAATGCTGAGAGA...AAATATGAGAAAACAACTGATGTTAAGTT 1205
811 roHisAlaGlnThrIleLysValAspTyrIleGlnArgTyrThrIle 827
1206 CCAATTTGAAACCACTGATGATATGTTGTAAGCAAGCAGACA 1250
828 GluAsnLeuAspProSerSerHisTyrValIleThrLeuLysAla 842

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seq_name: sp_invertebrate:094537

seq_documentation_block:
ID 094537 PRELIMINARY; PRT; 1375 AA.

AC 094537;
DT 01-FEB-1997 (TREMBLREL. 02, Created)
DT 01-FEB-1997 (TREMBLREL. 02, Last sequence update)
DT 01-NOV-1999 (TREMBLREL. 12, Last annotation update)
DE FRAZZLED.
GN FRAZZLED.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97015076.
RA KOLODZIEP P.A., TIMPE L., MITCHELL K.J., GOODMAN C.S., FRIED S.,
RT "Irazzled encodes a Drosophila member of the DCC immunoglobulin
subfamily and is required for CNS and motor axon guidance."
RL Cell 87:197-204(1996).
DR EXBL: U71001; AAC47314.1;
DR EMBASE: F89n0011592; fra.
DR PRAM: PR00041; fn3; 6.
DR PRAM: PR00047; 19; 3.
DR PRINTS: PR00014; FNTYPEIII.
SQ SEQUENCE 1375 AA; 151692 MW; 43806DBC CRC32;

alignment_scores:

Quality: 129.00 Length: 622
Ratio: 0.542 Gaps: 22
Percent Similarity: 38.264 Percent Identity: 16.399

alignment_block:

us-09-240-675-1 * 094537

Align seg 1/1 to: 094537 from: 1 to: 1375

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102 GGTGGAATAATCTPAAATCT.....CC 124
447 GlyGlyLysProLeuAspSerGlyLeuGlnAlaArgLeuProSerGlnP 463
125 TCAAAAGTAAAGTGCACATCATGATGACAACTTATC...CTGAGCT 171
463 oArgAspLeuValAlaGlnIleValIleValLysSerArgPheValThrLeuSerT 480
172 GG..... 173
480 TPValGlnProLeuGlnAlaAsnAlaGlyAspValValTyrTyrThrValTyr 496
174 ....AACAGAGCATGAGTCTGCGGATGAGACTTTTTCATT 214
497 TyrLysMetAsnAsnSerGlnArgGlnGlnLysMetValThrLysSerH 513
215 CGATTATCAAAAACCTGGATGATGATTAATGATAAATGTCTGGGTCTC 264
513 sAspAspGlnGlnValAsnIleGlnSerLeuLeuProGlyThrGlyTyrG 530
265 AGAATATACATAGTACCAATGCAACTTTCTCA..... 299
530 LnPheArgValGlnLysAsnThrAsnPheGlySerGlyAlaSerSerAla 546
300 ...CTCAGCTGAATGTTATGAGAATTAATTAATGCTT..... 335
547 ProLeuGlnValSerThrGlnProGluValAsnIleAlaGlyProProAr 563
336 .....ATAAGACAGAAAACAAACACTTCTTCATGCT 369
563 GAsnPheGlnGlyTyrAlaAspSerHisLysGlnIleTyrValLysTyrG 580

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370 ATGAG..... 374
    |||
580 IuglProthrValthrAsnGlyuileuLysTyrArgValTyrTyr 596
374 ..... 374
597 SerGluAsnAspSerGlyAlaAspLeuTyrHisAspSerThrAlaLeuGlu 613
375 ..... GTGACGCTATTTA 387
613 uAlaValLeuThrGluLeuArgProHisThrAspTyrValIleSerValV 630
388 CACCATTTCCGAAAGCTCAGATGCT..... 413
    |||
630 alProPheAsnArgAsnGlyMetGlyAspSerSerAlaGluIleArgVal 646
414 ..... CCTCCAGAGACATTTTGA 433
647 LysThrPheSerSerThrProSerGluProPheAsnValThrLeuGlu 663
434 A... GCTAGAGATAGGCAATAGTATACATCTCTCTCTGACAAAG 480
    |||
663 uValThrSerSerSerIleThrValHisThrGluProAlaGluG 680
481 ATAGTGTATGTGGCTTGGATGGTTAGCTTACATATAGCTTACTT 530
    |||
680 LuAspArgAsnGlyGlnIleThrGlyTyrLysIleArgTyrArgLys... 695
531 ATCTGAAAAAAGCTTTCAGGTGTAGAGAAAGGATGAAATATTATATTC 580
    |||
696 ... PheLysAspAlaProGluValLysSerThrProAlaAsnIle... Ar 710
581 CAGACATATAATTTTATAACTCTCCACGAGACACTTATGTCTAAAG 630
    |||
710 gTyrPheGluLeuSerAsnLeuAspArgAsnAlaGluTyrGluValLysI 727
631 TTAAGCGACACTACTT..... AGCTCATGGAATTT 662
    |||
727 leuAlaIleMetThrValAsnGlySerGlyProPheThrGluThrAsnArg 743
663 GGTGTCTATAGTCCAGTACATGTTTAAAGACACAGTGAATGAAGT 712
    |||
744 Ala..... AsnThrLeuGluAsnAspLeu 751
713 ACCT..... 716
751 uAspGluThrGluValProGlyLysProIleThrIleSerIleHisProG 768
717 ..... CCACCGAATAATATGAGTGC 737
    |||
768 LyAlaAsnAsnIleAlaIleuHisThrGlyProProGluHisProGluIle 784
738 AGGTCCAAATTCAGAACTATGTTCTTAAAGC..... 770
    |||
785 LysIle..... ArgAsnTyrValLeuGlyTyrGlyArgGlyIleProAs 799
770 ..... 770
799 pGluAsnThrIleGluLeuLysGluThrGluArgTyrHisIleLeuLysA 816
771 ..... GATTAT..... 776
    |||
816 snLeuGluSerAsnMetAspTyrValValSerLeuArgAlaArgAsnVal 832
776 ..... 776
833 LysGlyAspGlyProProIleTyrHisAsnIleLysThrArgAspGluGlu 849
776 ..... 776
849 uProValAspAlaLeuProThrProLeuGluValProValGlyLeuArgAlaI 866
777 ACATATGCAAAACATGACCTTTCATAGTTCAAGTGCCTCCACGCCCTTTTA 824

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    |||
866 leuThrMetSerSerSerSerIleValValTyrThrIleAspThrMetLeu 882
825 AAAGAGAT..... 833
    |||
883 AsnLysAsnGlnHisValThrAspAsnArgHisTyrThrValSerTyrGlu 899
834 ..... CTGGAACCATTTGTATAATGGAACAAATACCTGACCTGAAA 879
    |||
899 yIleThrGlySerAsnArgTyrArgTyr..... HisA 910
880 ATGCAAAACATACCAGCTGTCTTCTCCCAAGCTTTCCAAAAGAA 929
    |||
910 snThrThrAspLeuAsnGlyMetIle... AsnAspLeuArgProAsnThr 925
930 ATTACCTTCTCCGCTACAGACATCTGATGGAATACACATCTTTTGG 979
    |||
926 GlnTyrGluPheAlaValLysValValLysGlyArgGluSerSerThr 942
980 GTCGAAAGCATTAAGTTTGATCTGAAATACAGCTTCTCTACTCTC 1029
    |||
942 PserMetSerValLeuAsnSerThrTyrGluAsnValProValThrPro 959
1030 CAGCTTTACATTAAGATCCCTGTAGTATTCATTCATATCTATATGCGT 1079
    |||
959 ro..... ArgGluValThrValArg 965
1080 GCTCCAAACAGCTGTGAAACAGCCTGTGATCCGATTAATTCGA... 1124
    |||
966 LeuAspGluMetAsnProProThrValIleValGlnThrIleProPol 982
1125 ..... CTGATTTATGAATTTTGGGAAACA 1155
    |||
982 shIsthrLeuGlyGlnIleThrGlyTyrAsnIleTyrThrThrAspT 999
1156 CTTCAAATGCTGAGACA..... AAATATGCAAAAAA 1190
    |||
999 hThrLysArgAspArgAspTyrSerValGluAlaPheAlaGlyGlu 1015
1191 ACTGATGTTACAGTCTCTAATTGAAACACAGCTGATATATGTTGTA 1240
    |||
1016 ThrMetLeuMetLeuProAsnLeuLysProTyrThrThrTyrTyrPhe 1032
1241 AGCCAGACACACACC 1256
    |||
1032 sValGlnAlaArgThr 1037
seq_name: sp_invertebrate:094538
seq_documentation_block:
ID 094538 PRELIMINARY; PRT; 1526 AA
AC 094538:
DT 01-FEB-1997 (TRENDArel. 02, created)
DT 01-FEB-1997 (TRENDArel. 02, last sequence update)
DT 01-NOV-1999 (TRENDArel. 12, last annotation update)
DE FRAZZLED.
GN FRAZZLED.
OS Drosophila melanogaster (Fruit fly)
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila
RN [1] FRAZZLED.
RP SEQUENCE FROM N.A.
RX MEDLINE: 97015076.
RA KOLODZIEJ P.A., TIMPE L., MITCHELL K.J., GOODMAN C.S., FRIED S.,
RA JAN L.Y., JAN Y.N.
RT "frazzled encodes a Drosophila member of the DC immunoglobulin
RT subfamily and is required for CNS and motor axon guidance."
RL Cell 87:197-204(1996)
DR EMBL: U71002; AAC47315.1;
DR FLXBASE: FBgn0011592; fra.
DR PFAM: PF00041; fn3; 6.
DR PFAM: PF00047; fn3; 3.

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DR PRINTS: PR00014: FNTYPE11
SQ SEQUENCE 1526 AA: 168787 MW: F17B1EC9 CRC32;

Alignment_scores:

Quality: 129.00 Length: 622
Ratio: 0.542 Gaps: 22
Percent Similarity: 38.264 Percent Identity: 16.399

Alignment_block:
US-09-240-675-1 x 094538

Align seg 1/1 to: 094538 from: 1 to: 1526

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102 GGTGGAATAAATCTAAATCT...T.....CC 124
|||||  |||  |||
598 GlyGlyLysProLeuAspSerGlyLeuGlnAlaArgLeuProSerGlnPr 614
125 TCAAAAAGTAGAGTCGACATCATAGATGACAATTATC...CTGAGGT 171
|||  |||  |||  |||  |||  |||
614 CArgAspLeuValAlaGlnIleValLysSerArgPheValThrLeuSer 631
172 GG..... 173
||
631 rPvalGlnProLeuGlnAsnAlaGlyAspValValTyrTyrThrValTyr 647
174 .....ACAGAGCGATGAGTCTGTGGGAAATGCACTTTTCATT 214
|||||  |||  |||  |||  |||  |||
648 TyrLysMetAsnAsnSerGlnArgGlnLysMetValThrLysSerH1 664
215 CGATTATCAAAAAGTGGATGATGATTAATGATAATGTCGGTGC 264
|||  |||  |||  |||  |||  |||
664 sAspArgGlnGlnValAsnIleGlnSerLeuLeuProGlyArgThrTyrG 681
265 AGAAATTAAGTACCAATGCAACTTTCTCA..... 299
||
681 InPheArgValGlnAlaAsnThrAsnPheGlySerGlyAlaSerSerAla 697
300 ..CTCAAGCTGATGTTTATGAGAAATTAATGCGT..... 335
|||||  |||  |||  |||  |||  |||
698 ProLeuGlnValSerThrGlnProGlnValAsnIleAlaGlyProProAr 714
336 .....ATAGAGCGAAGAAAGAAACCTTCTCATGTT 369
|||||  |||  |||  |||  |||  |||
714 GAsnPheGlnGlyTyrAlaArgSerH1LysGlnIleTyrValLysTrpG 731
370 ATGAG..... 374
|||
731 LngLlnProThrValThrAsnGlyGlnIleLeuLysTyrArgValTyrTyr 747
374 ..... 374
748 SerGlnAsnAspSerGlyAlaAspLeuTyrH1AspSerThrAlaLeuG1 764
375 .....GTTGACGATTTA 387
764 ValAlaValLeuThrGlnLeuArgProH1AspPyrValIleSerValY 781
388 CACCAATTCGCAAGCTCAGATTGT..... 413
|||||  |||  |||  |||  |||  |||
781 alProPheAsnArgAsnGlyMetGlyAspSerSerAlaGlnIleArgVal 797
414 .....CTCCAGAAAGTACATTTCAGA 433
|||||  |||  |||  |||  |||  |||
798 LysThrPheSerSerThrProSerGlnProProAsnAsnValThrLeuG1 814
434 A...CCTGAAGATTAAGCATAGTATACATCTCTCGAAGAAAG 480
|||  |||  |||  |||  |||  |||
814 ValAlnHisSerSerSerIleThrValH1StrpGlnProProAlaGlnG 831
481 ATAGTGTATATGCGCTTGATGAGCTTAAGCTTACATATAGCTTACTT 530
|||  |||  |||  |||  |||  |||
831 LAspArgAsnGlnGlyH1IleThrGlyTyrLysIleArgTyrArgLys... 846
```

```
531 ATCTGAAAAAAGCTCTCAGGTGTAGAGAAAGATTGAAATATTATTC 580
|||||  |||  |||  |||  |||  |||
847 ..PheLysAspAlaProGlnValLysSerThrProAlaAsnIle...Ar 861
581 CAGACATTAATTTATTAACCTCTCACAGAGACTTACTTATGCTTAAG 630
|||||  |||  |||  |||  |||  |||
861 gTyrPheGlnLeuSerAsnLeuAspArgAsnAlaGlyTyrGlnValLysI 878
631 TTAAGCGACACTACTT.....ACGTATGGAAATT 662
|||||  |||  |||  |||  |||  |||
878 leAlaAlaMetThrValAsnGlySerGlyProPheThrGlnThrAsnArg 894
663 GGTGCTCTAGTCCAGTACATTGTATTAAGACACAGATTGAAATGAACT 712
|||  |||  |||  |||  |||  |||
895 Ala.....AsnThrLeuGlnAsnAspLe 902
713 ACCT..... 716
902 uAspGlnThrGlnValProGlyLysProIleTrpIleSerIleH1sProG 919
717 .....CCACGAGAAATATAGAGTC 737
|||||  |||  |||  |||  |||  |||
919 LAlaAsnAsnIleAlaLeuH1StrpGlyProProGlnH1sProGlnIle 935
738 AGTGTCAAAATCAGAACTATGTTCTTAATAG..... 770
|||||  |||  |||  |||  |||  |||
936 LysIle.....ArgAsnTyrValLeuGlyTyrPglYArgGlyIleProAs 950
770 ..... 770
950 pGlnAsnThrIleGlnLeuLysGlnThrGlnArgTyrH1sIleLeuLysA 967
771 .....GATPAT..... 776
967 snLeuGlnSerAsnMetAspTyrValValSerLeuAlaGlnArgAsnVal 983
776 ..... 776
984 LysGlyAspGlyProProIleTyrAspAsnIleLysThrArgAspGlnG1 1000
776 ..... 776
1000 uProValAspAlaProThrProLeuGlnValProValGlyLeuLysAlaI 1017
777 ..ACATATGCAAAACATGACCTTCAAGTCAAGTCCAGCCTTTTAA 824
|||||  |||  |||  |||  |||  |||
1017 IeThrMetSerSerSerSerIleValValTyrTrpIleAspThrMetLeu 1033
825 AAAAGCAAT..... 833
1034 AsnLysAsnGlnH1sValThrAspAsnArgH1sTyrThrValSerTyrG1 1050
834 ..CTGGAAACCATTTGTATTAAGAAACAAATACCTGACGTGAAA 879
|||||  |||  |||  |||  |||  |||
1050 YIleThrGlySerAsnArgTyrArgTyr.....H1sA 1061
880 ATGCAAAACATACCAGGTGTCTTCTCCAAAACGTTTCCAAAAGGA 929
|||||  |||  |||  |||  |||  |||
1061 snThrThrAspLeuAsnGlyMetIle...AsnAspLeuAsnProAsnThr 1076
930 ATTACCTCTCCGCGTCACAGATCTGAGGAATTAACATCTTTTG 979
|||||  |||  |||  |||  |||  |||
1077 GlnTyrGlnPheAlaValLysValValLysGlyArgArgLeuSerSer 1093
980 GTCTGAAGAGATTAAGTTGATGATAATTAAGCTTCTCTACTCTCTC 1029
|||||  |||  |||  |||  |||  |||
1093 pSerMetSerValLeuAsnSerThrTyrGlnAsnValProValAlnThrPro 1110
1030 CAGTCTTAAACATTAGATCCCTTAGTATTCATTCATTCATTCATTC 1079
|||  |||  |||  |||  |||  |||
1110 ro.....ArgGlnValThrValArg 1116
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1080 GCTCCAAACAGCTGTGAAACAGCCCTGATCAGATATGCA... 1124
 1117 LeuAspGluMetAsnProProThrValIleValGlnTrpIleProProly 1133
 1125CTGATTATGAAATATTTTGGGAAACA 1155
 1133 sHsThrLeuGlyGlnIleThrGlyTyrAsnIleTyrIleThrThrAspT 1150
 1156 CTTCAATCTGAGACA.....AAATATCGAAGAAAA 1190
 1150 hTThrLysArgAspArgAspTrpSerValGlnAlaPheLeuGlyGln 1166
 1191 ACTGATGTACAGTTCTTATTTGAACACAGTCACTGATATGTGTGAA 1240
 1167 ThrMetLeuMetLeuProAsnLeuLysProTyrThrThrTyrThrLeu 1183
 1241 AGCAGACAGACACACC 1256
 1183 sValGlnAlaArgThr 1188

seq_name: sp_vertibrate:090610

seq_documentation_block:
 ID 090610: PRELIMINARY; PRT: 1443 AA.
 AC 090610:
 DT 01-NOV-1996 (TREMBLER, 01, Created)
 DT 01-NOV-1996 (TREMBLER, 01, Last sequence update)
 DT 01-NOV-1999 (TREMBLER, 12, Last annotation update)
 DE NREGENIN (FRAGMENT).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
 NC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WHITE LEGHORN; TISSUE-BRAIN;
 RX MEDLINE; 95105243.
 RA VIELMEYER J., ROMAN J.M., DREYER W.J.;
 RT "Neogenin, an avian cell surface protein expressed during terminal
 RT neuronal differentiation, is closely related to the human tumor
 RT suppressor molecule deleted in colorectal cancer."
 RL J. Cell Biol. 127:2009-2020(1994).
 DR HSSP; P80362; 1MTL.
 DR PFAM; PF00041; fn3; 6.
 DR PFAM; PF00047; 19; 4.
 FT NON_TER
 SQ SEQUENCE 1443 AA; 158050 MW; 270877DC CRC32;

alignment_scores:
 Quality: 127.50 Length: 415
 Ratio: 0.644 Gaps: 19
 Percent Similarity: 47.711 Percent Identity: 22.169

alignment_block:
 US-09-240-675-1 x 090610

Align seg 1/1 to: 090610 from: 1 to: 1443
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 416 LeuAlaProAlaThrThrGlyProLeuProThrAlaPheArgAspValIle 432
 137 GGTGCACATCATAGATGACAACTTATC...CTGAGGTGGAACAGG... 179
 433 AlaThrLeuValSerThrArgPheIleArgLeuThrTrpArgThrProV 449
 180 ..AGGATAGAGTGTGCGGAATGCACTTTTCATTCATATATCAAAA 227
 449 AlSerAspProGlnGlyAspAsnLeuThrTyrSerIlePheTyrThrLys 465
 228 ACTGGATGATTAATGATTAATATGTGCGGTGTCAGAAATATATCTAG 277

466 GlnGly.....IleAsnArgLysArgValGlnAsn...These 477
 278 TACCAAAATGCAACTTTCTTCACTCAAGCTGAATGTTATGAGAAATTA 327
 477 hArgProGlyGlnThrGlnValMetIleGlnAsnLeuMetProGlyThrV 494
 328 AATGCGTATAGACAGAGAAAAGAAACACTTCTTCATGATGATGAGTT 377
 494 AlTyrValPheArgValValAlaGlnAsnLysIleGlyIleGlyGln 509
 378 GACTCATTTACACATTTCCGAAAGCTCAGATGCTCCAGAGTAGA 427
 510 ..SerSerAlaProLeuLysValAlaThr...GlnProGlnValIle 523
 428 TTTCAGAGCTGAAGTAAAGCCATAGTGAATACATCTCTCCGAGACA 477
 523 hLeuProGlyProAlaProAsnIleArgAlaTyrAlaGlySerProThrS 540
 478 AAGATAGGTATNGGGCTTG.....GATGCTTAACTT 515
 340 eValThrValThrTrpGlnThrProLeuSerGlyAsnGlyIleGln 556
 516 ACATATAGCTTACTTATCTGAAAAACTCTGAGGTGAGAGAAAGAT 565
 557 AsnTyrLysLeuTyrTyrMetLysGlyGlnAspSerGlnGlnAspVa 573
 566 TGAATATATTATTCAGACATATAATTTATTAAGCTCAGCAGAGACTA 615
 573 LAspValAlaGlyLeuSerTyrThrIleThrGlyLeuLysTyrThrG 590
 616 CTTATGTCTTAAGTATAAGAGACAGACTTACGTCAGAAATTTGTT 665
 590 LutySerPheArgValAla...TyrAsnLysIleGlyProGly 604
 666 GTCTATAGTCCAGTACATGATGTAAGACACAGGTGAAGAAAGTACC 715
 605 ValSerThrGlnAspValValAlaArgThrLeuSerAspValProSerAl 621
 716 TCCACAGAAATATAGAGTCAAGTCCAAAT...CAGACTATGTTG 762
 621 AlaLeuProGlnAsnLeuThrLeuGlnAlaArgAsnSerLysSerIleMet 638
 763 TTAATGGGATATACATATAGCAACAGACCTTCAAGTACGGCTC 812
 638 eHisTrpLeuProProAla... 645
 813 CAGGCTTTTAAAGGAATCTCGAACCATTG... 848
 646GlyThrHisSerGlyGlnIleThrG 654
 849 TATAATGGAACAAATACCTGAGTGTGAATGTCAAACTACCACT 897
 654 TyrLysIleArgTyrArgLysValSerArgLysSerAspValThrGus 671
 898 GTGCTCTTCCCAAAACCTTTCCAA...AAGCAATT... 932
 671 eValGlyLeuThrGlnLeuPheGlnLeuIleGlyGlyLeuGlnGly 687
 933TACCTTCCGCGTACAGACATCTGAGTAATACACA... 971
 688 ThrGlyTyrAsnPheArgIleAlaIleAlaMetThrValAsnGlyThrLys 704
 972 ...TCTTTTGCTGGAAGAGATTAAGTTGATCAATATCAAGCTT 1017
 704 AlaThrAspTrpValSerAlaGlnLeuThrPheGlnSerAspLeuAspGus 721
 1018 TCCACTTCCCTCCAGTC...TTTACATTAGTCCCTTATGAT 1058
 721 eArgValProGlnValProSerSerLeuHisValAlaArgProLeuValThr 737
 1059 TCATTCATATCTATATAGGTGCTCCAAAGAGTGTGAACACCGCTGT 1108
 738 SerIle...ValValSerTrpThrProProGlnAsnGlnAsnIle...Va 752

1109 GATCCAGGATTATCCACTGATTATGAAATATTATTTGGGAAACACTT 1158
 1159 CAATGCTGAGCA..AAATATCGAGAAAAAACTGATGTTACGTT 1205
 765 TGTATGAGTGTATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 781
 1206 CTTATTTGAAACCACTGATGATGATGATGATGATGATGATGATGAT 1250
 782 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 796
 seq_name: sp_vertebrate:098949

seq_documentation_block:
 ID 098949 PRELIMINARY: PRT: 873 AA.
 AC 098949
 DT 01-FEB-1997 (TREMBLER, 02, Created)
 DT 01-FEB-1997 (TREMBLER, 02, Last sequence update)
 DE AXL-RELATED RECEPTOR TYROSINE KINASE.
 GN REX.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
 CC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 97067156.
 RA BISCARDI J.S., DEMEYER F., RUEHLER G.F., CHESNUT D.A., BARAGONA S.C.,
 RT "Rek, a gene expressed in retina and brain, encodes a receptor
 RT tyrosine kinase of the Axl/Tyro3 family".
 RT J. Biol. Chem. 271:29049-29059(1996).
 DR EMBL: U70045; AAC60041.1.
 DR HSSP: P00523; 2PTK.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PFM: PF00047; 1n3; 2.
 DR PFM: PF00047; 1n3; 2.
 DR PFM: PF00069; PKinase; 1.
 SO SEQUENCE 873 AA; 96402 MW; 2918D550 CRC32;

alignment_scores:
 Quality: 123.00 Length: 453
 Ratio: 0.631 Gaps: 25
 Percent Similarity: 43.046 Percent Identity: 22.517

alignment_block:
 US-09-240-675-1 x 098949

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 98 CGCAGTGGGAAATCTAAATCTCTCAAAAGTAGAGTC.....140
 28 aAlaGlyMetLysPheThrGlySerProLeuLeuLeuLeuLeuLeuLeu 45
 141GACATCATGATGACAACTTT 161
 45 LysLysProValLysLeuAsnCysSerLeuGluGluMetGluAspProGlu 61
 162 ATCTGCGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 211
 62 MetLeu...TriPheLysAsp.....GlyAlaValValGlnSer 73
 212 ATTCGAT.....TATCAAAATCTGGATGATGATGATGATGATGATGAT 255
 73 TValAspGlnValLysLysLeuProValAspGluAspPheIle..... 87

256 CTGCTGCTCAGATATTACTAGTACCAAAATGCACTTTCTTCTCAGCAG 305
 88GlyPheLeuSerLeuLys 93
 306 CTGAATGTTATGAGAAATTAATATGCGTATAGAGCAAGAAAGAAA 355
 94SerValGlnLys 97
 356 CACTCTCTCA.....TGATAGAGTGTACCTATTTACCACTTC 396
 97 GlnAspSerGlyLysLysLysLysLysLysLysLysLysLysLysLys 114
 397 GCAAGCTCAG.....ATTGCTCTCCAGAAATGATAT 428
 114 LysLysSerGlnGlnValLysLysLysLysLysLysLysLysLysLys 130
 429 TTGAAAGCTGAAATAGGCAATAGTATGATGATGATGATGATGATGAT 478
 131 ValGluProGluLys.....ValSerValSerProAsnLys 143
 479 AGATAGTATGCTGGGCTTGGATGATGATGATGATGATGATGATGATGAT 528
 143 oPhenylMetAlaCysAlaValAlaValLysProGluProValThrLys 160
 529 TTTATCGAAA.....539
 160 AlrTrpMetGlyAspSerArgValGlyLeuProAspLysSerProSer 176
 540ACTCTGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 583
 177 LysLeuAsnValSerGlyLysLeuSerSerArgThrAlaThrValGlnLys 193
 584 ACATAAATTTAAACTCTCACAGAGAGATGATGATGATGATGATGATGAT 633
 193 AsnAsnValLysGlyLeuSerSerArgThrAlaThrValGlnLys 210
 634 AACACACACTTACTAGCTCATGAGAAATGGTGTATGATGATGATGATGAT 683
 210 LysAlaMetProLeu.....214
 684 TGTATTAAGACCACTGAAATGAAATGAAATGAAATGAAATGAAATGAA 733
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 220 ValSer.....GlnValThrSer 227
 784 CAACATGACCTTCAAGTTCAGTGGCTCCAGGCTTTTAAAGAGAT 833
 227 AsnAlaSer.....ValValThrValProLysPheAspGlyAla 241
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 242 ProLeuHisSerCysThrLeuGlnValAlaGluSerProAspGlyLys 258
 881 TGTCAAAATACCAAGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 930
 258 ValSerThrGln.....ValAlaProValProPheAlaLysGlyVal 273
 931 TT.....TACCTCTCGGCTGATGATGATGATGATGATGATGATGATGAT 956
 273 ValGlnLysLeuLysLysSerThrAspLysSerValArgValGlnCysSer 289
 957 GATGGAATTAACACATCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1006
 290 AsnGluMetGlySerSerProPheThrGlnValGlyValPhe..... 303
 1007 AATCAAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1056
 304GlnThrLeuGlnLeuAlaPro.....SerSerThrProG 315


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1057 ATTCATTCATATCTATTCGCTGCTCA.....AAACAGCT 1094
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315 LdaenlleHsVallleGlnApgspproGlyLeuValleuGlnUrpdu 331
      |||
1095 GGAACACGCTT...GTATCCAGGATTAATCCAGTATTATGAATAT 1141
      |||
332 GlyValAlaProAspValleuGlnUspValleuGlyTyArg...Le 347
      |||
1142 TTTTGG....GAAACACTTCAAATGCTGAGAGAAATATACGAGA 1185
      |||
347 uGluTrpIleGlnAspAsnValThrGlnGlyLeuIleValGlnAsp 364
      |||
1186 AAAAAGCATGTTACAGTCTTAT...TTGAACCACTGACTGTA... 1229
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364 hUysAlaAsnLeuThrThrPheProLeuUysAspLeuIleArg 380
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1230 TATGTGTG 1238
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381 ValCysVal 383

seq_name: sp_human:092859

seq_documentation_block:
ID 092859 PRELIMINARY; PRT; 1461 AA.
AC 092859:
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE NEOGENIN.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC -Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN
RP SEQUENCE FROM N.A.
RA MEYERHARDT J.A., LOOK A.T., BIGNER S.H., FEARON E.R.;
RL Oncogene 0:0-0(0).
RL EMBL: U61262; AAB17263.1;
DR HSSP: P02751; 1TTG.
DR PRAM: PR00041; fn3; 6
DR PRAM: PR00047; 19; 4.
DR PRINTS: PR00014; FNTYPEIII.
SQ SEQUENCE 1461 AA; 159958 MW; 0AB7247E CRC32;

alignment_scores:
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      Ratio: 0.581      Gaps: 20
Percent Similarity: 50.119 Percent Identity: 20.665

alignment_block:
US-09-240-675-1 x 092859

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      |||
107 AAAAATGTAAATCTCTCAAAAGTAGAGTGCATCATATGATGACA 156
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436 yProLeuProSerAlaProArgAspValValAlaSerLeuValSerThrA 453
      |||
157 ACTTATG...CTGAGGTGGAAC...AGAGGAGTACGCTGCGG 197
      |||
453 rPheIleUysLeuThrTrpArgTrpAlaSerAspProHsGlyAsp 469
      |||
198 AATGACTTTTTCATGATATCAAAAATCTGGAG...GATAA 241
      |||
470 AsnLeuThrTySerValPheTyThrIysGlnGlyIleAlaArgGluAr 486
      |||
242 TTGATAAAATGTCTGGGTGCACAAATATTAAGTACCAAAAGCACT 291
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486 gValGlnAsnThrSerHsIAspGlyGlnUetClnValThrIleGlnAsnL 503
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292 TTTCTTACACAGCTGAATGTTATAGAAATTAATTCGGATAGA 341
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503 eUeIProAlaThrValTyIlePhe.....AspValMet 514
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342 GCAGAAAAAGAAACACTTCTTCATGTATGATGCTCATTAATACAC 391
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515 AlAGlnAsnUysHsGlySerGly.....GluSerSerAlaPr 527
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392 ATTTGGCAACCTCAGATGCTCTCCAGAAATACATTAGAACCTGAG 441
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527 OleuArgValGlnUthr.....GlnProGlnValGlnLeuProGlyProA 542
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442 ATAAGCAATGATGATACACATCTCTCTGGAACAAAAGATAGCTATG 491
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542 lAProAsnLeuArgAlaTyAlaIAspProThrSerIleThrValThr 558
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492 TGGGCTTG.....GATGGTTAGCTTTCATATACATTAATCTTACT 529
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559 TrpGluThrProValSerGlyAsnGlyGlnIleGlnAsnTyTyIysLeuTy 575
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530 TATCTGAAAACCTTCAGGTGAGAGAAAGATGAAATATTAATT 579
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575 rTyMetGlnUysGlyThrAspIysGlnGlnAspValAspValSerSerH 592
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592 lSerTyThrIleAsnGlyLeuUysIysTyThrGlnUtySerPheArg 608
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630 GTTAAAGCAGCAGTACTAGCTCATGGAATTTGTTGCTTAAAGTCCAGT 679
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680 ACATTTGTTAAAGCACACAGTTGAAATGAATCACTCCACACAAATA 729
      |||
623 pValAlaValArgThrLeuSerAspValProSerAlaIAspProGlnAsnL 640
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730 TAGAAGTCAAGTCCAAAT...CAGAATATGCTTAAATGGAT... 773
      |||
640 eUserLeuGlnValArgAsnSerIysSerIleMetIleHsIAspGlnPro 656
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774 .....TATCATATGCAACATGACC...TTTCAGTTCAGTG 808
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657 ProIAspProAlaThrGlnAsnGlyGlnIleThrGlyTyIysIleArgTy 673
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809 GCTCCAGCCTTTTAAAGCAATCTGGAACCATTTGTAAAGAGA 858
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673 rArgGlyAlaSerArgIysSerAspValThrGlnThrLeuValSerGlyT 690
      |||
859 AACAAATACGCTGAGTGAATATGCAAAATACCCAGTGTCTTCCCT 908
      |||
690 hGlnLeu.....SerGlnLeuIle... 696
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909 CAACAGCTTTTCAAAAAGAAATTTACCTTCCGCGTACAGCATGTA 958
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697 GluGlyLeuAspArgGlyThrGlnTyAspPheArgValAlaIleLeuTh 713
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959 TGGAAATACACA.....TCTTTTGGTCTGAAGAGTAAAGTTTG 999
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713 rIleAsnGlyThrGlyProAlaThrAspTrpLeuSerAlaGlnUthrPheG 730
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1000 ATAGCAAAATCAAGCTTCTCTACTCTCTCAGTC...TTTAA 1040
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730 lUserAspLeuAspGlnUthrArgValProGlnValProSerSerLeuHsI 746
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1041 ATTAGATCCCTTAGTGTATTCATTCATATCATATTCGCTGCCAAAC 1090
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747 ValArgProLeuValThrSerIle...ValValSerThrPheProGly 762
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762 lAsnGlnAsnIle...ValValArgGlyTyAlaIleGlyTyGlyIle
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666 GTCTAAGCCAGTACATCTGTATAAGACCAACAGTTGAATGAACTAC 715
608 ValSerSerGluGluIuHhIshValValIhIhrLeuSerhPvalProSerAl 624
716 TCCACCAGAAATATATGAAGTCAGTGTCCMAATCAGAACTATGTCTTA 765
624 aMetProGlnAspValSerLeuGluIValAlaAsn..... 635
766 AATGGATTATACATATGAAACATGACCTTCAAGTTCAGTGCCTCAC 815
636 .....SerArgSerIleLeuValSerTyr..... 643
816 GCCTTTTAAAAAGAAATCCTCGAAGCAACCTTTG.....TA 850
644 .....LeuProProProGlyIhrgIAsnGlyPheIleIhrgIyTy 658
851 TAAATGGAACAATATCTGCACTGTGGAATGTCAAACTAC..... 893
658 rIAs.....IleArgHisIAsnGlyThrIhrrArgArg 669
894 .....CAGTGTGCTTCTCTCAAAAGCTTTC..... 920
669 LysIuLeuIuIhIhrLeuGluProhAsnAsnLeuTrrTyLeuPhehIcLy 685
921 ...CAAAAGGAATT...TACCTTCCGCGGTACAGCATGTGATGAA 964
686 LeuGluIuLysGlySerGlnIuYrSerPheGluIValAlaAlaMetIhValAs 702
965 TAAACATCTTTTGGCTCGAAGACATTAAGTTTACT..... 1004
702 nGlyIhrrGlyProSerSerhPrrTyTrhAlaGluIhrrProGluAsnA 719
1005 .....GAATATACAGCTTCTACTCTCTCCAGCTTATACATTAGA 1046
719 sPLeuAspIuSerGluIValIProArgGlnProSerSerLeuIhIValArg 735
1047 TCCCTAAGCATTCATTCATATCTATATACGCTGTCCAAAAGCTGCG 1096
736 ProLeuThrTrhSerIle...IleMetSerTrrPthrProLeuAsnPr 751
1097 AAACAGCGCTGATCAAGAGATTATCAACATGATTTATGAATTTATTTT 1146
751 oAsnIle...ValValArgGlyTyIleIleGlyTyrcIyVal..... 764
1147 GGGAAACACTTCAATGCTAGAGA...AAATATTCGAAAGAAAAAACT 1193
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